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(54) Title: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE
EXPRESSION IN HUMAN HEART

(57) Abstract: A single exon nucleic acid microarray comprising a plurality of single exon nucleic acid probes for measuring gene
expression in a sample derived from human heart is described. Also described are single exon nucleic acid probes expressed in the
heart and their use in methods for detecting gene expression.



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HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
FOR ANALYSIS OF GENE EXPRESSION IN HUMAN HEART

CROSS REFERENCE TO RELATED APPLICATIONS

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The present application is a continuation-in-part of U.S. patent application serial nos. 09/632,366, filed August 3, 2000 and 09/608,408, filed June 30, 2000; claims the benefit under 35 U.S.C. s 119(e) of U.S. provisional patent application serial nos. 60/236,359, filed September 27, 2000, 60/234,687, filed September 21, 2000, 60/207,456, filed May 26, 2000, and 60/180,312, filed February 4, 2000; and further claims the benefit under 35 U.S.C. s 119(a) of UK patent application no. 0024263.6, filed October 4, 2000, the disclosures of which are incorporated herein by reference in their entireties.

REFERENCE TO SEQUENCE LISTING AND INCORPORATION BY
REFERENCE THEREOF

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The present application includes a Sequence Listing in electronic format, filed pursuant to PCT Administrative Instructions 801 - 806 on a single CD-R disc, in triplicate, containing a file named pto_HEART.txt, created 24 January 2001, having 20,186,946 bytes. The Sequence Listing contained in said file on said disc is incorporated herein by reference in its entirety.

Field of the Invention

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The present invention relates to genome-derived single exon microarrays useful for verifying the expression of regions of genomic DNA predicted to encode protein. In particular, the present invention relates to unique genome-derived single exon nucleic acid probes expressed in human

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heart and single exon nucleic acid microarrays that include such probes.

Background of the Invention

5 For almost two decades following the invention of general techniques for nucleic acid sequencing, Sanger et al., *Proc. Natl. Acad. Sci. USA* 70(4):1209-13 (1973); Gilbert et al., *Proc. Natl. Acad. Sci. USA* 70(12):3581-4 (1973), these techniques were used principally as tools to
10 further the understanding of proteins - known or suspected - about which a basic foundation of biological knowledge had already been built. In many cases, the cloning effort that preceded sequence identification had been both informed and directed by that antecedent
15 biological understanding.

 For example, the cloning of the T cell receptor for antigen was predicated upon its known or suspected cell type-specific expression, by its suspected membrane association, and by the predicted assembly of its gene via
20 T cell-specific somatic recombination. Subsequent sequencing efforts at once confirmed and extended understanding of this family of proteins. Hedrick et al., *Nature* 308(5955):153-8 (1984).

 More recently, however, the development of high
25 throughput sequencing methods and devices, in concert with large public and private undertakings to sequence the human and other genomes, has altered this investigational paradigm: today, sequence information often precedes understanding of the basic biology of the encoded protein
30 product.

 One of the approaches to large-scale sequencing is predicated upon the proposition that expressed sequences - that is, those accessible through isolation of mRNA - are of greatest initial interest. This "expressed
35 sequence tag" ("EST") approach has already yielded vast

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amounts of sequence data (see for example Adams *et al.*,
Science 252:1651 (1991); Williamson, *Drug Discov. Today*
4:115 (1999)). For nucleic acids sequenced by this
approach, often the only biological information that is
5 known *a priori* with any certainty is the likelihood of
biologic expression itself. By virtue of the species and
tissue from which the mRNA had originally been obtained,
most such sequences are also annotated with the identity of
the species and at least one tissue in which expression
10 appears likely.

More recently, the pace of genomic sequencing has
accelerated dramatically. When genomic DNA serves as the
initial substrate for sequencing efforts, expression cannot
be presumed; often the only *a priori* biological information
15 about the sequence includes the species and chromosome (and
perhaps chromosomal map location) of origin.

With the ever-accelerating pace of sequence
accumulation by directed, EST, and genomic sequencing
approaches - and in particular, with the accumulation of
20 sequence information from multiple genera, from multiple
species within genera, and from multiple individuals within
a species - there is an increasing need for methods that
rapidly and effectively permit the functions of nucleic
sequences to be elucidated. And as such functional
25 information accumulates, there is a further need for
methods of storing such functional information in
meaningful and useful relationship to the sequence itself;
that is, there is an increasing need for means and
apparatus for annotating raw sequence data with known or
30 predicted functional information.

Although the increase in the pace of genomic
sequencing is due in large part to technological changes in
sequencing strategies and instrumentation, Service, *Science*
280:995 (1998); Pennisi, *Science* 283: 1822-1823 (1999),
35 there is an important functional motivation as well.

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While it was understood that the EST approach would rarely be able to yield sequence information about the noncoding portions of the genome, it now also appears the EST approach is capable of capturing only a fraction of a genome's actual expression complexity.

For example, when the *C. elegans* genome was fully sequenced, gene prediction algorithms identified over 19,000 potential genes, of which only 7,000 had been found by EST sequencing. *C. elegans* Sequencing Consortium, *Science* 282:2012 (1998). Analogously, the recently completed sequence of chromosome 2 of *Arabidopsis* predicts over 4000 genes, Lin et al., *Nature*, 402:761 (1999), of which only about 6% had previously been identified via EST sequencing efforts. Although the human genome has the greatest depth of EST coverage, it is still woefully short of surrendering all of its genes. One recent estimate suggests that the human genome contains more than 146,000 genes, which would at this point leave greater than half of the genes undiscovered. It is now predicted that many genes, perhaps 20 to 50%, will only be found by genomic sequencing.

There is, therefore, a need for methods that permit the functional regions of genomic sequence – and most importantly, but not exclusively, regions that function to encode genes – to be identified.

Much of the coding sequence of the human genome is not homologous to known genes, making detection of open reading frames ("ORFs") and predictions of gene function difficult. Computational methods exist for predicting coding regions in eukaryotic genomes. Gene prediction programs such as GRAIL and GRAIL II, Uberbacher et al., *Proc. Natl. Acad. Sci. USA* 88(24):11261-5 (1991); Xu et al., *Genet. Eng.* 16:241-53 (1994); Uberbacher et al., *Methods Enzymol.* 266:259-81 (1996); GENEFINDER, Solovyev et al., *Nucl. Acids. Res.* 22:5156-63 (1994); Solovyev et al.,

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Ismb 5:294-302 (1997); and GENESCAN, Burge et al., *J. Mol. Biol.* 268:78-94 (1997), predict many putative genes without known homology or function. Such programs are known, however, to give high false positive rates. Burset et al., *Genomics* 34:353-367 (1996). Using a consensus obtained by a plurality of such programs is known to increase the reliability of calling exons from genomic sequence. Ansari-Lari et al., *Genome Res.* 8(1):29-40 (1998)

Identification of functional genes from genomic data remains, however, an imperfect art. For example, in reporting the full sequence of human chromosome 21, the Chromosome 21 Mapping and Sequencing Consortium reports that prior bioinformatic estimates of human gene number may need to be revised substantially downwards. *Nature* 405:311-199 (2000); Reeves, *Nature* 405:283-284 (2000).

Thus, there is a need for methods and apparatus that permit the functions of the regions identified bioinformatically - and specifically, that permit the expression of regions predicted to encode protein - readily to be confirmed experimentally.

Recently, the development of nucleic acid microarrays has made possible the automated and highly parallel measurement of gene expression. Reviewed in Schena (ed.), DNA Microarrays : A Practical Approach (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); *Nature Genet.* 21(1)(suppl):1 - 60 (1999); Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376).

It is common for microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, such as those from the I.M.A.G.E. consortium, Lennon et al., *Genomics* 33(1):151-2 (1996), or from the construction of "problem specific" libraries targeted at a particular biological question, R.S. Thomas

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et al., *Cancer Res.* (in press). Such microarrays by definition can measure expression only of those genes found in EST libraries, and thus have not been useful as probes for genes discovered solely by genomic sequencing.

5 The utility of using whole genome nucleic acid microarrays to answer certain biological questions has been demonstrated for the yeast *Saccharomyces cerevisiae*. De Risi et al., *Science* 278:680 (1997). The vast majority of yeast nuclear genes, approximately 95% however, are single
10 exon genes, i.e., lack introns, Lopez et al., *RNA* 5:1135-1137 (1999); Goffeau et al., *Science* 274:563-67 (1996), permitting coding regions more readily to be identified. Whole genome nucleic acid microarrays have not generally been used to probe gene expression from more complex
15 eukaryotic genomes, and in particular from those averaging more than one intron per gene.

Diseases of the heart and vascular system are a significant cause of human morbidity and mortality. Increasingly, genetic factors are being found that
20 contribute to predisposition, onset, and/or aggressiveness of most, if not all, of these diseases. Although mutations in single genes have on occasion been identified as causative, these disorders are for the most part believed to have polygenic etiologies. There is a need for methods
25 and apparatus that permit prediction, diagnosis and prognosis of diseases of the human heart, particularly those diseases with polygenic etiology.

Summary of the Invention

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 The present invention solves these and other problems in the art by providing methods and apparatus for predicting, confirming, and displaying functional information derived from genomic sequence. The present
35 invention also provides apparatus for verifying the

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expression of putative genes identified within genomic sequence.

In particular, the invention provides novel genome-derived single exon nucleic acid microarrays useful
5 for verifying the expression of putative genes identified within genomic sequence.

The present invention also provides compositions and kits for the ready production of nucleic acids identical in sequence to, or substantially identical in
10 sequence to, probes on the genome-derived single exon microarrays of the present invention.

Accordingly, in a first aspect of the invention, there is provided a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a
15 sample derived from human heart, comprising a plurality of single exon nucleic acid probes according to any one of the nucleotide sequences set out in SEQ ID NOs: 1 - 9,980 or a complementary sequence, or a portion of such a sequence.

By plurality is meant at least two, suitably at
20 least 20, most suitably at least 100, preferably at least 1000 and, most preferably, upto 5000.

In one embodiment of the first aspect, each of said plurality of probes is separately and addressably amplifiable.

25 In an alternative embodiment, each of said plurality of probes is separately and addressably isolatable from said plurality.

In a preferred embodiment, each of said plurality of probes is amplifiable using at least one common primer.
30 Preferably, each of said plurality of probes is amplifiable using a first and a second common primer.

In yet another embodiment, said set of single exon nucleic acid probes comprises between 50 - 20,000 probes, for example, 50 - 5000.

35 Suitably, said set of single exon nucleic acid

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probes comprises at least 50 - 1000 discrete single exon nucleic acid probes having a sequence as set out in any of SEQ ID NOS.: 1 - 19,771 or a complimentary sequence, or a portion of such a sequence.

5 Preferably, the average length of the single exon nucleic acid probes is between 200 and 500 bp. It is preferred that the average length should be at least 200bp, suitably at least 250bp, most suitably at least 300bp, preferably at least 400bp and, most preferably, 500 bp.

10 In another embodiment, the single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence. It is preferred that at least 50%, suitably at least 60%, most suitably at least 70%, preferably at least 75%, more preferably at least 80, 85, 90, 95 or 99% of said
15 single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence.

 In another preferred embodiment, said single exon nucleic acid lack homopolymeric stretches of A or T. It is preferred that at least 50%, suitably at least 60%, most
20 suitably at least 70%, preferably at least 75%, more preferably at least 80, 85, 90, 95 or 99% of said single exon nucleic acid probes lack homopolymeric stretches of A or T.

 Preferably, a spatially-addressable set of single
25 exon nucleic acid probes in accordance with the first aspect of the invention is addressably disposed upon a substrate.

 Suitable substrates include a filter membrane which may, preferably, be nitrocellulose or nylon. The
30 nylon may preferably, be positively-charged. Other suitable substrates include glass, amorphous silicon, crystalline silicon, and plastic. Further suitable materials include polymethylacrylic, polyethylene, polypropylene, polyacrylate, polymethylmethacrylate, polyvinylchloride,
35 polytetrafluoroethylene, polystyrene, polycarbonate,

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polyacetal, polysulfone, celluloseacetate, cellulosenitrate, nitrocellulose, and mixtures thereof.

In a second aspect of the invention, there is provided a microarray comprising a spatially addressable
5 set of single exon nucleic acid probes in accordance with the first aspect of the invention.

In one embodiment, a genome-derived single-exon microarray is packaged together with such an ordered set of amplifiable probes corresponding to the probes, or one or
10 more subsets of probes, thereon. In alternative embodiments, the ordered set of amplifiable probes is packaged separately from the genome-derived single exon microarray.

In another aspect, the invention provides genome-
15 derived single exon nucleic acid probes useful for gene expression analysis, and particularly for gene expression analysis by microarray. In particular embodiments of this aspect, the present invention provides human single-exon probes that include specifically-hybridizable fragments of
20 SEQ ID Nos. 9,981 - 19,771, wherein the fragment hybridizes at high stringency to an expressed human gene. In particular embodiments, the invention provides single exon probes comprising SEQ ID Nos. 1 - 9,980.

Accordingly, in a third aspect of the invention,
25 there is provided a single exon nucleic acid probe for measuring human gene expression in a sample derived from human heart which is a nucleic acid molecule comprising a nucleotide sequence as set out in any of SEQ ID NOs.: 1 - 9,980 or a complementary sequence or a fragment thereof
30 wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human heart.

In one embodiment, a single exon nucleic acid probe in accordance with the third aspect comprises a nucleotide sequence as set out in any of SEQ ID NOs.: 9,981
35 - 19,771 or a complementary sequence or a fragment thereof.

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In a fourth aspect of the invention, there is provided a single exon nucleic acid probe for measuring human gene expression in a sample derived from human heart which is a nucleic acid molecule having a sequence encoding
5 a peptide comprising a peptide sequence as set out in any of SEQ ID NOs.: 19,772 - 29,119 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human heart.

Preferably, a single exon nucleic acid probe in
10 accordance with the third or fourth aspects of the invention comprises between at least 15 and 50 contiguous nucleotides of said SEQ ID NO:. It is preferred that the single exon nucleic acid probe comprises at least 15, suitably at least 20, more suitably at least 25 or
15 preferably at least 50 contiguous nucleotides of said SEQ ID NO:.

In another preferred embodiment, a single exon nucleic acid probe in accordance with the third or fourth aspects of the invention is between 3kb and 25kb in length.
20 It is preferred that said probe is no more than 3kb, suitably no more than 5kb, more suitably no more than 10kb, preferably 15kb, more preferably 20kb or, most preferably, no more than 20kb in length.

Preferably, a single exon nucleic acid probe in
25 accordance with either the fifth or sixth aspect of the invention is DNA, preferably single-stranded DNA, RNA or PNA.

In another embodiment of either the third or fourth aspect of the invention, a single exon nucleic acid
30 probe is detectably labeled. Suitable detectable labels include a radionuclide, a fluorescent label or a first member of a specific binding pair. Suitable fluorescent labels include dyes such as cyanine dyes, preferably Cy3 and Cy5 although other suitable dyes will be known to those
35 skilled in the art.

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In a particularly preferred embodiment, a single exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks prokaryotic and bacteriophage vector sequence. In yet another embodiment, a single exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks homopolymeric stretches of A or T.

In a fifth aspect of the invention, there is provided an amplifiable nucleic acid composition, comprising:

the single exon nucleic acid probe in accordance with either of the third or fourth aspects of the invention; and at least one nucleic acid primer;

wherein said at least one primer is sufficient to prime enzymatic amplification of said probe.

In an sixth aspect of the invention, there is provided a method of measuring gene expression in a sample derived from human heart, comprising:

contacting the single exon microarray in accordance with the second aspect of the invention, with a first collection of detectably labeled nucleic acids, said first collection of nucleic acids derived from mRNA of human heart; and then

measuring the label detectably bound to each probe of said microarray.

In a seventh aspect of the invention, there is provided a method of identifying exons in a eukaryotic genome, comprising:

algorithmically predicting at least one exon from genomic sequence of said eukaryote; and then

detecting specific hybridization of detectably labeled nucleic acids to a single exon probe,

wherein said detectably labeled nucleic acids are derived from mRNA from the heart of said eukaryote, said probe is a single exon probe having a fragment identical in

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sequence to, or complementary in sequence to, said
predicted exon, said probe is included within a single exon
microarray in accordance with the first aspect of the
invention, and said fragment is selectively hybridizable at
5 high stringency.

In a eighth aspect of the invention, there is
provided a method of assigning exons to a single gene,
comprising:

identifying a plurality of exons from genomic
10 sequence in accordance with the seventh aspect of the
invention; and then

measuring the expression of each of said exons in
a plurality of tissues and/or cell types using
hybridization to single exon microarrays having a probe
15 with said exon,

wherein a common pattern of expression of said
exons in said plurality of tissues and/or cell types
indicates that the exons should be assigned to a single
gene.

20 In an ninth aspect of the invention, there is
provided a nucleic acid sequence as set out in any of SEQ
ID NOS: 1 - 19,771 wherein said sequence encodes a peptide.

In a tenth aspect of the invention, there is
provided a peptide encoded by a sequence comprising a
25 sequence as set out in any of SEQ ID NOS: 9,981 - 19,771,
or a complementary sequence or coding portion thereof.

In a preferred embodiment, a peptide may be
encoded by a sequence comprising a sequence set out in any
of SEQ ID NOS.: 1 - 9,980.

30 In a further aspect, the invention provides
peptides comprising an amino acid sequence translated from
the DNA fragments, said amino acid sequences comprising SEQ
ID NOS.: 9,981 - 19,771.

Accordingly in a eleventh aspect of the invention
35 there is provided a peptide comprising a sequence as set

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out in any of SEQ ID NOs: 19,772 - 29,119, or fragment thereof.

In another aspect, the invention provides means for displaying annotated sequence, and in particular, for displaying sequence annotated according to the methods and apparatus of the present invention. Further, such display can be used as a preferred graphical user interface for electronic search, query, and analysis of such annotated sequence.

10

Detailed Description of the Invention

Definitions

As used herein, the term "microarray" and phrase "nucleic acid microarray" refer to a substrate-bound collection of plural nucleic acids, hybridization to each of the plurality of bound nucleic acids being separately detectable. The substrate can be solid or porous, planar or non-planar, unitary or distributed.

As so defined, the term "microarray" and phrase "nucleic acid microarray" include all the devices so called in Schena (ed.), DNA Microarrays: A Practical Approach (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); *Nature Genet.* 21(1)(suppl):1 - 60 (1999); and Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376). As so defined, the term "microarray" and phrase "nucleic acid microarray" further include substrate-bound collections of plural nucleic acids in which the nucleic acids are distributably disposed on a plurality of beads, rather than on a unitary planar substrate, as is described, *inter alia*, in Brenner et al., *Proc. Natl. Acad. Sci. USA* 97(4):166501670 (2000); in such case, the term "microarray" and phrase "nucleic

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acid microarray" refer to the plurality of beads in aggregate.

As used herein with respect to a nucleic acid microarray, the term "probe" refers to the nucleic acid that is, or is intended to be, bound to the substrate; in such context, the term "target" thus refers to nucleic acid intended to be bound thereto by Watson-Crick complementarity. As used herein with respect to solution phase hybridization, the term "probe" refers to the nucleic acid of known sequence that is detectably labeled.

As used herein, the expression "probe comprising SEQ ID NO.", and variants thereof, intends a nucleic acid probe, at least a portion of which probe has either (i) the sequence directly as given in the referenced SEQ ID NO., or (ii) a sequence complementary to the sequence as given in the referenced SEQ ID NO., the choice as between sequence directly as given and complement thereof dictated by the requirement that the probe hybridize to mRNA.

As used herein, the term "open reading frame" and the equivalent acronym "ORF" refer to that portion of an exon that can be translated in its entirety into a sequence of contiguous amino acids i.e. a nucleic acid sequence that, in at least one reading frame, does not possess stop codons; the term does not require that the ORF encode the entirety of a natural protein.

As used herein, the term "amplicon" refers to a PCR product amplified from human genomic DNA, containing the predicted exon.

As used herein the term "exon" refers to the consensus prediction of the various exon and gene predicting algorithms i.e. a nucleic acid sequence bioinformatically predicted to encode a portion of a natural protein.

As used herein, the term "peptide" refers to a sequence of amino acids. The sequences referred to as

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PEPTIDE SEQ ID NOS.: are the predicted peptide sequences that would be translated from one of the exons, or a portion thereof set out in exon SEQ ID NOS.:. The codons encoding the peptide are wholly contained within the exon.

5 As used herein, a "portions" of a defined nucleotide sequence or sequences can be and, preferably, are fragments unique to that sequence or to one or a combination of those sequences. A fragment unique to a nucleic acid molecule is one that is a signature for the
10 larger nucleic acid molecule.

As used herein, the phrase "expression of a probe" and its linguistic variants means that the ORF present within the probe, or its complement, is present within a target mRNA.

15 As used herein, "stringent conditions" refers to parameters well known to those skilled in the art. When a nucleic acid molecule is said to be hybridisable to another of a given sequence under "stringent conditions" it is meant that it is homologous to the given sequence.

20 As used herein, the phrase "specific binding pair" intends a pair of molecules that bind to one another with high specificity. Binding pairs are said to exhibit specific binding when they exhibit avidity of at least 10^7 , preferably at least 10^8 , more preferably at least 10^9
25 liters/mole. Nonlimiting examples of specific binding pairs are: antibody and antigen; biotin and avidin; and biotin and streptavidin.

As used herein with respect to the visual display of annotated genomic sequence, the term "rectangle" means
30 any geometric shape that has at least a first and a second border, wherein the first and second borders each are capable of mapping uniquely to a point of another visual object of the display.

As used herein, a "Mondrian" means a visual
35 display in which a single genomic sequence is annotated

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with predicted and experimentally confirmed functional information.

5 Brief Description of the Drawings

The present invention is further illustrated with reference to the following non-limiting figures and examples in which:

10 FIG. 1 illustrates a process for predicting functional regions from genomic sequence, confirming the functional activity of such regions experimentally, and associating and displaying the data so obtained in meaningful and useful relationship to the original sequence data;

FIG. 2 further elaborates that portion of the process schematized in FIG. 1 for predicting functional regions from genomic sequence;

FIG. 3 illustrates a Mondrian visual display;

20 FIG. 4 presents a Mondrian showing a hypothetical annotated genomic sequence;

FIG. 5 is a histogram showing the distribution of ORF length and PCR products as obtained, with ORF length shown in black and PCR product length shown in dotted

25 lines;

FIG. 6 is a histogram showing the distribution, among exons predicted according to the methods described, of expression as measured using simultaneous two color hybridization to a genome-derived single exon microarray.

30 The graph shows the number of sequence-verified products that were either not expressed ("0"), expressed in one or more but not all tested tissues ("1" - "9"), or expressed in all tissues tested ("10");

35 FIG. 7 is a pictorial representation of the expression of verified sequences that showed expression

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with signal intensity greater than 3 in at least one tissue, with: FIG. 7A showing the expression as measured by microarray hybridization in each of the 10 measured tissues, and the expression as measured "bioinformatically" by query of EST, NR and SwissProt databases; with FIG. 7B showing the legend for display of physical expression (ratio) in FIG. 7A; and with FIG. 7C showing the legend for scoring EST hits as depicted in FIG. 7A;

FIG. 8 shows a comparison of normalized CY3 signal intensity for arrayed sequences that were identical to sequences in existing EST, NR and SwissProt databases or that were dissimilar (unknown), where black denotes the signal intensity for all sequence-verified products with a BLAST Expect ("E") value of greater than $1e-30$ (1×10^{-30}) ("unknown") and a dotted line denotes sequence-verified spots with a BLAST expect ("E") value of less than $1e-30$ (1×10^{-30}) ("known");

FIG. 9 presents a Mondrian of BAC AC008172 (bases 25,000 to 130,000), containing the carbamyl phosphate synthetase gene (AF154830.1); and

FIG. 10 is a Mondrian of BAC A049839.

Methods and Apparatus for Predicting, Confirming, Annotating, and Displaying Functional Regions From Genomic Sequence Data

FIG. 1 is a flow chart illustrating in broad outline a process for predicting functional regions from genomic sequence, confirming and characterizing the functional activity of such regions experimentally, and then associating and displaying the information so obtained in meaningful and useful relationship to the original sequence data.

The initial input into process 10 of the present

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invention is drawn from one or more databases 100 containing genomic sequence data. Because genomic sequence is usually obtained from subgenomic fragments, the sequence data typically will be stored in a series of records corresponding to these subgenomic sequenced fragments. Some fragments will have been catenated to form larger contiguous sequences ("contigs"); others will not. A finite percentage of sequence data in the database will typically be erroneous, consisting *inter alia* of vector sequence, sequence created from aberrant cloning events, sequence of artificial polylinkers, and sequence that was erroneously read.

Each sequence record in database 100 will minimally contain as annotation a unique sequence identifier (accession number), and will typically be annotated further to identify the date of accession, species of origin, and depositor. Because database 100 can contain nongenomic sequence, each sequence will typically be annotated further to permit query for genomic sequence. Chromosomal origin, optionally with map location, can also be present. Data can be, and over time increasingly will be, further annotated with additional information, in part through use of the present invention, as described below. Annotation can be present within the data records, in information external to database 100 and linked to the records thereto, or through a combination of the two.

Databases useful as genomic sequence database 100 in the present invention include GenBank, and particularly include several divisions thereof, including the htgs(draft), NT (nucleotide, command line), and NR (nonredundant) divisions. GenBank is produced by the National Institutes of Health and is maintained by the National Center for Biotechnology Information (NCBI). Databases of genomic sequence from species other than human, such as mouse, rat, Arabidopsis, *C. elegans*, *C.*

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brigsii, *Drosophila*, zebra fish, and other higher eukaryotic organisms will also prove useful as genomic sequence database 100.

Genomic sequence obtained by query of genomic sequence database 100 is then input into one or more processes 200 for identification of regions therein that are predicted to have a biological function as specified by the user. Such functions include, but are not limited to, encoding protein, regulating transcription, regulating message transport after transcription into mRNA, regulating message splicing after transcription into mRNA, of regulating message degradation after transcription into mRNA, and the like. Other functions include directing somatic recombination events, contributing to chromosomal stability or movement, contributing to allelic exclusion or X chromosome inactivation, and the like.

The particular genomic sequence to be input into process 200 will depend upon the function for which relevant sequence is to be identified as well as upon the approach chosen for such identification. Process step 200 can be iterated to identify different functions within a given genomic region. In such case, the input often will be different for the several iterations.

Sequences predicted to have the requisite function by process 200 are then input into process 300, where a subset of the input sequences suitable for experimental confirmation is identified. Experimental confirmation can involve physical and/or bioinformatic assay. Where the subsequent experimental assay is bioinformatic, rather than physical, there are fewer constraints on the sequences that can be tested, and in this latter case therefore process 300 can output the entirety of the input sequence.

The subset of sequences output from process 300 is then used in process 400 for experimental verification

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and characterization of the function predicted in process 200, which experimental verification can, and often will, include both physical and bioinformatic assay.

Process 500 annotates the sequence data with the functional information obtained in the physical and/or bioinformatic assays of process 400. Such annotation can be done using any technique that usefully relates the functional information to the sequence, as, for example, by incorporating the functional data into the sequence data record itself, by linking records in a hierarchical or relational database, by linking to external databases, by a combination thereof, or by other means well known within the database arts. The data can even be submitted for incorporation into databases maintained by others, such as GenBank, which is maintained by NCBI.

As further noted in FIG. 1, additional annotation can be input into process 500 from external sources 600.

The annotated data is then displayed in process 800, either before, concomitantly with, or after optional storage 700 on nontransient media, such as magnetic disk, optical disc, magneto-optical disk, flash memory, or the like.

FIG. 1 shows that the experimental data output from process 400 can be used in each preceding step of process 10: e.g., facilitating identification of functional sequences in process 200, facilitating identification of an experimentally suitable subset thereof in process 300, and facilitating creation of physical and/or informational substrates for, and performance of subsequent assay, of functional sequences in process 400.

Information from each step can be passed directly to the succeeding process, or stored in permanent or interim form prior to passage to the succeeding process. Often, data will be stored after each, or at least a plurality, of such process steps. Any or all process steps

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can be automated.

FIG. 2 further elaborates the prediction of functional sequence within genomic sequence according to process 200.

5 Genomic sequence database 100 is first queried 20 for genomic sequence.

 The sequence required to be returned by query 20 will depend, in the first instance, upon the function to be identified.

10 For example, genomic sequences that function to encode protein can be identified *inter alia* using gene prediction approaches, comparative sequence analysis approaches, or combinations of the two. In gene prediction analysis, sequence from one genome is input into process
15 200 where at least one, preferably a plurality, of algorithmic methods are applied to identify putative coding regions. In comparative sequence analysis, by contrast, corresponding, e.g., syntenic, sequence from a plurality of sources, typically a plurality of species, is input into
20 process 200, where at least one, possibly a plurality, of algorithmic methods are applied to compare the sequences and identify regions of least variability.

 The exact content of query 20 will also depend upon the database queried. For example, if the database
25 contains both genomic and nongenomic sequence, perhaps derived from multiple species, and the function to be determined is protein coding regions in human genomic sequence, the query will accordingly require that the sequence returned be genomic and derived from humans.

30 Query 20 can also incorporate criteria that compel return of sequence that meets operative requirements of the subsequent analytical method. Alternatively, or in addition, such operative criteria can be enforced in subsequent preprocess step 24.

35 For example, if the function sought to be

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identified is protein coding, query 20 can incorporate criteria that return from genomic sequence database 100 only those sequences present within contigs sufficiently long as to have obviated substantial fragmentation of any
5 given exon among a plurality of separate sequence fragments.

Such criteria can, for example, consist of a required minimal individual genomic sequence fragment length, such as 10 kb, more typically 20 kb, 30 kb, 40kb,
10 and preferably 50 kb or more, as well as an optional further or alternative requirement that sequence from any given clone, such as a bacterial artificial chromosome ("BAC"), be presented in no more than a finite maximal number of fragments, such as no more than 20 separate
15 pieces, more typically no more than 15 fragments, even more typically no more than about 10 - 12 fragments.

Results using the present invention have shown that genomic sequence from bacterial artificial chromosomes (BACs) is sufficient for gene prediction analysis according
20 to the present invention if the sequence is at least 50 kb in length, and if additionally the sequence from any given BAC is presented in fewer than 15, and preferably fewer than 10, fragments. Accordingly, query 20 can incorporate a requirement that data accessioned from BAC sequencing be
25 in fewer than 15, preferably fewer than 10, fragments.

An additional criterion that can be incorporated into the query can be the date, or range of dates, of sequence accession. Although the process has been described above as if genomic sequence database 100 were
30 static, it is of course understood that the genomic sequence databases need not be static, and indeed are typically updated on a frequent, even hourly, basis. Thus, as further described in Examples 1 and 2, *infra*, it is possible to query the database for newly added sequence,
35 either newly added after an absolute date, or newly added

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relative to a prior analysis performed using the methods and apparatus of the present invention. In this way, the process herein described can incorporate a dynamic, temporal component.

One utility of such temporal limitation is to identify, from newly accessioned genomic sequence, the presence of novel genes, particularly those not previously identified by EST sequencing (or other sequencing efforts that are similarly based upon gene expression). As further described in Example 1, such an approach has shown that newly accessioned human genomic sequence, when analyzed for sequences that function to encode protein, readily identifies genes that are novel over those in existing EST and other expression databases. This makes the methods of the present invention extremely powerful gene discovery tools. And as would be appreciated, such gene discovery can be performed using genomic sequence from species other than human.

If query 20 incorporates multiple criteria, such as above-described, the multiple criteria can be performed as a series of separate queries or as a single query, depending in part upon the query language, the complexity of the query, and other considerations well known in the database arts.

If query 20 returns no genomic sequence meeting the query criteria, the negative result can be reported by process 22, and process 200 (and indeed, entire process 10) ended 23, as shown. Alternatively, or in addition to report and termination of the initial inquiry, a new query 20 can be generated that takes into account the initial negative result.

When query 20 returns sequence meeting the query criteria, the returned sequence is then passed to optional preprocessing 24, suitable and specific for the desired analytical approach and the particular analytical methods

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thereof to be used in process 25.

Preprocessing 24 can include processes suitable for many approaches and methods thereof, as well as processes specifically suited for the intended subsequent
5 analysis.

Preprocessing 24 suitable for most approaches and methods will include elimination of sequence irrelevant to, or that would interfere with, the subsequent analysis. Such sequence includes repetitive sequence, such as Alu
10 repeats and LINE elements, vector sequence, artificial sequence, such as artificial polylinkers, and the like. Such removal can readily be performed by identification and subsequent masking of the undesired sequence.

Identification can be effected by comparing the
15 genomic sequence returned by query 20 with public or private databases containing known repetitive sequence, vector sequence, artificial sequence, and other artifactual sequence. Such comparison can readily be done using programs well known in the art, such as CROSS_MATCH, or by
20 proprietary sequence comparison programs the engineering of which is well within the skill in the art.

Alternatively, or in addition, undesirable, including artifactual, sequence can be identified algorithmically without comparison to external databases
25 and thereafter removed. For example, synthetic polylinker sequence can be identified by an algorithm that identifies a significantly higher than average density of known restriction sites. As another example, vector sequence can be identified by algorithms that identify nucleotide or
30 codon usage at variance with that of the bulk of the genomic sequence.

Once identified, undesired sequence can be removed. Removal can usefully be done by masking the undesired sequence as, for example, by converting the
35 specific nucleotide references to one that is unrecognized

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by the subsequent bioinformatic algorithms, such as "X".
Alternatively, but at present less preferred, the undesired
sequence can be excised from the returned genomic sequence,
leaving gaps.

- 5 Preprocessing 24 can further include selection
from among duplicative sequences of that one sequence of
highest quality. Higher quality can be measured as a lower
percentage of, fewest number of, or least densely clustered
occurrence of ambiguous nucleotides, defined as those
10 nucleotides that are identified in the genomic sequence
using symbols indicating ambiguity. Higher quality can
also or alternatively be valued by presence in the longest
contig.

- Preprocessing 24 can, and often will, also
15 include formatting of the data as specifically appropriate
for passage to the analytical algorithms of process 25.
Such formatting can and typically will include, *inter alia*,
addition of a unique sequence identifier, either derived
from the original accession number in genomic sequence
20 database 100, or newly applied, and can further include
additional annotation. Formatting can include conversion
from one to another sequence listing standard, such as
conversion to or from FASTA or the like, depending upon the
input expected by the subsequent process.

- 25 Preprocessing, which can be optional depending
upon the function desired to be identified and the
informational requirements of the methods for effecting
such identification, is followed by sequence processing 25,
where sequences with the desired function are identified
30 within the genomic sequence.

- As mentioned above, such functions can include,
but are not limited to, encoding protein, regulating
transcription, regulating message transport after
transcription into mRNA, regulating message splicing after
35 transcription, of regulating message degradation, and the

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like. Other functions include directing somatic recombination events, contributing to chromosomal stability or movement, contributing to allelic exclusion or X chromosome inactivation, or the like.

5 The methods of the present invention are particularly useful for gene discovery, that is, for identifying, from genomic sequence, regions that function to encode genes, and in a particularly useful embodiment, for identifying regions that function to encode genes not
10 hitherto identified by expression-based or directed cloning and sequencing. In conjunction with verification using the novel single exon microarrays of the present invention, as further described below, the methods herein described become powerful gene discovery tools.

15 Accordingly, in a preferred embodiment of the present invention, process 25 is used to identify putative coding regions. Two preferred approaches in process 25 for identifying sequence that encodes putative genes are gene prediction and comparative sequence analysis.

20 Gene prediction can be performed using any of a number of algorithmic methods, embodied in one or more software programs, that identify open reading frames (ORFs) using a variety of heuristics, such as GRAIL, DICTION, and GENEFINDER. Comparative sequence analysis similarly can be
25 performed using any of a variety of known programs that identify regions with lower sequence variability.

 As further described in Example 1, below, gene finding software programs yield a range of results. For the newly accessioned human genomic sequence input in
30 Example 1, for example, GRAIL identified the greatest percentage of genomic sequence as putative coding region, 2% of the data analyzed; GENEFINDER was second, calling 1%; and DICTION yielded the least putative coding region, with 0.8% of genomic sequence called as coding region.

35 Increased reliability can be obtained when

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consensus is required among several such methods. Although discussed herein particularly with respect to exon calling, consensus among methods will in general increase reliability of predicting other functions as well.

5 Thus, as indicated by query 26, sequence processing 25, optionally with preprocessing 24, can be repeated with a different method, with consensus among such iterations determined and reported in process 27.

Process 27 compares the several outputs for a
10 given input genomic sequence and identifies consensus among the separately reported results. The consensus itself, as well as the sequence meeting that consensus, is then stored in process 29a, displayed in process 29b, and/or output to process 300 for subsequent identification of a subset
15 thereof suitable for assay.

Multiple levels of consensus can be calculated and reported by process 27. For example, as further described in Example 1, *infra*, process 27 can report consensus as between all specific pairs of methods of gene
20 prediction, as consensus among any one or more of the pairs of methods of gene prediction, or as among all of the gene prediction algorithms used. Thus, in Example 1, process 27 reported that GRAIL and GENEFINDER programs agreed on 0.7% of genomic sequence, that GRAIL and DICTION agreed on 0.5%
25 of genomic sequence, and that the three programs together agreed on 0.25% of the data analyzed. Put another way, 0.25% of the genomic sequence was identified by all three of the programs as containing putative coding region.

Furthermore, consensus can be required among
30 different approaches to identifying a chosen function.

For example, if the function desired to be identified is coding of protein sequence, and a first used approach to exon calling is gene prediction, the process can be repeated on the same input sequence, or subset
35 thereof, with another approach, such as comparative

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sequence analysis. In such a case, where comparative sequence analysis follows gene prediction, the comparison can be performed not only on genomic nucleic acid sequence, but additionally or alternatively can be performed on the
5 predicted amino acid sequence translated from the ORFs prior identified by the gene prediction approach.

Although shown as an iterative process, the multiple analyses required to achieve consensus can be done in series, in parallel, or some combination thereof.

10 Predicted functional sequence, optionally representing a consensus among a plurality of methods and approaches for determination thereof, is passed to process 300 for identification of a subset thereof for functional assay.

15 In the preferred embodiment of the methods of the present invention, wherein the function sought to be identified is protein coding, process 300 is used to identify a subset thereof suitable for experimental verification by physical and/or bioinformatic approaches.

20 For example, putative ORFs identified in process 200 can be classified, or binned, bioinformatically into putative genes. This binning can be based *inter alia* upon consideration of the average number of exons/gene in the species chosen for analysis, upon density of exons that
25 have been called on the genomic sequence, and other empirical rules. Thereafter, one or more among the gene-specific ORFs can be chosen for subsequent use in gene expression assay.

Where such subsequent gene expression assay uses
30 amplified nucleic acid, considerations such as desired amplicon length, primer synthesis requirements, putative exon length, sequence GC content, existence of possible secondary structure, and the like can be used to identify and select those ORFs that appear most likely successfully
35 to amplify. Where subsequent gene expression assay relies

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upon nucleic acid hybridization, whether or not using amplified product, further considerations involving hybridization stringency can be applied to identify that subset of sequences that will most readily permit sequence-specific discrimination at a chosen hybridization and wash stringency. One particular such consideration is avoidance of putative exons that span repetitive sequence; such sequence can hybridize spuriously to nonspecific message, reducing specific signal in the hybridization.

For bioinformatic assay, there are fewer constraints on the sequences that can be tested experimentally, and in this latter case therefore process 300 can output the entirety of the input sequence.

The subset of sequences identified by process 300 as suitable for use in assay is then used in process 400 to create the physical and/or informational substrate for experimental verification of the predictions made in process 200, and thereafter to assay those substrates.

As mentioned, the methods of the present invention are particularly useful for identifying potential coding regions within genomic sequence. In a preferred embodiment of process 400, therefore, the expression of the sequences predicted to encode protein is verified. The combination of the predictive and experimental methods provides a powerful gene discovery engine.

Thus, in another aspect, the present invention provides methods and apparatus for verifying the expression of putative genes identified within genomic sequence. In particular, the invention provides a novel method of verifying gene expression in which expression of predicted ORFs is measured and confirmed using a novel type of nucleic acid microarray, the genome-derived single exon nucleic acid microarrays of the present invention.

Putative ORFs as predicted by a consensus of gene calling, particularly gene prediction, algorithms in

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process 200, and as further identified as suitable by
process 300, are amplified from genomic DNA using the
polymerase chain reaction (PCR). Although PCR is
conveniently used, other amplification approaches can also
5 be used.

Amplification schemes can be designed to capture
the entirety of each predicted ORF in an amplicon with
minimal additional (that is, intronic or intergenic)
sequence. Because ORFs predicted from human genomic
10 sequence using the methods of the present invention differ
in length, such an approach results in amplicons of varying
length.

However, most predicted ORFs are shorter than 500
bp in length, and although amplicons of at least about 100
15 or 200 base pairs can be immobilized as probes on nucleic
acid microarrays, early experimental results using the
methods of the present invention have suggested that longer
amplicons, at least about 400 or 500 base pairs, are more
effective. Furthermore, certain advantages derive from
20 application to the microarray of amplicons of defined size.

Therefore, amplification schemes can
alternatively, and preferably, be designed to amplify
regions of defined size, preferably at least about 300, 400
or 500 bp, centered about each predicted ORF. Such an
25 approach results in a population of amplicons of limited
size diversity, but that typically contain intronic and/or
intergenic nucleic acid in addition to putative ORF.

Conversely, somewhat fewer than 10% of ORFs
predicted from human genomic sequence according to the
30 methods of the present invention exceed 500 bp in length.
Portions of such extended ORFs, preferably at least about
300, 400 or 500 bp in length, can be amplified. However, it
has been discovered that the percentage success at
amplifying pieces of such ORFs is low, and that such
35 putative exons are more effectively amplified when larger

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fragments, at least about 1000 or 1500 bp, and even as large as 2000 bp are amplified.

The putative ORFs selected in process 300 are thus input into one or more primer design programs, such as PRIMER3 (available online for use at <http://www-genome.wi.mit.edu/cgi-bin/primer/>), with a goal of amplifying at least about 500 base pairs of genomic sequence centered within or about ORFs predicted to be no more than about 500 bp, or at least about 1000 - 1500 bp of genomic sequence for ORFs predicted to exceed 500 bp in length, and the primers synthesized by standard techniques. Primers with the requisite sequences can be purchased commercially or synthesized by standard techniques.

Conveniently, a first predetermined sequence can be added commonly to the ORF-specific 5' primer and a second, typically different, predetermined sequence commonly added to each 3' ORF-unique primer. This serves to immortalize the amplicon, that is, serves to permit further amplification of any amplicon using a single set of primers complementary respectively to the common 5' and common 3' sequence elements. The presence of these "universal" priming sequences further facilitates later sequence verification, providing a sequence common to all amplicons at which to prime sequencing reactions. The common 5' and 3' sequences further serve to add a cloning site should any of the ORFs warrant further study.

Such predetermined sequence is usefully at least about 10, 12 or 15 nt in length, and usually does not exceed about 25 nt in length. The "universal" priming sequences used in the examples presented *infra* were each 16 nt long.

The genomic DNA to be used as substrate for amplification will come from the eukaryotic species from which the genomic sequence data had originally been obtained, or a closely related species, and can

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- conveniently be prepared by well known techniques from somatic or germline tissue or cultured cells of the organism. See, e.g., Short Protocols in Molecular Biology : A Compendium of Methods from Current Protocols in
- 5 Molecular Biology, Ausubel et al. (eds.), 4th edition (April 1999), John Wiley & Sons (ISBN: 047132938X) and Maniatis et al., Molecular Cloning : A Laboratory Manual, 2nd edition (December 1989), Cold Spring Harbor Laboratory Press (ISBN: 0879693096). Many such prepared genomic DNAs
- 10 are available commercially, with the human genomic DNAs additionally having certification of donor informed consent.

- Although the intronic and intergenic material flanking putative coding regions in the amplicons could
- 15 potentially interfere with hybridizations during microarray experiments, we have found, surprisingly, that differential expression ratios are not significantly affected. Rather, the predominant effect of exon size is to alter the absolute signal intensity, rather than its ratio. Equally
- 20 surprising, the art had suggested that single exon probes would not provide sufficient signal intensity for high stringency hybridization analyses; we find that such probes not only provide adequate signal, but have substantial advantages, as herein described.

- 25 After partial purification, as by size exclusion spin column, with or without confirmation as to amplicon quality as by gel electrophoresis, each amplicon (single exon probe) is disposed in an array upon a support substrate.

- 30 Methods for creating microarrays by deposition and fixation of nucleic acids onto support substrates are well known in the art (Reviewed by Schena et al., see above).

- Typically, the support substrate will be glass,
- 35 although other materials, such as amorphous or crystalline

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- silicon or plastics. Such plastics include polymethylacrylic, polyethylene, polypropylene, polyacrylate, polymethylmethacrylate, polyvinylchloride, polytetrafluoroethylene, polystyrene, polycarbonate, 5 polyacetal, polysulfone, celluloseacetate, cellulosenitrate, nitrocellulose, or mixtures thereof, can also be used. Typically, the support will be rectangular, although other shapes, particularly circular disks and even spheres, present certain advantages. Particularly 10 advantageous alternatives to glass slides as support substrates for array of nucleic acids are optical discs, as described in WO 98/12559.

- The amplified nucleic acids can be attached covalently to a surface of the support substrate or, more 15 typically, applied to a derivatized surface in a chaotropic agent that facilitates denaturation and adherence by presumed noncovalent interactions, or some combination thereof.

- Robotic spotting devices useful for arraying 20 nucleic acids on support substrates can be constructed using public domain specifications (The MGuide, version 2.0, <http://cmgm.stanford.edu/pbrown/mguide/index.html>), or can conveniently be purchased from commercial sources (MicroArray GenII Spotter and MicroArray GenIII Spotter, 25 Molecular Dynamics, Inc., Sunnyvale, CA). Spotting can also be effected by printing methods, including those using ink jet technology.

- As is well known in the art, microarrays typically also contain immobilized control nucleic acids. 30 For controls useful in providing measurements of background signal for the genome-derived single exon microarrays of the present invention, a plurality of *E. coli* genes can readily be used. As further described in Example 1, 16 or 32 *E. coli* genes suffice to provide a robust measure of 35 background noise in such microarrays.

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As is well known in the art, the amplified product disposed in arrays on a support substrate to create a nucleic acid microarray can consist entirely of natural nucleotides linked by phosphodiester bonds, or

5 alternatively can include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as complementary binding can be obtained in the hybridization. If enzymatic amplification is used to produce the immobilized probes, the amplifying enzyme will impose

10 certain further constraints upon the types of nucleic acid analogs that can be generated.

Although particularly described herein as using high density microarrays constructed on planar substrates, the methods of the present invention for confirming the

15 expression of ORFs predicted from genomic sequence can use any of the known types of microarrays, as herein defined, including lower density planar arrays, and microarrays on nonplanar, nonunitary, distributed substrates.

For example, gene expression can be confirmed

20 using hybridization to lower density arrays, such as those constructed on membranes, such as nitrocellulose, nylon, and positively-charged derivatized nylon membranes. Further, gene expression can also be confirmed using nonplanar, bead-based microarrays such as are described in

25 Brenner et al., *Proc. Natl. Acad. Sci. USA* 97(4):166501670 (2000); U.S. Patent No. 6,057,107; and U.S. Patent No. 5,736,330. In theory, a packed collection of such beads provides in aggregate a higher density of nucleic acid probe than can be achieved with spotting or lithography

30 techniques on a single planar substrate.

Planar microarrays on solid substrates, however, provide certain useful advantages, including high throughput and compatibility with existing readers. For example, each standard microscope slide can include at

35 least 1000, typically at least 2000, preferably 5000 and

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upto 10,000 - 50,000 or more nucleic acid probes of discrete sequence. The number of sequences deposited will depend on their required application.

Each putative gene can be represented in the array by a single predicted ORF. Alternatively, genes can be represented by more than one predicted ORF. For purposes of measuring differential splicing, more than one predicted ORF will be provided for a putative gene. And as is well known in the art, each probe of defined sequence, representing a single predicted ORF, can be deposited in a plurality of locations on a single microarray to provide redundancy of signal.

The genome-derived single exon microarrays described above differ in several fundamental and advantageous ways from microarrays presently used in the gene expression art, including (1) those created by deposition of mRNA-derived nucleic acids, (2) those created by *in situ* synthesis of oligonucleotide probes, and (3) those constructed from yeast genomic DNA.

Most nucleic acid microarrays that are in use for study of eukaryotic gene expression have as immobilized probes nucleic acids that are derived - either directly or indirectly - from expressed message. As discussed above, it is common, for example, for such microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, see Lennon et al., or from the *de novo* construction of "problem specific" libraries targeted at a particular biological question, R.S. Thomas et al., *Cancer Res.* (in press). Such microarrays are herein collectively denominated "EST microarrays".

Such EST microarrays by definition can measure expression only of those genes found in EST libraries, shown herein to represent only a fraction of expressed genes. Furthermore, such libraries - and thus microarrays

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based thereupon - are biased by the tissue or cell type of message origin, by the expression levels of the respective genes within the tissues, and by the ability of the message successfully to have been reverse-transcribed and cloned.

5 Thus, as further discussed in Example 1, the methods of the present invention enable sequences that do not appear in EST or other expression databases to be determined - subsequently arrayed for expression measurements could not, therefore, have been represented as
10 probes on an EST microarray. And as further demonstrated in the examples, *infra*, the remaining population of genes identified from genomic sequence by the methods of the present invention - that is, the one third of sequences that had previously been accessioned in EST or other
15 expression databases - are biased toward genes with higher expression levels.

Representation of a message in an EST and/or cDNA library depends upon the successful reverse transcription, optionally but typically with subsequent successful
20 cloning, of the message. This introduces substantial bias into the population of probes available for arraying in EST microarrays.

In contrast, neither reverse transcription nor cloning is required to produce the probes arrayed on the
25 genome-derived single exon microarrays of the present invention. And although the ultimate deposition of a probe on the genome-derived single exon microarray of the present invention depends upon a successful amplification from genomic material, a priori knowledge of the sequence of the
30 desired amplicon affords greater opportunity to recover any given probe sequence recalcitrant to amplification than is afforded by the requirement for successful reverse transcription and cloning of unknown message in EST approaches.

35 Thus, the genome-derived single exon microarrays

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of the present invention present a far greater diversity of probes for measuring gene expression, with far less bias, than do EST microarrays presently used in the art.

As a further consequence of their ultimate origin
5 from expressed message, the probes in EST microarrays often contain poly-A (or complementary poly-T) stretches derived from the poly-A tail of mature mRNA. These homopolymeric stretches contribute to cross-hybridization, that is, to a spurious signal occasioned by hybridization to the
10 homopolymeric tail of a labeled cDNA that lacks sequence homology to the gene-specific portion of the probe.

In contrast, the probes arrayed in the genome-derived single exon microarrays of the present invention lack homopolymeric stretches derived from message
15 polyadenylation, and thus can provide more specific signal. Typically, at least about 50, 60 or 75% of the probes on the genome-derived single exon microarrays of the present invention lack homopolymeric regions consisting of A or T, where a homopolymeric region is defined for purposes herein
20 as stretches of 25 or more, typically 30 or more, identical nucleotides.

A further distinction, which also affects the specificity of hybridization, is occasioned by the typical derivation of EST microarray probes from cloned material.
25 Because much of the probe material disposed as probes on EST microarrays is excised or amplified from plasmid, phage, or phagemid vectors, EST microarrays typically include a fair amount of vector sequence, more so when the probes are amplified, rather than excised, from the vector.

30 In contrast, the vast majority of probes in the genome-derived single exon microarrays of the present invention contain no prokaryotic or bacteriophage vector sequence, having been amplified directly or indirectly from genomic DNA. Typically, therefore, at least about 50, 60,
35 70 or 80% or more of individual exon-including probes

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disposed on a genome-derived single exon microarray of the present invention lack vector sequence, and particularly lack sequences drawn from plasmids and bacteriophage. Preferably, at least about 85, 90 or more than 90% of exon-
5 including probes in the genome-derived single exon microarray of the present invention lack vector sequence. With attention to removal of vector sequences through preprocessing 24, percentages of vector-free exon-including probes can be as high as 95 - 99%. The substantial absence
10 of vector sequence from the genome-derived single exon microarrays of the present invention results in greater specificity during hybridization, since spurious cross-hybridization to a probe vector sequence is reduced.

As a further consequence of excision or
15 amplification of probes from vectors in construction of EST microarrays, the probes arrayed thereon often contain artificial sequence, derived from vector polylinker multiple cloning sites, at both 5' and 3' ends. The probes disposed upon the genome-derived single exon microarrays
20 need have no such artificial sequence appended thereto.

As mentioned above, however, the ORF-specific primers used to amplify putative ORFs can include artificial sequences, typically 5' to the ORF-specific primer sequence, useful for "universal" (that is,
25 independent of ORF sequence) priming of subsequent amplification or sequencing reactions. When such "universal" 5' and/or 3' priming sequences are appended to the amplification primers, the probes disposed upon the genome-derived single exon microarray will include
30 artificial sequence similar to that found in EST microarrays. However, the genome-derived single exon microarray of the present invention can be made without such sequences, and if so constructed, presents an even smaller amount of nonspecific sequence that would
35 contribute to nonspecific hybridization.

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Yet another consequence of typical use of cloned material as probes in EST microarrays is that such microarrays contain probes that result from cloning artifacts, such as chimeric molecules containing coding region of two separate genes. Derived from genomic material, typically not thereafter cloned, the probes of the genome-derived single exon microarrays of the present invention lack such cloning artifacts, and thus provide greater specificity of signal in gene expression measurements.

A further consequence of the cloned origin of probes on many EST microarrays is that the individual probes often have disparate sizes, which can cause the optimal hybridization stringency to vary among probes on a single microarray. In contrast, as discussed above, the probes arrayed on the genome-derived single exon microarrays of the present invention can readily be designed to have a narrow distribution in sizes, with the range of probe sizes no greater than about 10% of the average size, typically no greater than about 5% of the average probe size.

Because of their origin from fully- or partially-spliced message, probes disposed upon EST arrays will often include multiple exons. The percentage of such exon-spanning probes in an EST microarray can be calculated, on average, based upon the predicted number of exons/gene for the given species and the average length of the immobilized probes. For human genes, the near-complete sequence of human chromosome 22, Dunham et al., *Nature* 402(6761):489-95 (1999), predicts that human genes average 5.5 exons/gene. Even with probes of 200 - 500 bp, the vast majority of human EST microarray probes include more than one exon.

In contrast, by virtue of their origin from algorithmically identified ORFs in genomic sequence, the probes in the genome-derived single exon microarrays of the

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present invention can consist of individual exons. Thus, in contrast to EST microarrays, at least about 50, 60, 70, 75, 80, 85, 95 or 99% of probes deposited in the genome-derived microarray of the present invention consist of, or
5 include, no more than one predicted ORF.

This provides the ability, not readily achieved using EST microarrays, to use the genome-derived single exon microarrays of the present invention to measure tissue-specific expression of individual exons, which in
10 turn allows differential splicing events to be detected and characterized, and in particular, allows the correlation of differential splicing to tissue-specific expression patterns.

Furthermore, the exons that are represented in
15 EST microarrays are often biased toward the 3' or 5' end of their respective genes, since sequencing strategies used for EST identification are so biased. In contrast, no such 3' or 5' bias necessarily inheres in the selection of exons for disposition on the genome-derived single exon
20 microarrays of the present invention.

Conversely, the probes provided on the genome-derived single exon microarrays of the present invention typically, but need not necessarily, include intronic and/or intergenic sequence that is absent from EST
25 microarrays, which are derived from mature mRNA. Typically, at least about 50, 60, 70, 80 or 90% of the exon-including probes on the genome-derived single exon microarrays of the present invention include sequence drawn from noncoding regions. As discussed above, the additional
30 presence of noncoding region does not significantly interfere with measurement of gene expression, and provides the additional opportunity to assay pre-spliced RNA, and thus measure such phenomena such as nuclear export control.

The genome-derived single exon microarrays of the
35 present invention are also quite different from *in situ*

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synthesis microarrays, where probe size is severely constrained by inadequacies in the photolithographic synthesis process.

Typically, probes arrayed on *in situ* synthesis microarrays are limited to a maximum of about 25 bp. As a well known consequence, hybridization to such chips must be performed at low stringency. In order, therefore, to achieve unambiguous sequence-specific hybridization results, the *in situ* synthesis microarray requires substantial redundancy, with concomitant programmed arraying for each probe of probe analogues with altered (*i.e.*, mismatched) sequence.

In contrast, the longer probe length of the genome-derived single exon microarrays of the present invention allows much higher stringency hybridization and wash. Typically, therefore, exon-including probes on the genome-derived single exon microarrays of the present invention average at least about 100, 200, 300, 400 or 500 bp in length. By obviating the need for substantial probe redundancy, this approach permits a higher density of probes for discrete exons or genes to be arrayed on the microarrays of the present invention than can be achieved for *in situ* synthesis microarrays.

A further distinction is that the probes in *in situ* synthesis microarrays typically are covalently linked to the substrate surface. In contrast, the probes disposed on the genome-derived microarray of the present invention typically are, but need not necessarily be, bound noncovalently to the substrate.

Furthermore, the short probe size on *in situ* microarrays causes large percentage differences in the melting temperature of probes hybridized to their complementary target sequence, and thus causes large percentage differences in the theoretically optimum stringency across the array as a whole.

In contrast, the larger probe size in the microarrays of the present invention create lower percentage differences in melting temperature across the range of arrayed probes.

5 A further significant advantage of the microarrays of the present invention over *in situ* synthesized arrays is that the quality of each individual probe can be confirmed before deposition. In contrast, the quality of probes cannot be assessed on a probe-by-probe
10 basis for the *in situ* synthesized microarrays presently being used.

The genome-derived single exon microarrays of the present invention are also distinguished over, and present substantial benefits over, the genome-derived microarrays
15 from lower eukaryotes such as yeast. Lashkari et al., *Proc. Natl. Acad. Sci. USA* 94:13057-13062 (1997).

Only about 220 - 250 of the 6100 or so nuclear genes in *Saccharomyces cerevisiae* - that is, only about 4 - 5% - have standard, spliceosomal, introns, Lopez et al.,
20 *Nucl. Acids Res.* 28:85-86 (2000); Spingola et al., *RNA* 5(2):221-34 (1999). Furthermore, the entire yeast genome has already been sequenced. These two facts permit the ready amplification and disposition of single-ORF amplicons on such microarray without the requirement for antecedent
25 use of gene prediction and/or comparative sequence analyses.

Thus, a significant aspect of the present invention is the ability to identify and to confirm expression of predicted coding regions in genomic sequence
30 drawn from eukaryotic organisms that have a higher percentage of genes having introns than do yeast such as *Saccharomyces cerevisiae*, particularly in genomic sequence drawn from eukaryotes in which at least about 10, 20 or 50% of protein-encoding genes have introns. In preferred
35 embodiments, the methods and apparatus of the present

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invention are used to identify and confirm expression of novel genes from genomic sequence of eukaryotes in which the average number of introns per gene is at least about one, two or three or more.

5 After the physical substrate is prepared, experimental verification of predicted function is performed.

 In a preferred embodiment of the present invention, where the function sought to be identified in
10 genomic sequence is protein coding, experimental verification is performed by measuring expression of the putative ORFs, typically through nucleic acid hybridization experiments, and in particularly preferred embodiments, through hybridization to genome-derived single exon
15 microarrays prepared as above- described.

 Expression is conveniently measured and expressed for each probe in the microarray as a ratio of the expression measured concurrently in a plurality of mRNA sources, according to techniques well known in the
20 microarray art, *Reviewed in* Schena et al., and as further described in Example 2, below. The mRNA source for the reference against which specific expression is measured can be drawn from a homogeneous mRNA source, such as a single cultured cell-type, or alternatively can be heterogeneous,
25 as from a pool of mRNA derived from multiple tissues and/or cell types, as further described in Example 2, *infra*.

 mRNA can be prepared by standard techniques, see Ausubel et al. and Maniatis et al., or purchased commercially. The mRNA is then typically reverse-
30 transcribed in the presence of labeled nucleotides: the index source (that in which expression is desired to be measured) is reverse transcribed in the presence of nucleotides labeled with a first label, typically a fluorophore (fluorochrome; fluor; fluorescent dye); the
35 reference source is reverse transcribed in the presence of

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a second label, typically a fluorophore, typically fluorometrically-distinguishable from the first label. As further described in Example 2, *infra*, Cy3 and Cy5 dyes prove particularly useful in these methods. After partial
5 purification of the index and reference targets, hybridization to the probe array is conducted according to standard techniques, typically under a coverslip.

After wash, microarrays are conveniently scanned using a commercial microarray scanning device, such as a
10 Gen3 Scanner (Molecular Dynamics, Sunnyvale, CA). Data on expression is then passed, with or without interim storage, to process 500, where the results for each probe are related to the original sequence.

Often, hybridization of target material to the
15 genome-derived single exon microarray will identify certain of the probes thereon as of particular interest. Thus, it is often desirable that the user be able readily to obtain sufficient quantities of an individual probe, either for subsequent arrayed deposition upon an additional support
20 substrate, often as part of a microarray having a plurality of probes so identified, or alternatively or additionally as a solitary solid-phase or solution-phase probe, for further use.

Thus, in another aspect, the present invention
25 provides compositions and kits for the ready production of nucleic acids identical in sequence to, or substantially identical in sequence to, probes on the genome-derived single exon microarrays of the present invention.

In this aspect, a small quantity of each probe is
30 disposed, typically without attachment to substrate, in a spatially-addressable ordered set, typically one per well of a microtiter dish. Although a 96 well microtiter plate can be used, greater efficiency is obtained using higher density arrays, such as are provided by microtiter plates
35 having 384, 864, 1536, 3456, 6144, or 9600 wells, and

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although microtiter plates having physical depressions (wells) are conveniently used, any device that permits addressable withdrawal of reagent from fluidly-noncommunicating areas can be used.

5 In this aspect of the invention, therefore, a fluidly noncommunicating addressable ordered set of individual probes, corresponding to those on a genome-derived single exon microarray, is provided, with each probe in sufficient quantity to permit amplification, such
10 as by PCR. As earlier mentioned, the ORF-specific 5' primers used for genomic amplification can have a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification can have a second, different, common sequence added thereto, thus permitting,
15 in this preferred embodiment, the use of a single set of 5' and 3' primers to amplify any one of the probes from the amplifiable ordered set.

Each discrete amplifiable probe can also be packaged with amplification primers, solutes, buffers,
20 etc., and can be provided in dry (e.g., lyophilized) form or wet, in the latter case typically with addition of agents that retard evaporation.

In another aspect of the present invention, a genome-derived single-exon microarray is packaged together
25 with such an ordered set of amplifiable probes corresponding to the probes, or one or more subsets of probes, thereon. In alternative embodiments, the ordered set of amplifiable probes is packaged separately from the genome-derived single exon microarray.

30 In some embodiments, the microarray and/or ordered probe set are further packaged with recordable media that provide probe identification and addressing information, and that can additionally contain annotation information, such as gene expression data. Such recordable
35 media can be packaged with the microarray, with the ordered

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probe set, or with both.

If the microarray is constructed on a substrate that incorporates recordable media, such as is described in international patent application no. WO 98/12559, then
5 separate packaging of the genome-derived single exon microarray and the bioinformatic information is not required.

The amount of amplifiable probe material should be sufficient to permit at least one amplification
10 sufficient for subsequent hybridization assay.

Although the use of high density genome-derived microarrays on solid planar substrates is presently a preferred approach for the physical confirmation and characterization of the expression of sequences predicted
15 to encode protein, other types of microarrays (as herein defined) can also be used.

Furthermore, as earlier mentioned, experimental verification of the function predicted from genomic sequence in process 200 can be bioinformatic, rather than,
20 or additional to, physical verification.

For example, where the function desired to be identified is protein coding, the predicted ORFs can be compared bioinformatically to sequences known or suspected of being expressed.

Thus, the sequences output from process 300 (or process 200), can be used to query expression databases, such as EST databases, SNP ("single nucleotide polymorphism") databases, known cDNA and mRNA sequences, SAGE ("serial analysis of gene expression") databases, and
30 more generalized sequence databases that allow query for expressed sequences. Such query can be done by any sequence query algorithm, such as BLAST ("basic local alignment search tool"). The results of such query - including information on identical sequences and
35 information on nonidentical sequences that have diffuse or

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focal regions of sequence homology to the query sequence – can then be passed directly to process 500, or used to inform analyses subsequently undertaken in process 200, process 300, or process 400.

5 Experimental data, whether obtained by physical or bioinformatic assay in process 400, is passed to process 500 where it is usefully related to the sequence data itself, a process colloquially termed "annotation". Such annotation can be done using any technique that usefully
10 relates the functional information to the sequence, as, for example, by incorporating the functional data into the record itself, by linking records in a hierarchical or relational database, by linking to external databases, or by a combination thereof. Such database techniques are
15 well within the skill in the art.

The annotated sequence data can be stored locally, uploaded to genomic sequence database 100, and/or displayed 800.

The methods and apparatus of the present
20 invention rapidly produce functional information from genomic sequence. Coupled with the escalating pace at which sequence now accumulates, the rapid pace of sequence annotation produces a need for methods of displaying the information in meaningful ways.

25 FIG. 3 shows visual display 80 presenting a single genomic sequence annotated according to the present invention. Because of its nominal resemblance to artistic works of Piet Mondrian, visual display 80 is alternatively described herein as a "Mondrian".

30 Each of the visual elements of display 80 is aligned with respect to the genomic sequence being annotated (hereinafter, the "annotated sequence"). Given the number of nucleotides typically represented in an annotated sequence, representation of individual
35 nucleotides would rarely be readable in hard copy output of

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display 80. Typically, therefore, the annotated sequence is schematized as rectangle 89, extending from the left border of display 80 to its right border. By convention herein, the left border of rectangle 89 represents the first nucleotide of the sequence and the right border of rectangle 89 represents the last nucleotide of the sequence.

As further discussed below, however, the Mondrian visual display of annotated sequence can serve as a convenient graphical user interface for computerized representation, analysis, and query of information stored electronically. For such use, the individual nucleotides can conveniently be linked to the X axis coordinate of rectangle 89. This permits the annotated sequence at any point within rectangle 89 readily to be viewed, either automatically - for example, by time-delayed appearance of a small overlaid window upon movement of a cursor or other pointer over rectangle 89 - or through user intervention, as by clicking a mouse or other pointing device at a point in rectangle 89.

Visual display 80 is generated after user specification of the genomic sequence to be displayed. Such specification can consist of or include an accession number for a single clone (e.g., a single BAC accessioned into GenBank), wherein the starting and stopping nucleotides are thus absolutely identified, or alternatively can consist of or include an anchor or fulcrum point about which a chosen range of sequence is anchored, thus providing relative endpoints for the sequence to be displayed. For example, the user can anchor such a range about a given chromosomal map location, gene name, or even a sequence returned by query for similarity or identity to an input query sequence. When visual display 80 is used as a graphical user interface to computerized data, additional control over the first and

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last displayed nucleotide will typically be dynamically selectable, as by use of standard zooming and/or selection tools.

Field 81 of visual display 80 is used to present the output from process 200, that is, to present the bioinformatic prediction of those sequences having the desired function within the genomic sequence. Functional sequences are typically indicated by at least one rectangle 83 (83a, 83b, 83c), the left and right borders of which respectively indicate, by their X-axis coordinates, the starting and ending nucleotides of the region predicted to have function.

Where a single bioinformatic method or approach identifies a plurality of regions having the desired function, a plurality of rectangles 83 is disposed horizontally in field 81. Where multiple methods and/or approaches are used to identify function, each such method and/or approach can be represented by its own series of horizontally disposed rectangles 83, each such horizontally disposed series of rectangles offset vertically from those representing the results of the other methods and approaches.

Thus, rectangles 83a in FIG. 3 represent the functional predictions of a first method of a first approach for predicting function, rectangles 83b represent the functional predictions of a second method and/or second approach for predicting that function, and rectangles 83c represent the predictions of a third method and/or approach.

Where the function desired to be identified is protein coding, field 81 is used to present the bioinformatic prediction of sequences encoding protein. For example, rectangles 83a can represent the results from GRAIL or GRAIL II, rectangles 83b can represent the results from GENEFINDER, and rectangles 83c can represent the

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results from DICTION.

Optionally, and preferably, rectangles 83 collectively representing predictions of a single method and/or approach are identically colored and/or textured, and are distinguishable from the color and/or texture used for a different method and/or approach.

Alternatively, or in addition, the color, hue, density, or texture of rectangles 83 can be used further to report a measure of the bioinformatic reliability of the prediction. For example, many gene prediction programs will report a measure of the reliability of prediction. Thus, increasing degrees of such reliability can be indicated, e.g., by increasing density of shading. Where display 80 is used as a graphical user interface, such measures of reliability, and indeed all other results output by the program, can additionally or alternatively be made accessible through linkage from individual rectangles 83, as by time-delayed window ("tool tip" window), or by pointer (e.g., mouse)-activated link.

As earlier described, increased predictive reliability can be achieved by requiring consensus among methods and/or approaches to determining function. Thus, field 81 can include a horizontal series of rectangles 83 that indicate one or more degrees of consensus in predictions of function.

Although FIG. 3 shows three series of horizontally disposed rectangles in field 81, display 80 can include as few as one such series of rectangles and as many as can discriminably be displayed, depending upon the number of methods and/or approaches used to predict a given function.

Furthermore, field 81 can be used to show predictions of a plurality of different functions. However, the increased visual complexity occasioned by such display makes more useful the ability of the user to select

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a single function for display. When display 80 is used as a graphical user interface for computer query and analysis, such function can usefully be indicated and user-selectable, as by a series of graphical buttons or tabs
5 (not shown in FIG. 3).

Rectangle 89 is shown in FIG. 3 as including interposed rectangle 84. Rectangle 84 represents the portion of annotated sequence for which predicted functional information has been assayed physically, with
10 the starting and ending nucleotides of the assayed material indicated by the X axis coordinates of the left and right borders of rectangle 84. Rectangle 85, with optional inclusive circles 86 (86a, 86b, and 86c) displays the results of such physical assay.

15 Although a single rectangle 84 is shown in FIG. 3, physical assay is not limited to just one region of annotated genomic sequence. It is expected that an increasing percentage of regions predicted to have function by process 200 will be assayed physically, and that display
20 80 will accordingly, for any given genomic sequence, have an increasing number of rectangles 84 and 85, representing an increased density of sequence annotation.

Where the function desired to be identified is protein coding, rectangle 84 identifies the sequence of the
25 probe used to measure expression. In embodiments of the present invention where expression is measured using genome-derived single exon microarrays, rectangle 84 identifies the sequence included within the probe immobilized on the support surface of the microarray. As
30 noted supra, such probe will often include a small amount of additional, synthetic, material incorporated during amplification and designed to permit reamplification of the probe, which sequence is typically not shown in display 80.

Rectangle 87 is used to present the results of
35 bioinformatic assay of the genomic sequence. For example,

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where the function desired to be identified is protein coding, process 400 can include bioinformatic query of expression databases with the sequences predicted in process 200 to encode exons. And as earlier discussed, because bioinformatic assay presents fewer constraints than does physical assay, often the entire output of process 200 can be used for such assay, without further subsetting thereof by process 300. Therefore, rectangle 87 typically need not have separate indicators therein of regions submitted for bioinformatic assay; that is, rectangle 87 typically need not have regions therein analogous to rectangles 84 within rectangle 89.

Rectangle 87 as shown in FIG. 3 includes smaller rectangles 880 and 88. Rectangles 880 indicate regions that returned a positive result in the bioinformatic assay, with rectangles 88 representing regions that did not return such positive results. Where the function desired to be predicted and displayed is protein coding, rectangles 880 indicate regions of the predicted exons that identify sequence with significant similarity in expression databases, such as EST, SNP, SAGE databases, with rectangles 88 indicating genes novel over those identified in existing expression data bases.

Rectangles 880 can further indicate, through color, shading, texture, or the like, additional information obtained from bioinformatic assay.

For example, where the function assayed and displayed is protein coding, the degree of shading of rectangles 880 can be used to represent the degree of sequence similarity found upon query of expression databases. The number of levels of discrimination can be as few as two (identity, and similarity, where similarity has a user-selectable lower threshold). Alternatively, as many different levels of discrimination can be indicated as can visually be discriminated.

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Where display 80 is used as a graphical user interface, rectangles 880 can additionally provide links directly to the sequences identified by the query of expression databases, and/or statistical summaries thereof.

5 As with each of the precedingly-discussed uses of display 80 as a graphical user interface, it should be understood that the information accessed via display 80 need not be resident on the computer presenting such display, which often will be serving as a client, with the linked

10 information resident on one or more remotely located servers.

Rectangle 85 displays the results of physical assay of the sequence delimited by its left and right borders.

15 Rectangle 85 can consist of a single rectangle, thus indicating a single assay, or alternatively, and increasingly typically, will consist of a series of rectangles (85a, 85b, 85c) indicating separate physical assays of the same sequence.

20 Where the function assayed is gene expression, and where gene expression is assayed as herein described using simultaneous two-color fluorescent detection of hybridization to genome-derived single exon microarrays, individual rectangles 85 can be colored to indicate the

25 degree of expression relative to control. Conveniently, shades of green can be used to depict expression in the sample over control values, and shades of red used to depict expression less than control, corresponding to the spectra of the Cy3 and Cy5 dyes conventionally used for

30 respective labeling thereof. Additional functional information can be provided in the form of circles 86 (86a, 86b, 86c), where the diameter of the circle can be used to indicate expression intensity. As discussed *infra*, such relative expression (expression ratios) and absolute

35 expression (signal intensity) can be expressed using

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normalized values.

Where display 80 is used as a graphical user interface, rectangle 85 can be used as a link to further information about the assay. For example, where the assay is one for gene expression, each rectangle 85 can be used to link to information about the source of the hybridized mRNA, the identity of the control, raw or processed data from the microarray scan, or the like.

FIG. 4 is rendition of display 80 representing gene prediction and gene expression for a hypothetical BAC, showing conventions used in the Examples presented infra. BAC sequence ("Chip seq.") 89 is presented, with the physically assayed region thereof (corresponding to rectangle 84 in FIG. 3) shown in white. Algorithmic gene predictions are shown in field 81, with predictions by GRAIL shown, predictions by GENEFINDER, and predictions by DICTION shown. Within rectangle 87, regions of sequence that, when used to query expression databases, return identical or similar sequences ("EST hit") are shown as white rectangles (corresponding to rectangles 880 in FIG. 3), gray indicates low homology, and black indicates unknowns (where black and gray would correspond to rectangles 88 in FIG. 3).

Although FIGS. 3 and 4 show a single stretch of sequence, uninterrupted from left to right, longer sequences are usefully represented by vertical stacking of such individual Mondrians, as shown in FIGS. 9 and 10.

Single Exon Probes Useful For Measuring Gene Expression

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The methods and apparatus of the present invention rapidly produce functional information from genomic sequence. Where the function to be identified is protein coding, the methods and apparatus of the present invention rapidly identify and confirm the expression of

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portions of genomic sequence that function to encode protein. As a direct result, the methods and apparatus of the present invention rapidly yield large numbers of single-exon nucleic acid probes, the majority from
5 previously unknown genes, each of which is useful for measuring and/or surveying expression of a specific gene in one or more tissues or cell types.

It is, therefore, another aspect of the present invention to provide genome-derived single exon nucleic
10 acid probes useful for gene expression analysis, and particularly for gene expression analysis by microarray.

Using the methods and genome-derived single-exon microarrays of the present invention, we have for example readily identified a large number of unique ORFs from human
15 genomic sequence. Using single exon probes that encompass these ORFs, we have demonstrated, through microarray hybridization analysis, the expression of 9,980 of these ORFs in heart.

As would immediately be appreciated by one of
20 skill in the art, each single exon probe having demonstrable expression in heart is currently available for use in measuring the level of its ORF's expression in heart.

Diseases of the heart and vascular system are a
25 significant cause of human morbidity and mortality. Increasingly, genetic factors are being found that contribute to predisposition, onset, and/or aggressiveness of most, if not all, of these diseases. Although mutations in single genes have on occasion been identified as
30 causative, these disorders are for the most part believed to have polygenic etiologies.

For example, cardiovascular disease (CVD), which includes coronary heart disease, stroke, and peripheral
arterial vascular disease, is the leading cause of death in
35 the United States and other developed countries. In

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developing regions, coronary heart disease and stroke are ranked second and third, respectively, as causes of mortality. In the United States alone, about 1 million deaths (about 42% of total deaths per year) result from CVD each year. CVD is also a significant cause of morbidity, with about 1.5 million people suffering myocardial infarction, and about 500,000 suffering strokes in the United States each year. With risk for CVD increasing with age, and an increasingly aging population, CVD will continue to be a major health problem into the future.

CVD is caused by arterial lesions that begin as fatty streaks, which consist of lipid-laden foam cells, and develop into fibrous plaques. The atherosclerotic plaque may grow slowly, and over several decades may produce a severe stenosis or result in arterial occlusion. Some plaques are stable, but other, more unstable, ones may rupture and induce thrombosis. The thrombi may embolize, rapidly occluding the lumen and leading to myocardial infarction or acute ischemic syndrome.

Risk factors for CVD include age and gender. In addition, a family history of CVD significantly increases risk, indicating a genetic basis for development of this disease complex. Obesity, especially truncal obesity, the cause of which is suspected to be genetic, is yet another risk factor for CVD. Familial disorders such as hyperlipidemia, hypoalphalipoproteinemia, hypertriglyceridemia, hypercholesterolemia, hyperinsulinemia, homocystinuria, and dysbetalipoproteinemia, all of which lead to lipid or lipoprotein abnormalities, can predispose one to the development of CVD. Both insulin-dependent and non-insulin-dependent diabetes mellitus, both of which have genetic components, have been also linked to the development of atherosclerosis.

The literature is replete with evidence for

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genetic causes of cardiovascular diseases. For example, studies by Allayee et al., *Am. J. Hum. Genet.* 63:577-585(1998), indicated a genetic association between familial combined hyperlipidemia (FCHL) and small dense LDL particles. The studies also concluded that the genetic determinants for LDL particle size are shared, at least in part, among FCHL families and the more general population at risk for CVD. Juo et al., *Am. J. Hum. Genet.* 63: 586-594 (1998) demonstrated that small, dense LDL particles and elevated apolipoprotein B levels, both of which are commonly found in members of FCHL families, share a common major gene plus individual polygenic components.

The common major gene was estimated to explain 37% of the variants of adjusted LDL particle size and 23% of the variants of adjusted apoB levels.

The atherogenic lipoprotein phenotype (ALP) is a common heritable trait, symptoms of which include a prevalence of small, dense LDL particles, increased levels of triglyceride-rich lipoproteins, reduced levels of high density lipoprotein, and increased risk of CVD, particularly myocardial infarction. Both Nishina et al., *Proc. Nat. Acad. Sci.* 89: 708-712 (1992) and Rotter et al., *Am. J. Hum. Genet.* 58: 585-594(1996) demonstrated linkage between ALP and the LDLR locus. Rotter et al., *supra*, also reported linkage to the CETP locus on chromosome 16 and to the SOD1 locus on chromosome 6, and possibly also to the APOA1/APOC3/APOA4 cluster on chromosome 11.

Mutations in genes identified as components of lipid metabolism, e.g., apolipoprotein E (apoE) and LDL receptor (LDLR), have been shown to be associated with predisposition to the development of CVD. For example, several apoE variants had been found to be associated with familial dysbetalipoproteinemia, characterized by elevated plasma cholesterol and triglyceride levels and an increased risk for atherosclerosis (de Knijff et al., *Mutat* 4: 178-

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194 (1994)). Mutations in the LDLR gene have been associated with the familial hypercholesterolemia, an autosomal dominant disorder characterized by elevation of serum cholesterol bound to low density lipoprotein (LDL), that can lead to increased susceptibility to CVD.

To date, mutations in numerous genes have been shown to be associated with increased CVD susceptibility. However, the identified genetic associations are believed not to account for all genetic contributions to CVD.

As yet another example, hypertension is a major health problem because of its high prevalence and its association with increased risk of CVD. Approximately 25% of all adults and over 60% of persons older than 60 years in the United States have high blood pressure.

Arterial or systemic hypertension is diagnosed when the average of two or more diastolic BP measurements on at least two subsequent visits is 90 mm Hg or more, or when the average of multiple systolic BP readings on two or more subsequent visits is consistently greater than 140 mm Hg. Pulmonary hypertension is defined as pressure within the pulmonary arterial system elevated above the normal range; pulmonary hypertension may lead to right ventricle (RV) failure.

Hypertension, together with other cardiovascular risk factors, leads to atherosclerosis and other forms of CVD, primarily by damaging the vascular endothelium. In more than 40% of the U.S. population, hypertension is accompanied by hyperlipidemia and leads to the development of atherosclerotic plaques. In the absence of hyperlipidemia, intimal thickening occurs. Non-atherosclerotic hypertension-induced vascular damage can lead to stroke or heart failure.

Familial diseases associated with secondary hypertension include familial renal disease, polycystic kidney disease, medullary thyroid cancer, pheochromocytoma,

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and hyperparathyroidism. Hypertension is also twice as common in patients with diabetes mellitus.

More than 95% of all hypertension cases are essential hypertension, that is, lack identifiable antecedent clinical cause. Essential hypertension shows clustering in families and can result from a variety of genetic diseases. In most cases, high blood pressure results from a complex interaction of factors with both genetic and environmental components. The recent search for genes that contribute to the development of essential hypertension has shown that the disorder is polygenic in origin. However, with several exceptions (such as angiotensinogen, angiotensin receptor-1, beta-3 subunit of guanine nucleotide-binding protein, tumor necrosis factor receptor-2, and "-adducin), the particular genes involved are still being sought.

Susceptibility loci for essential hypertension have been mapped to chromosomes 17 and 15q. Hasstedt et al., Am. J. Hum. Genet. 43: 14-22 (1988) measured red cell sodium in 1,800 normotensive members of 16 Utah pedigrees ascertained through hypertensive or normotensive probands, siblings with early stroke death, or brothers with early coronary disease, and suggested that red blood cell sodium was determined by 4 alleles at a single locus. This major locus was thought to explain 29% of the variance in red cell sodium, and polygenic inheritance explained another 54.6%. A higher frequency of the high red blood cell sodium genotype in pedigrees in which the proband was hypertensive rather than normotensive provided evidence that this major locus increases susceptibility to hypertension.

From a study of systolic blood pressure in 278 pedigrees, Perusse et al., Am. J. Hum. Genet. 49: 94-105 (1991) reported that variability in systolic blood pressure is likely influenced by allelic variation of a single gene, with gender and age dependence. They also suggested that a

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single gene may be associated with a steeper increase of blood pressure with age among males and females.

There is strong evidence, however, for additional as yet uncharacterized, hypertension-associated loci on
5 other chromosomes.

For example, Xu et al., Am. J. Hum. Genet. 64: 1694-1701 (1999) carried out a systematic search for chromosomal regions containing genes that regulate blood pressure by scanning the entire autosomal genome using 367
10 polymorphic markers. Because of the sampling design, the number of sib pairs, and the availability of genotyped parents, this study represented one of the most powerful of its kind. Although no regions achieved a 5% genomewide significance level, maximum lod scores were greater than
15 2.0 for regions of chromosomes 3, 11, 15, 16, and 17.

As another example, cardiac arrhythmias account for several thousand deaths each year. Arrhythmias such as ventricular fibrillation, which causes more than 300,000 sudden deaths annually in the United States alone,
20 encompass a multitude of disorders. Another type of arrhythmia, idiopathic dilated cardiomyopathy, of which familial dilated cardiomyopathy accounts for 20-25%, is responsible for more than 10,000 deaths in the United States annually and is the predominant indication for
25 cardiac transplantation.

Cardiac arrhythmias can be divided into bradyarrhythmias (slowed rhythms) or tachyarrhythmias (speeded rhythms). Bradyarrhythmias result from abnormalities of intrinsic automatic behavior or
30 conduction, primarily within the atrioventricular node and the His-Purkinje's network. Tachyarrhythmias are caused by altered automaticity, reentry, or triggered automaticity.

Bradyarrhythmias arising from suspected polygenic disorders include Long QT syndrome 4, atrioventricular
35 block, familial sinus node disease, progressive cardiac

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conduction defect, and familial cardiomyopathy.

Tachyarrhythmias with possible underlying polygenic causes include familial ventricular tachycardia, Wolff-Parkinson-White syndrome, familial arrhythmogenic right ventricular dysplasia, heart-hand syndrome V, Mal de Meleda, familial ventricular fibrillation, and familial noncompaction of left ventricular myocardium.

For some of the arrhythmias, one or more of the causative genes have been identified.

For example, atrioventricular block has been associated with mutations in the SCN5A gene, as well as mutations in a locus mapped to 19q13. Studies have shown linkage of familial sinus node disease to a marker on 10q22-q24. Familial ventricular tachycardia has been linked to mutations in genes encoding the G protein subunit alpha-i2 (GNAI1), and/or related genes. Examination of families with Wolff-Parkinson-White syndrome suggest an autosomal dominant pattern of inheritance and evidence of linkage of the disorder to DNA markers on band 7q3. Linkage analysis shows strong evidence for localization of a gene for Mal de Meleda disease on 8qter. Familial ventricular fibrillation can be caused by mutations in the cardiac sodium channel gene SCN5A. Familial noncompaction of left ventricular myocardium has been linked to mutations in the gene encoding tafazzin (TAZ), or in the FK506-binding protein 1A gene (FKBP1A).

Familial dilated cardiomyopathy is characterized by an autosomal dominant pattern of inheritance with age-related penetrance. The linkage of familial dilated cardiomyopathy to several loci indicate that it is polygenic. These loci include CMD1A on 1p11-q11, CMD1B on 9q13, CMD1C on 10q21, CMD1D on 1q32, CMD1E on 3p, CMD1F on 6q, CMD1G on 2q31, CMD1H on 2q14-q22, and CMD1I, which results from mutation in the DES gene on 2q35.

In addition, cardiomyopathy can also be caused by

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mutations in the ACTC gene, the cardiac beta-myosin heavy chain gene (MYH7), or the cardiac troponin T gene.

Familial arrhythmogenic right ventricular dysplasia is inherited as an autosomal dominant with reduced penetrance and is one of the major genetic causes of juvenile sudden death. It is estimated that the prevalence of familial arrhythmogenic right ventricular dysplasia ranges from 6 per 10,000 in the general population to 4.4 per 1,000 in some areas.

Several loci for familial arrhythmogenic right ventricular dysplasia have been mapped indicating that this disease is also polygenic in nature. These loci include ARVD1 on 14q23-q24, ARVD2 on 1q42-q43, ARVD3 on 14q12-q22, ARVD4 on 2q32.1-q32.3, ARVD5 on 3p23, and ARVD6 on 10p14-p12.

Progressive cardiac conduction defect (PCCD), also called Lenegre-Lev disease, is one of the most common cardiac conduction diseases. It is characterized by progressive alteration of cardiac conduction through the His-Purkinje system with right or left bundle branch block and widening of QRS complexes, leading to complete atrioventricular block and ultimately causing syncope and sudden death. It represents the major cause of pacemaker implantation in the world (0.15 implantations per 1,000 inhabitants per year in developed countries). The cause of PCCD is unknown but familial cases with right bundle branch block have been reported suggesting that at least some cases are of genetic origin. Reports have linked PCCD to HB1 on 19q13.3, and to mutations in the SCN5A gene (Schott et al., Nature Genet. 23: 20-21 (1999)).

As yet a further example, congenital heart disease occurs at a rate of 8 per 1000 live births, which corresponds to approximately 32,000 infants with newly diagnosed congenital heart disease each year in the United States. Twenty percent of infants with congenital heart

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disease die within the first year of life. Approximately 80% of the first-year survivors live to reach adulthood. Congenital heart disease also has economic impact due to the estimated 20,000 surgical procedures performed to correct circulatory defects in these patients. The estimated number of adults with congenital heart disease in the United States is currently about 900,000.

In 90% of patients, congenital heart disease is attributable to multifactorial inheritance. Only 5-10% of malformations are due to primary genetic factors, which are either chromosomal or a result of a single mutant gene.

The most common congenital heart disease found in adults is bicuspid aortic valve. This defect occurs in 2% of the general population and accounts for approximately 50% of operated cases of aortic stenosis in adults. Atrial septal defect is responsible for 30-40% of congenital heart disease seen in adults. The most common congenital cardiac defect observed in the pediatric population is ventricular septal defect, which accounts for 15-20% of all congenital lesions. Tetralogy of Fallot is the most common cyanotic congenital anomaly observed in adults. Other congenital heart diseases include Eisenmenger's syndrome, patent ductus arteriosus, pulmonary stenosis, coarctation of the aorta, transposition of the great arteries, tricuspid atresia, univentricular heart, Ebstein's anomaly, and double-outlet right ventricle.

A number of studies have identified putative genetic loci associated with one or more congenital heart diseases.

Congenital heart disease affects more than 40% of all Down syndrome patients. The candidate chromosomal region containing the putative gene or genes for congenital heart disease associated with Down syndrome is 21q22.2-q22.3, between ETS2 and MX1.

DiGeorge syndrome (DGS) is characterized by

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several symptoms including outflow tract defects of the heart such as teratology of Fallot. Most cases result from a deletion of chromosome 22q11.2 (the DiGeorge syndrome chromosome region, or DGCR). The 22q11 deletion is the second most common cause of congenital heart disease after Down syndrome. Several genes are lost in this deletion including the putative transcription factor TUPLE1. This deletion is associated with a variety of phenotypes, e.g., Shprintzen syndrome; conotruncal anomaly face (or Takao syndrome); and isolated outflow tract defects of the heart including Tetralogy of Fallot, truncus arteriosus, and interrupted aortic arch.

Whereas 90% of cases of DGS may now be attributed to a 22q11 deletion, other associated chromosome defects have been identified. For example, Greenberg et al., Am. J. Hum. Genet. 43:605-611 (1988), reported 1 case of DGS with del10p13 and one with a 18q21.33 deletion. Fukushima et al., Am. J. Hum. Genet. 51 (suppl.):A80 (1992) reported linkage with a deletion of 4q21.3-q25. Gottlieb et al., Am. J. Hum. Genet. 62: 495-498 (1998) concluded that the deletion of more than 1 region on 10p could be associated with the DGS phenotype. The association of the DiGeorge syndrome with at least 2 and possibly more chromosomal locations suggests strongly the involvement of several genes in this disease.

Digilio et al., J. Med. Genet. 34: 188-190 (1997), calculated empiric risk figures for recurrence of isolated Tetralogy of Fallot in families after exclusion of del(22q11), and concluded that gene(s) different from those located on 22q11 must be involved in causing familial aggregation of nonsyndromic Tetralogy of Fallot. Johnson et al., Am. J. Med. Genet. (1997) conducted a cytogenetic evaluation of 159 cases of Tetralogy of Fallot. They reported that a del(22q11) was identified in 14% who underwent fluorescence in situ hybridization (FISH) testing

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with the N25 cosmid probe.

Other congenital heart disease are also suspected to be of polygenic origin. For example, Holmes et al., Birth Defects Orig. Art. Ser. X(4): 228-230 (1974) described familial clustering of hypoplastic left heart syndrome in siblings consistent with multifactorial causation.

Other significant diseases of the heart and vascular system are also believed to have a genetic, typically polygenic, etiological component. These diseases include, for example, hypoplastic left heart syndrome, cardiac valvular dysplasia, Pfeiffer cardiocranial syndrome, oculofaciocardiodental syndrome, Kapur-Toriello syndrome, Sonoda syndrome, Ohdo Blepharophimosis syndrome, heart-hand syndrome, Pierre-Robin syndrome, Hirschsprung disease, Kousseff syndrome, Grange occlusive arterial syndrome, Kearns-Sayre syndrome, Kartagener syndrome, Alagille syndrome, Ritscher-Schinzel syndrome, Ivemark syndrome, Young-Simpson syndrome, hemochromatosis, Holzgreve syndrome, Barth syndrome, Smith-Lemli-Opitz syndrome, glycogen storage disease, Gaucher-like disease, Fabry disease, Lowry-Maclean syndrome, Rett syndrome, Opitz syndrome, Marfan syndrome, Miller-Dieker lissencephaly syndrome, mucopolysaccharidosis, Bruada syndrome, humerospinal dysostosis, Phaver syndrome, McDonough syndrome, Marfanoid hypermobility syndrome, atransferrinemia, Cornelia de Lange syndrome, Leopard syndrome, Diamond-Blackfan anemia, Steinfeld syndrome, progeria, and Williams-Beuren syndrome.

The human genome-derived single exon nucleic acid probes and microarrays of the present invention are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of human heart and vascular system, particularly those diseases with polygenic etiology. With each of the single exon probes described herein shown to be

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expressed at detectable levels in human heart, and with about 2/3 of the probes identifying novel genes, the single exon microarrays of the present invention provide exceptionally high informational content for such studies.

5 For example, diagnosis (including differential diagnosis among clinically indistinguishable disorders), staging, and/or grading of a disease can be based upon the quantitative relatedness of a patient gene expression profile to one or more reference expression profiles known
10 to be characteristic of a given heart or vascular disease, or to specific grades or stages thereof.

In one embodiment, the patient gene expression profile is generated by hybridizing nucleic acids obtained directly or indirectly from transcripts expressed in the
15 patient's heart or vascular tissues to the genome-derived single exon microarray of the present invention. Reference profiles are obtained similarly by hybridizing nucleic acids obtained directly or indirectly from transcripts expressed in heart or vascular tissue of individuals with
20 known disease. Methods for quantitatively relating gene expression profiles, without regard to the function of the protein encoded by the gene, are disclosed in WO 99/58720, incorporated herein by reference in its entirety.

In another approach, the genome-derived single
25 exon probes and microarrays of the present invention can be used to interrogate genomic DNA, rather than pools of expressed message; this latter approach permits predisposition to and/or prognosis of heart or vascular disease to be assessed through the massively parallel
30 determination of altered copy number, deletion, or mutation in the patient's genome of exons known to be expressed in human heart. The algorithms set forth in WO 99/58720 can be applied to such genomic profiles without regard to the function of the protein encoded by the interrogated gene.

35 The utility is specific to the probe; at

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sufficiently high hybridization stringency, which stringencies are well known in the art — see Ausubel *et al.* and Maniatis *et al.* — each probe reports the level of expression of message specifically containing that ORF.

5 It should be appreciated, however, that the probes of the present invention, for which expression in the heart has been demonstrated are useful for both measurement in the heart and for survey of expression in other tissues.

10 Significant among such advantages is the presence of probes for novel genes.

As mentioned above and further detailed in Examples 1 and 2, the methods described enable ORFs which are not present in existing expression databases to be
15 identified. And the fewer the number of tissues in which the ORF can be shown to be expressed, the more likely the ORF will prove to be part of a novel gene: as further discussed in Example 2, ORFs whose expression was measurable in only a single of the tested tissues were
20 represented in existing expression databases at a rate of only 11%, whereas 36% of ORFs whose expression was measurable in 9 tissues were present in existing expression databases, and fully 45% of those ORFs expressed in all ten tested tissues were present in existing expressed sequence
25 databases.

Either as tools for measuring gene expression or tools for surveying gene expression, the genome-derived single exon probes of the present invention have significant advantages over the cDNA or EST-based probes
30 that are currently available for achieving these utilities.

The genome-derived single exon probes of the present invention are useful in constructing genome-derived single exon microarrays; the genome-derived single exon microarrays, in turn, are useful devices for measuring and
35 for surveying gene expression in the human.

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Gene expression analysis using microarrays – conventionally using microarrays having probes derived from expressed message – is well-established as useful in the biological research arts (see Lockhart et al. *Nature* 405, 5 827-836).

Microarrays have been used to determine gene expression profiles in cells in response to drug treatment (see, for example, Kaminski et al., "Global Analysis of Gene Expression in Pulmonary Fibrosis Reveals Distinct 10 Programs Regulating Lung Inflammation and Fibrosis," *Proc. Natl. Acad. Sci. USA* 97(4):1778-83 (2000); Bartosiewicz et al., "Development of a Toxicological Gene Array and Quantitative Assessment of This Technology," *Arch. Biochem. Biophys.* 376(1):66-73 (2000)), viral infection (see for 15 example, Geiss et al., "Large-scale Monitoring of Host Cell Gene Expression During HIV-1 Infection Using cDNA Microarrays," *Virology* 266(1):8-16 (2000)) and during cell processes such as differentiation, senescence and apoptosis (see, for example, Shelton et al., "Microarray Analysis of 20 Replicative Senescence," *Curr. Biol.* 9(17):939-45 (1999); Voehringer et al., "Gene Microarray Identification of Redox and Mitochondrial Elements That Control Resistance or Sensitivity to Apoptosis," *Proc. Natl. Acad. Sci. USA* 97(6):2680-5 (2000)).

Microarrays have also been used to determine abnormal gene expression in diseased tissues (see, for example, Alon et al., "Broad Patterns of Gene Expression Revealed by Clustering Analysis of Tumor and Normal Colon Tissues Probed by Oligonucleotide Arrays," *Proc. Natl. 30 Acad. Sci. USA* 96(12):6745-50 (1999); Perou et al., "Distinctive Gene Expression Patterns in Human Mammary Epithelial Cells and Breast Cancers," *Proc. Natl. Acad. Sci. USA* 96(16):9212-7 (1999); Wang et al., "Identification of Genes Differentially Over-expressed in Lung Squamous Cell 35 Carcinoma Using Combination of cDNA Subtraction and

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Microarray Analysis," *Oncogene* 19(12):1519-28 (2000);
Whitney et al., "Analysis of Gene Expression in Multiple
Sclerosis Lesions Using cDNA Microarrays," *Ann. Neurol.*
46(3):425-8 (1999)), in drug discovery screens (see, for
5 example, Scherf et al., "A Gene Expression Database for the
Molecular Pharmacology of Cancer," *Nat. Genet.* 24(3):236-44
(2000)) and in diagnosis to determine appropriate treatment
strategies (see, for example, Sgroi et al., "In vivo Gene
Expression Profile Analysis of Human Breast Cancer
10 Progression," *Cancer Res.* 59(22):5656-61 (1999)).

In microarray-based gene expression screens of
pharmacological drug candidates upon cells, each probe
provides specific useful data. In particular, it should be
appreciated that even those probes that show no change in
15 expression are as informative as those that do change,
serving, in essence, as negative controls.

For example, where gene expression analysis is
used to assess toxicity of chemical agents on cells, the
failure of the agent to change a gene's expression level is
20 evidence that the drug likely does not affect the pathway
of which the gene's expressed protein is a part.
Analogously, where gene expression analysis is used to
assess side effects of pharmacological agents - whether in
lead compound discovery or in subsequent screening of lead
25 compound derivatives - the inability of the agent to alter
a gene's expression level is evidence that the drug does
not affect the pathway of which the gene's expressed
protein is a part.

WO 99/58720 provides methods for quantifying the
30 relatedness of a first and second gene expression profile
and for ordering the relatedness of a plurality of gene
expression profiles. The methods so described permit
useful information to be extracted from a greater
percentage of the individual gene expression measurements
35 from a microarray than methods previously used in the art.

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Other uses of microarrays are described in Gerhold et al., *Trends Biochem. Sci.* 24(5):168-173 (1999) and Zweiger, *Trends Biotechnol.* 17(11):429-436 (1999); Schena et al.

5 The invention particularly provides genome-derived single-exon probes known to be expressed in heart.

The individual single exon probes can be provided in the form of substantially isolated and purified nucleic acid, typically, but not necessarily, in a quantity
10 sufficient to perform a hybridization reaction.

Such nucleic acid can be in any form directly hybridizable to the message that contains the probe's ORF, such as double stranded DNA, single-stranded DNA complementary to the message, single-stranded RNA
15 complementary to the message, or chimeric DNA/RNA molecules so hybridizable. The nucleic acid can alternatively or additionally include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as complementary binding can be obtained. For example, probes
20 can include phosphorothioates, methylphosphonates, morpholino analogs, and peptide nucleic acids (PNA), as are described, for example, in U.S. Patent Nos. 5,142,047; 5,235,033; 5,166,315; 5,217,866; 5,184,444; 5,861,250.

Usefully, however, such probes are provided in a
25 form and quantity suitable for amplification, where the amplified product is thereafter to be used in the hybridization reactions that probe gene expression. Typically, such probes are provided in a form and quantity suitable for amplification by PCR or by other well known
30 amplification technique. One such technique additional to PCR is rolling circle amplification, as is described, *inter alia*, in U.S. Patent Nos. 5,854,033 and 5,714,320 and international patent publications WO 97/19193 and WO 00/15779. As is well understood, where the probes are
35 to be provided in a form suitable for amplification, the

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range of nucleic acid analogues and/or internucleotide linkages will be constrained by the requirements and nature of the amplification enzyme.

Where the probe is to be provided in form
5 suitable for amplification, the quantity need not be sufficient for direct hybridization for gene expression analysis, and need be sufficient only to function as an amplification template, typically at least about 1, 10 or 100 pg or more.

Each discrete amplifiable probe can also be packaged with amplification primers, either in a single composition that comprises probe template and primers, or in a kit that comprises such primers separately packaged therefrom. As earlier mentioned, the ORF-specific
15 5' primers used for genomic amplification can have a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification can have a second, different, common sequence added thereto, thus permitting, in this embodiment, the use of a single set of 5' and 3'
20 primers to amplify any one of the probes. The probe composition and/or kit can also include buffers, enzyme, etc., required to effect amplification.

As mentioned earlier, when intended for use on a genome-derived single exon microarray of the present
25 invention, the genome-derived single exon probes of the present invention will typically average at least about 100, 200, 300, 400 or 500 bp in length, including (and typically, but not necessarily centered about) the ORF. Furthermore, when intended for use on a genome-derived
30 single exon microarray of the present invention, the genome-derived single exon probes of the present invention will typically not contain a detectable label.

When intended for use in solution phase hybridization, however — that is, for use in a
35 hybridization reaction in which the probe is not first

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bound to a support substrate (although the target may indeed be so bound) - length constraints that are imposed in microarray-based hybridization approaches will be relaxed, and such probes will typically be labeled.

5 In such case, the only functional constraint that dictates the minimum size of such probe is that each such probe must be capable of specifically identifying in a hybridization reaction the exon from which it is drawn. In theory, a probe of as little as 17 nucleotides is capable
10 of uniquely identifying its cognate sequence in the human genome. For hybridization to expressed message - a subset of target sequence that is much reduced in complexity as compared to genomic sequence - even fewer nucleotides are required for specificity.

15 Therefore, the probes of the present invention can include as few as 20, 25 or 50 bp or ORF, or more. In particular embodiments, the ORF sequences are given in SEQ ID NOS. 9,981 - 19,771, respectively, for probe SEQ ID NOS. 1 - 9,980. The minimum amount of ORF required to be
20 included in the probe of the present invention in order to provide specific signal in either solution phase or microarray-based hybridizations can readily be determined for each of ORF SEQ ID NOS. 9,981 - 19,771 individually by routine experimentation using standard high stringency
25 conditions.

Such high stringency conditions are described, *inter alia*, in Ausubel et al. and Maniatis et al. For microarray-based hybridization, standard high stringency conditions can usefully be 50% formamide, 5X SSC, 0.2 µg/µl
30 poly(dA), 0.2 µg/µl human c₆t1 DNA, and 0.5 % SDS, in a humid oven at 42°C overnight, followed by successive washes of the microarray in 1X SSC, 0.2% SDS at 55°C for 5 minutes, and then 0.1X SSC, 0.2% SDS, at 55°C for 20 minutes. For solution phase hybridization, standard high
35 stringency conditions can usefully be aqueous hybridization

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at 65°C in 6X SSC. Lower stringency conditions, suitable for cross-hybridization to mRNA encoding structurally- and functionally-related proteins, can usefully be the same as the high stringency conditions but with reduction in
5 temperature for hybridization and washing to room temperature (approximately 25°C).

When intended for use in solution phase hybridization, the maximum size of the single exon probes of the present invention is dictated by the proximity of
10 other expressed exons in genomic DNA: although each single exon probe can include intergenic and/or intronic material contiguous to the ORF in the human genome, each probe of the present invention will include portions of only one expressed exon.

15 Thus, each single exon probe will include no more than about 25 kb of contiguous genomic sequence, more typically no more than about 20 kb of contiguous genomic sequence, more usually no more than about 15 kb, even more usually no more than about 10 kb. Usually, probes that are
20 maximally about 5 kb will be used, more typically no more than about 3 kb.

It will be appreciated that the Sequence Listing appended hereto presents, by convention, only that strand of the probe and ORF sequence that can be directly
25 translated reading from 5' to 3' end. As would be well understood by one of skill in the art, single stranded probes must be complementary in sequence to the ORF as present in an mRNA; it is well within the skill in the art to determine such complementary sequence. It will further
30 be understood that double stranded probes can be used in both solution-phase hybridization and microarray-based hybridization if suitably denatured.

Thus, it is an aspect of the present invention to provide single-stranded nucleic acid probes that have
35 sequence complementary to those described herein above and

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below, and double-stranded probes one strand of which has sequence complementary to the probes described herein.

The probes can, but need not, contain intergenic and/or intronic material that flanks the ORF, on one or both sides, in the same linear relationship to the ORF that the intergenic and/or intronic material bears to the ORF in genomic DNA. The probes do not, however, contain nucleic acid derived from more than one expressed ORF.

And when intended for use in solution hybridization, the probes of the present invention can usefully have detectable labels. Nucleic acid labels are well known in the art, and include, *inter alia*, radioactive labels, such as ^3H , ^{32}P , ^{33}P , ^{35}S , ^{125}I , ^{131}I ; fluorescent labels, such as Cy3, Cy5, Cy5.5, Cy7, SYBR[®]

Green and other labels described in Haugland, *Handbook of Fluorescent Probes and Research Chemicals*, 7th ed., Molecular Probes Inc., Eugene, OR (2000), or fluorescence resonance energy transfer tandem conjugates thereof; labels suitable for chemiluminescent and/or enhanced chemiluminescent detection; labels suitable for ESR and NMR detection; and labels that include one member of a specific binding pair, such as biotin, digoxigenin, or the like.

The probes, either in quantity sufficient for hybridization or sufficient for amplification, can be provided in individual vials or containers.

Alternatively, such probes can usefully be packaged as a plurality of such individual genome-derived single exon probes.

When provided as a collection of plural individual probes, the probes are typically made available in amplifiable form in a spatially-addressable ordered set, typically one per well of a microtiter dish. Although a 96 well microtiter plate can be used, greater efficiency is obtained using higher density arrays.

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If, as earlier mentioned, the ORF-specific 5' primers used for genomic amplification had a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification had a second, different, common sequence added thereto, a single set of 5' and 3' primers can be used to amplify all of the probes from the amplifiable ordered set.

Such collections of genome-derived single exon probes can usefully include a plurality of probes chosen for the common attribute of expression in the human heart.

In such defined subsets, typically at least 50, 60, 75, 80, 85, 90 or 95% or more of the probes will be chosen by their expression in the defined tissue or cell type.

The single exon probes of the present invention, as well as fragments of the single exon probes comprising selectively hybridizable portions of the probe ORF, can be used to obtain the full length cDNA that includes the ORF by (i) screening of cDNA libraries; (ii) rapid amplification of cDNA ends ("RACE"); or (iii) other conventional means, as are described, *inter alia*, in Ausubel et al. and Maniatis et al.

It is another aspect of the present invention to provide genome-derived single exon nucleic acid microarrays useful for gene expression analysis, where the term "microarray" has the meaning given in the definitional section of this description, *supra*.

The invention particularly provides genome-derived single-exon nucleic acid microarrays comprising a plurality of probes known to be expressed in human heart. In preferred embodiments, the present invention provides human genome-derived single exon microarrays comprising a plurality of probes drawn from the group consisting of SEQ ID NOS.: 1 - 9,980.

When used for gene expression analysis, the

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genome-derived single exon microarrays provide greater physical informational density than do the genome-derived single exon microarrays that have lower percentages of probes known to be expressed commonly in the tested tissue.

5 At a fixed probe density, for example, a given microarray surface area of the defined subset genome-derived single exon microarray can yield a greater number of expression measurements. Alternatively, at a given probe density, the same number of expression measurements can be obtained from

10 a smaller substrate surface area. Alternatively, at a fixed probe density and fixed surface area, probes can be provided redundantly, providing greater reliability in signal measurement for any given probe. Furthermore, with a higher percentage of probes known to be expressed in the

15 assayed tissue, the dynamic range of the detection means can be adjusted to reveal finer levels discrimination among the levels of expression.

Although particularly described with respect to their utility as probes of gene expression, particularly as

20 probes to be included on a genome-derived single exon microarray, each of the nucleic acids having SEQ ID NOS.: 1 - 9,980 contains an open-reading frame, set forth respectively in SEQ ID NOS.: 9,981 - 19,771, that encodes a protein domain. Thus, each of SEQ ID NOS. 1 - 9,980 can be

25 used, or that portion thereof in SEQ ID NOS. 9,981 - 19,771 used, to express a protein domain by standard in vitro recombinant techniques. See Ausubel et al. and Maniatis et al.

Additionally, kits are available commercially

30 that readily permit such nucleic acids to be expressed as protein in bacterial cells, insect cells, or mammalian cells, as desired (e.g., HAT[™] Protein Expression & Purification System, ClonTech Laboratories, Palo Alto, CA; Adeno-X[™] Expression System, ClonTech Laboratories, Palo

35 Alto, CA; Protein Fusion & Purification (pMAL[™]) System, New

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England Biolabs, Beverley, MA)

- Furthermore, shorter peptides can be chemically synthesized using commercial peptide synthesizing equipment and well known techniques. Procedures are described, *inter alia*, in Chan et al. (eds.), Fmoc Solid Phase Peptide Synthesis: A Practical Approach (Practical Approach Series, (Paper)), Oxford Univ. Press (March 2000) (ISBN: 0199637245); Jones, Amino Acid and Peptide Synthesis (Oxford Chemistry Primers, No 7) , Oxford Univ. Press (August 1992) (ISBN: 0198556683); and Bodanszky, Principles of Peptide Synthesis (Springer Laboratory), Springer Verlag (December 1993) (ISBN: 0387564314).

- It is, therefore, another aspect of the invention to provide peptides comprising an amino acid sequence translated from SEQ ID NOS.: 9,981 - 19,771. Such amino acid sequences are set out in SEQ ID NOS: 19,772 - 29,119. Any such recombinantly-expressed or synthesized peptide of at least 8, and preferably at least about 15, amino acids, can be conjugated to a carrier protein and used to generate antibody that recognizes the peptide. Thus, it is a further aspect of the invention to provide peptides that have at least 8, preferably at least 15, consecutive amino acids.

- The following examples are offered by way of illustration and not by way of limitation.

EXAMPLE 1

- Preparation of Single Exon Microarrays from ORFs Predicted in Human Genomic Sequence

Bioinformatics Results

- All human BAC sequences in fewer than 10 pieces that had been accessioned in a five month period immediately preceding this study were downloaded from

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GenBank. This corresponds to ~2200 clones, totaling ~350 MB of sequence, or approximately 10% of the human genome.

After masking repetitive elements using the program CROSS_MATCH, the sequence was analyzed for open reading frames using three separate gene finding programs. The three programs predict genes using independent algorithmic methods developed on independent training sets: GRAIL uses a neural network, GENEFINDER uses a hidden Markoff model, and DICTION, a program proprietary to Genetics Institute, operates according to a different heuristic. The results of all three programs were used to create a prediction matrix across the segment of genomic DNA.

The three gene finding programs yielded a range of results. GRAIL identified the greatest percentage of genomic sequence as putative coding region, 2% of the data analyzed. GENEFINDER was second, calling 1%, and DICTION yielded the least putative coding region, with 0.8% of genomic sequence called as coding region.

The consensus data were as follows. GRAIL and GENEFINDER agreed on 0.7% of genomic sequence, GRAIL and DICTION agreed on 0.5% of genomic sequence, and the three programs together agreed on 0.25% of the data analyzed. That is, 0.25% of the genomic sequence was identified by all three of the programs as containing putative coding region.

ORFs predicted by any two of the three programs ("consensus ORFs") were assorted into "gene bins" using two criteria: (1) any 7 consecutive exons within a 25 kb window were placed together in a bin as likely contributing to a single gene, and (2) all ORFs within a 25 kb window were placed together in a bin as likely contributing to a single gene if fewer than 7 exons were found within the 25 kb window.

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PCR

The largest ORF from each gene bin that did not span repetitive sequence was then chosen for amplification, as were all consensus ORFs longer than 500 bp. This method approximated one exon per gene; however, a number of genes were found to be represented by multiple elements.

Previously, we had determined that DNA fragments fewer than 250 bp in length do not bind well to the amino-modified glass surface of the slides used as support substrate for construction of microarrays; therefore, amplicons were designed in the present experiments to approximate 500 bp in length.

Accordingly, after selecting the largest ORF per gene bin, a 500 bp fragment of sequence centered on the ORF was passed to the primer picking software, PRIMER3 (available online for use at <http://www-genome.wi.mit.edu/cgi-bin/primer/>). A first additional sequence was commonly added to each ORF-unique 5' primer, and a second, different, additional sequence was commonly added to each ORF-unique 3' primer, to permit subsequent reamplification of the amplicon using a single set of "universal" 5' and 3' primers, thus immortalizing the amplicon. The addition of universal priming sequences also facilitates sequence verification, and can be used to add a cloning site should some ORFs be found to warrant further study.

The ORFs were then PCR amplified from genomic DNA, verified on agarose gels, and sequenced using the universal primers to validate the identity of the amplicon to be spotted in the microarray.

Primers were supplied by Operon Technologies (Alameda, CA). PCR amplification was performed by standard techniques using human genomic DNA (Clontech, Palo Alto, CA) as template. Each PCR product was verified by SYBR[®] green (Molecular Probes, Inc., Eugene, OR) staining of

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agarose gels, with subsequent imaging by Fluorimager (Molecular Dynamics, Inc., Sunnyvale, CA). PCR amplification was classified as successful if a single band appeared.

- 5 The success rate for amplifying ORFs of interest directly from genomic DNA using PCR was approximately 75%. FIG. 5 graphs the distribution of predicted ORF (exon) length and distribution of amplified PCR products, with ORF length shown in red and PCR product length shown in blue
- 10 (which may appear black in the figure). Although the range of ORF sizes is readily seen to extend to beyond 900 bp, the mean predicted exon size was only 229 bp, with a median size of 150 bp (n=9498). With an average amplicon size of 475 ± 25 bp, approximately 50% of the average PCR
- 15 amplification product contained predicted coding region, with the remaining 50% of the amplicon containing either intron, intergenic sequence, or both.

- Using a strategy predicated on amplifying about 500 bp, it was found that long exons had a higher PCR
- 20 failure rate. To address this, the bioinformatics process was adjusted to amplify 1000, 1500 or 2000 bp fragments from exons larger than 500 bp. This improved the rate of successful amplification of exons exceeding 500 bp, constituting about 9.2% of the exons predicted by the gene
- 25 finding algorithms.

- Approximately 75% of the probes disposed on the array (90% of those that successfully PCR amplified) were sequence-verified by sequencing in both the forward and reverse direction using MegaBACE sequencer (Molecular
- 30 Dynamics, Inc., Sunnyvale, CA), universal primers, and standard protocols.

- Some genomic clones (BACs) yielded very poor PCR and sequencing results. The reasons for this are unclear, but may be related to the quality of early draft sequence
- 35 or the inclusion of vector and host contamination in some

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submitted sequence data.

Although the intronic and intergenic material flanking coding regions could theoretically interfere with hybridization during microarray experiments, subsequent empirical results demonstrated that differential expression ratios were not significantly affected by the presence of noncoding sequence. The variation in exon size was similarly found not to affect differential expression ratios significantly; however, variation in exon size was observed to affect the absolute signal intensity (data not shown).

The 350 MB of genomic DNA was, by the above-described process, reduced to 9750 discrete probes, which were spotted in duplicate onto glass slides using commercially available instrumentation (MicroArray GenII Spotter and/or MicroArray GenIII Spotter, Molecular Dynamics, Inc., Sunnyvale, CA). Each slide additionally included either 16 or 32 *E. coli* genes, the average hybridization signal of which was used as a measure of background biological noise.

Each of the probe sequences was BLASTed against the human EST data set, the NR data set, and SwissProt GenBank (May 7, 1999 release 2.0.9).

One third of the probe sequences (as amplified) produced an exact match (BLAST Expect ("E") values less than 1×10^{-100}) to either an EST (20% of sequences) or a known mRNA (13% of sequences). A further 22% of the probe sequences showed some homology to a known EST or mRNA (BLAST E values from 1×10^{-5} to 1×10^{-99}). The remaining 45% of the probe sequences showed no significant sequence homology to any expressed, or potentially expressed, sequences present in public databases.

All of the probe sequences (as amplified) were then analyzed for protein similarities with the SwissProt database using BLASTX, Gish et al., *Nature Genet.* 3:266

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(1993). The predicted functional breakdowns of the 2/3 of probes identical or homologous to known sequences are presented in Table 1.

5

Table 1

Function of Predicted ORFs As Deduced From Comparative Sequence Analysis			
Total	V6 chip	V7 chip	Function Predicted from Comparative Sequence Analysis
211	96	115	Receptor
120	43	77	Zinc Finger
30	11	19	Homeobox
25	9	16	Transcription Factor
17	11	7	Transcription
118	57	61	Structural
95	39	56	Kinase
36	18	18	Phosphatase
83	31	52	Ribosomal
45	19	26	Transport
21	17	14	Growth Factor
17	12	5	Cytochrome
50	33	17	Channel

As can be seen, the two most common types of genes were transcription factors and receptors, making up 2.2% and 1.8% of the arrayed elements, respectively.

10

EXAMPLE 2

Gene Expression Measurements From Genome-Derived Single Exon Microarrays

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The two genome-derived single exon microarrays prepared according to Example 1 were hybridized in a series of simultaneous two-color fluorescence experiments to (1) Cy3-labeled cDNA synthesized from message drawn individually from each of brain, heart, liver, fetal liver, placenta, lung, bone marrow, HeLa, BT 474, or HBL 100 cells, and (2) Cy5-labeled cDNA prepared from message pooled from all ten tissues and cell types, as a control in each of the measurements. Hybridization and scanning were carried out using standard protocols and Molecular Dynamics equipment.

Briefly, mRNA samples were bought from commercial sources (Clontech, Palo Alto, CA and Amersham Pharmacia Biotech (APB)). Cy3-dCTP and Cy5-dCTP (both from APB) were incorporated during separate reverse transcriptions of 1 µg of polyA⁺ mRNA performed using 1 µg oligo(dT)12-18 primer and 2 µg random 9mer primers as follows. After heating to 70°C, the RNA:primer mixture was snap cooled on ice. After snap cooling on ice, added to the RNA to the stated final concentration was: 1X Superscript II buffer, 0.01 M DTT, 100µM dATP, 100 µM dGTP, 100 µM dTTP, 50 µM dCTP, 50 µM Cy3-dCTP or Cy5-dCTP 50 µM, and 200 U Superscript II enzyme. The reaction was incubated for 2 hours at 42°C. After 2 hours, the first strand cDNA was isolated by adding 1 U Ribonuclease H, and incubating for 30 minutes at 37°C. The reaction was then purified using a Qiagen PCR cleanup column, increasing the number of ethanol washes to 5. Probe was eluted using 10 mM Tris pH 8.5.

Using a spectrophotometer, probes were measured for dye incorporation. Volumes of both Cy3 and Cy5 cDNA corresponding to 50 pmoles of each dye were then dried in a Speedvac, resuspended in 30 µl hybridization solution containing 50% formamide, 5X SSC, 0.2 µg/µl poly(dA), 0.2 µg/µl human c₅t1 DNA, and 0.5 % SDS.

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Hybridizations were carried out under a coverslip, with the array placed in a humid oven at 42°C overnight. Before scanning, slides were washed in 1X SSC, 0.2% SDS at 55°C for 5 minutes, followed by 0.1X SSC, 0.2% SDS, at 55°C for 20 minutes. Slides were briefly dipped in water and dried thoroughly under a gentle stream of nitrogen.

Slides were scanned using a Molecular Dynamics Gen3 scanner, as described. Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376).

Although the use of pooled cDNA as a reference permitted the survey of a large number of tissues, it attenuates the measurement of relative gene expression, since every highly expressed gene in the tissue/cell type-specific fluorescence channel will be present to a level of at least 10% in the control channel. Because of this fact, both signal and expression ratios (the latter hereinafter, "expression" or "relative expression") for each probe were normalized using the average ratio or average signal, respectively, as measured across the whole slide.

Data were accepted for further analysis only when signal was at least three times greater than biological noise, the latter defined by the average signal produced by the *E. coli* control genes.

The relative expression signal for these probes was then plotted as function of tissue or cell type, and is presented in FIG. 6.

FIG. 6 shows the distribution of expression across a panel of ten tissues. The graph shows the number of sequence-verified products that were either not expressed ("0"), expressed in one or more but not all tested tissues ("1" - "9"), and expressed in all tissues tested ("10").

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Of 9999 arrayed elements on the two microarrays (including positive and negative controls and "failed" products), 2353 (51%) were expressed in at least one tissue or cell type. Of the gene elements showing significant
5 signal -- where expression was scored as "significant" if the normalized Cy3 signal was greater than 1, representing signal 5-fold over biological noise (0.2) -- 39% (991) were expressed in all 10 tissues. The next most common class (15%) consisted of gene elements expressed in only a single
10 tissue.

The genes expressed in a single tissue were further analyzed, and the results of the analyses are compiled in FIG. 7.

FIG. 7A is a matrix presenting the expression of
15 all verified sequences that showed expression greater than 3 in at least one tissue. Each clone is represented by a column in the matrix. Each of the 10 tissues assayed is represented by a separate row in the matrix, and relative expression of a clone in that tissue is indicated at the
20 respective node by intensity of green shading, with the intensity legend shown in panel B. The top row of the matrix ("EST Hit") contains "bioinformatic" rather than "physical" expression data -- that is, presents the results returned by query of EST, NR and SwissProt databases using
25 the probe sequence. The legend for "bioinformatic expression" (i.e., degree of homology returned) is presented in panel C. Briefly, white is known, black is novel, with gray depicting nonidentical with significant homology (white: E values < 1e-100; gray: E values from 1e-
30 05 to 1e-99; black: E values > 1e-05).

As FIG. 7 readily shows, heart and brain were demonstrated to have the greatest numbers of genes that were shown to be uniquely expressed in the respective tissue. In brain, 200 uniquely expressed genes were
35 identified; in heart, 150. The remaining tissues gave the

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following figures for uniquely expressed genes: liver, 100; lung, 70; fetal liver, 150; bone marrow, 75; placenta, 100; HeLa, 50; HBL, 100; and BT474, 50.

It was further observed that there were many more "novel" genes among those that were up-regulated in only one tissue, as compared with those that were down-regulated in only one tissue. In fact, it was found that ORFs whose expression was measurable in only a single of the tested tissues were represented in sequencing databases at a rate of only 11%, whereas 36% of the ORFs whose expression was measurable in 9 of the tissues were present in public databases. As for those ORFs expressed in all ten tissues, fully 45% were present in existing expressed sequence databases. These results are not unexpected, since genes expressed in a greater number of tissues have a higher likelihood of being, and thus of having been, discovered by EST approaches.

Comparison of Signal from Known and Unknown Genes

The normalized signal of the genes found to have high homology to genes present in the GenBank human EST database were compared to the normalized signal of those genes not found in the GenBank human EST database. The data are shown in FIG. 8.

FIG. 8 shows the normalized Cy3 signal intensity for all sequence-verified products with a BLAST Expect ("E") value of greater than $1e-30$ (designated "unknown") upon query of existing EST, NR and SwissProt databases, and shows in blue the normalized Cy3 signal intensity for all sequence-verified products with a BLAST Expect value of less than $1e-30$ ("known"). Note that biological background noise has an averaged normalized Cy3 signal intensity of 0.2.

As expected, the most highly expressed of the ORFs were "known" genes. This is not surprising, since

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very high signal intensity correlates with very commonly-expressed genes, which have a higher likelihood of being found by EST sequence.

However, a significant point is that a large number of even the high expressers were "unknown". Since the genomic approach used to identify genes and to confirm their expression does not bias exons toward either the 3' or 5' end of a gene, many of these high expression genes will not have been detected in an end-sequenced cDNA library.

The significant point is that presence of the gene in an EST database is *not* a prerequisite for incorporation into a genome-derived microarray, and further, that arraying such "unknown" exons can help to assign function to as-yet undiscovered genes.

Verification of Gene Expression

To ascertain the validity of the approach described above to identify genes from raw genomic sequence, expression of two of the probes was assayed using reverse transcriptase polymerase chain reaction (RT-PCR) and northern blot analysis.

Two microarray probes were selected on the basis of exon size, prior sequencing success, and tissue-specific gene expression patterns as measured by the microarray experiments. The primers originally used to amplify the two respective ORFs from genomic DNA were used in RT-PCR against a panel of tissue-specific cDNAs (Rapid-Scan gene expression panel 24 human cDNAs) (OriGene Technologies, Inc., Rockville, MD).

Sequence AL079300_1 was shown by microarray hybridization to be present in cardiac tissue, and sequence AL031734_1 was shown by microarray experiment to be present in placental tissue (data not shown). RT-PCR on these two sequences confirmed the tissue-specific gene expression as

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measured by microarrays, as ascertained by the presence of a correctly sized PCR product from the respective tissue type cDNAs.

Clearly, all microarray results cannot, and indeed should not, be confirmed by independent assay methods, or the high throughput, highly parallel advantages of microarray hybridization assays will be lost. However, in addition to the two RT-PCR results presented above, the observation that 1/3 of the arrayed genes exist in expression databases provides powerful confirmation of the power of our methodology - which combines bioinformatic prediction with expression confirmation using genome-derived single exon microarrays - to identify novel genes from raw genomic data.

To verify that the approach further provides correct characterization of the expression patterns of the identified genes, a detailed analysis was performed of the microarrayed sequences that showed high signal in brain.

For this latter analysis, sequences that showed high (normalized) signal in brain, but which showed very low (normalized) signal (less than 0.5, determined to be biological noise) in all other tissues, were further studied. There were 82 sequences that fit these criteria, approximately 2% of the arrayed elements. The 10 sequences showing the highest signal in brain in microarray hybridizations are detailed in Table 2, along with assigned function, if known or reasonably predicted.

Table 2

Function of the Most Highly Expressed Genes Expressed Only in Brain
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Microarray Sequence Name	Normal ized Signal	Expressi on Ratio	Homology to EST present in GenBank	Gene Function as described by GenBank
AP000217-1	5.2	+7.7	High	S-100 protein, b-chain, Ca ²⁺ binding protein expressed in central nervous system
AP000047-1	2.3		High	Unknown Function
AC006548-9	1.7		High	Similar to mouse membrane glyco-protein M6, expressed in central nervous system
AC007245-5	1.5		High	Similar to amphiphysin, a synaptic vesicle- associated protein. Ref 21
L44140-4	1.2	+2.0	High	Endothelial actin-binding protein found in nonmuscle filamin

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AC004689-9	1.2	+3.5	High	Protein Phosphatase PP2A, neuronal/ downregulates activated protein kinases
AL031657-1	1.2	+3.0	High	Unknown function/ Contains the anhyrin motif, a common protein sequence motif
AC009266-2	1.1	+3.7	Low	Low homology to the Synaptotagmin I protein in rat/present at low levels throughout rat brain
AP000086-1	1.0	+2.7	Low	Unknown, very poor homology to collagen
AC004689-3	1.0		High	Protein Phosphatase PP2A, neuronal/ downregulates activated protein kinases

Of the ten sequences studied by these latter confirmatory approaches, eight were previously known. Of these eight, six had previously been reported to be important in the central nervous system or brain. The exon

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giving the highest signal (AP00217-1) was found to be the gene encoding an S100B Ca^{2+} binding protein, reported in the literature to be highly and uniquely expressed in the central nervous system. Heizmann, *Neurochem. Res.* 9:1097
5 (1997).

A number of the brain-specific probe sequences (including AC006548-9, AC009266-2) did not have homology to any known human cDNAs in GenBank but did show homology to rat and mouse cDNAs. Sequences AC004689-9 and AC004689-3
10 were both found to be phosphatases present in neurons (Millward *et al.*, *Trends Biochem. Sci.* 24(5):186-191 (1999)). Two microarray sequences, AP000047-1 and AP000086-1 have unknown function, with AP000086-1 being absent from GenBank. Functionality can now be narrowed
15 down to a role in the central nervous system for both of these genes, showing the power of designing microarrays in this fashion.

Next, the function of the chip sequences with the highest (normalized) signal intensity in brain, regardless
20 of expression in other tissues, was assessed. In this latter analysis, we found expression of many more common genes, since the sequences were not limited to those expressed only in brain. For example, looking at the 20 highest signal intensity spots in brain, 4 were similar to
25 tubulin (AC00807905; AF146191-2; AC007664-4; AF14191-2), 2 were similar to actin (AL035701-2; AL034402-1), and 6 were found to be homologous to glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (AL035604-1; Z86090-1; AC006064-L, AC006064-K; AC035604-3; AC006064-L). These genes are often
30 used as controls or housekeeping genes in microarray experiments of all types.

Other interesting genes highly expressed in brain were a ferritin heavy chain protein, which is reported in the literature to be found in brain and liver (Joshi *et al.*, *J. Neurol. Sci.* 134(Suppl):52-56 (1995)), a result
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duplicated with the array. Other highly expressed chip sequences included a translation elongation factor 1 α (AC007564-4), a DEAD-box homolog (AL023804-4), and a Y-chromosome RNA-binding motif (Chai et al., *Genomics* 49(2):283-89 (1998)) (AC007320-3). A low homology analog (AP00123-1/2) to a gene, DSCR1, thought to be involved in trisomy 21 (Down's syndrome), showed high expression in both brain and heart, in agreement with the literature (Fuentes et al., *Mol. Genet.* 4(10):1935-44 (1995)).

- As a further validation of the approach, we selected the BAC AC006064 to be included on the array. This BAC was known to contain the GAPDH gene, and thus could be used as a control for the ORF selection process. The gene finding and exon selection algorithms resulted in choosing 25 exons from BAC AC006064 for spotting onto the array, of which four were drawn from the GAPDH gene. Table 3 shows the comparison of the average expression ratio for the 4 exons from BAC006064 compared with the average expression ratio for 5 different dilutions of a commercially available GAPDH cDNA (Clontech).

Table 3

Comparison of Expression Ratio, for each tissue, of GAPDH		
	AC006064 (n = 4)	Control (n = 5)
Bone Marrow	-1.81 \pm 0.11	-1.85 \pm 0.08
Brain	-1.41 \pm 0.11	-1.17 \pm 0.05
BT474	1.85 \pm 0.09	1.66 \pm 0.12
Fetal Liver	-1.62 \pm 0.07	-1.41 \pm 0.05
HBL100	1.32 \pm 0.05	2.64 \pm 0.12
Heart	1.16 \pm 0.09	1.56 \pm 0.10
HeLa	1.11 \pm 0.06	1.30 \pm 0.15
Liver	-1.62 \pm 0.22	-2.07 \pm

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Lung	-4.95 ± 0.93	-3.75 ± 0.21
Placenta	-3.56 ± 0.25	-3.52 ± 0.43

Each tissue shows excellent agreement between the experimentally chosen exons and the control, again demonstrating the validity of the present exon mining approach. In addition, the data also show the variability of expression of GAPDH within tissues, calling into question its classification as a housekeeping gene and utility as a housekeeping control in microarray experiments.

EXAMPLE 3

Representation of Sequence and Expression Data as a "Mondrian"

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For each genomic clone processed for microarray as above-described, a plethora of information was accumulated, including full clone sequence, probe sequence within the clone, results of each of the three gene finding programs, EST information associated with the probe sequences, and microarray signal and expression for multiple tissues, challenging our ability to display the information.

Accordingly, we devised a new tool for visual display of the sequence with its attendant annotation which, in deference to its visual similarity to the paintings of Piet Mondrian, is hereinafter termed a "Mondrian". FIGS. 3 and 4 present the key to the information presented on a Mondrian.

FIG. 9 presents a Mondrian of BAC AC008172 (bases 25,000 to 130,000 shown), containing the carbamyl phosphate synthetase gene (AF154830.1). Purple background within the region shown as field 81 in FIG. 3 indicates all 37 known

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exons for this gene.

As can be seen, GRAIL II successfully identified 27 of the known exons (73%), GENEFINDER successfully identified 37 of the known exons (100%), while DICTION 5 identified 7 of the known exons (19%).

Seven of the predicted exons were selected for physical assay, of which 5 successfully amplified by PCR and were sequenced. These five exons were all found to be from the same gene, the carbamyl phosphate synthetase gene 10 (AF154830.1).

The five exons were arrayed, and gene expression measured across 10 tissues. As is readily seen in the Mondrian, the five chip sequences on the array show identical expression patterns, elegantly demonstrating the 15 reproducibility of the system.

FIG. 10 is a Mondrian of BAC AL049839. We selected 12 exons from this BAC, of which 10 successfully sequenced, which were found to form between 5 and 6 genes. Interestingly, 4 of the genes on this BAC are protease 20 inhibitors. Again, these data elegantly show that exons selected from the same gene show the same expression patterns, depicted below the red line. From this figure, it is clear that our ability to find known genes is very good. A novel gene is also found from 86.6 kb to 88.6 kb, 25 upon which all the exon finding programs agree. We are confident we have two exons from a single gene since they show the same expression patterns and the exons are proximal to each other. Backgrounds in the following colors indicate a known gene (top to bottom):

30 red = kallistatin protease inhibitor (P29622);
purple = plasma serine protease inhibitor (P05154);
turquoise = α 1 anti-chymotrypsin (P01011); mauve = 40S ribosomal protein (P08865). Note that chip sequence 8 and 12 did not sequence verify.

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EXAMPLE 4Genome-Derived Single Exon Probes Useful For Measuring
Human Gene Expression

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The protocols set forth in Examples 1 and 2, *supra*, were applied to additional human genomic sequence as it became newly available in GenBank to identify unique exons in the human genome that could be shown to be expressed at significant levels in heart tissue.

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These unique exons are within longer probe sequences. Each probe was completely sequenced on both strands prior to its use on a genome-derived single exon microarray; sequencing confirms the exact chemical structure of each probe. An added benefit of sequencing is that it placed us in possession of a set of single base-incremented fragments of the sequenced nucleic acid, starting from the sequencing primer 3' OH. (Since the single exon probes were first obtained by PCR amplification from genomic DNA, we were of course additionally in possession of an even larger set of single base incremented fragments of each of the 9,980 single exon probes, each fragment corresponding to an extension product from one of the two amplification primers.)

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The structures of the 9,980 unique single exon probes are clearly presented in the Sequence Listing as SEQ ID Nos.: 1 - 9,980. The 16 nt 5' primer sequence and 16 nt 3' primer sequence present on the amplicon are not included in the sequence listing. The sequences of the exons present within each of these probes is presented in the Sequence Listing as SEQ ID Nos.: 9,981 - 19,771, respectively. It will be noted that some amplicons have more than one exon, some exons are contained in more than one amplicon.

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As detailed in Example 2, expression was

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demonstrated by disposing the amplicons as single exon probes on nucleic acid microarrays and then performing two-color fluorescent hybridization analysis; significant expression is based on a statistical confidence that the signal is significantly greater than negative biological control spots. The negative biological control is formed from spotted DNA sequences from a different species. Here, 32 sequences from E.Coli were spotted in duplicate to give a total of 64 spots.

For each hybridisation (each slide, each colour) the median value of the signal from all of the spots is determined. The normalised signal value is the arithmetic mean of the signal from duplicate spots divided by the population median.

Control spots are eliminated if there is more than a five-fold difference between each one of the duplicate spots raw signals.

The median of the signal from the remaining control spots is calculated and all subsequent calculations are done with normalised signals.

Control spots having a signal of greater than median + 2.4 (the value 2.4 is roughly 12 times the observed standard deviation of control spot populations) are eliminated. Spots with such high signals are considered to be "outliers".

The mean and standard deviation of the modified control spot populations are calculated.

The mean + 3x the standard deviation (mean + (3*SD)) is used as the signal threshold qualifier for that particular hybridisation. Thus, individual thresholds are determined for each channel and each hybridisation.

This means that, assuming that the data is distributed normally, there is a 99% confidence that any signal exceeding the threshold is significant.

The probes and their expression data are

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presented in Table 4, set forth respectively in Example 5. Example 5 presents the subset of probes that is significantly expressed in the human heart and thus presents the subset of probes that was recognized to be useful for measuring expression of their cognate genes in human heart tissue.

The sequence of each of the exon probes identified by SEQ ID NOS.: 9,981 - 19,771 was individually used as a BLAST (or, for SWISSPROT, BLASTX) query to identify the most similar sequence in each of dbEST, SwissProt (BLASTX), and NR divisions of GenBank. Because the query sequences are themselves derived from genomic sequence in GenBank, only nongenic hits from NR were scored.

The smallest in value of the BLAST (or BLASTX) expect ("E") scores for each query sequence across the three database divisions was used as a measure of the "expression novelty" of the probe's ORF. Table 4 is sorted in descending order based on this measure, reported as "Most Similar (top) Hit BLAST E Value". Those sequences for which no "Hit E Value" is listed are those exons which were found to have no similar sequences.

As sorted, Table 4 thus lists its respective probes (by "AMPLICON SEQ ID NO.:" and additionally by the SEQ ID NO.: of the exon contained within the probe: "EXON SEQ ID NO.:" from least similar to sequences known to be expressed (i.e., highest BLAST E value), at the beginning of the table, to most similar to sequences known to be expressed (i.e., lowest BLAST E value), at the bottom of the table.

Table 4 further provides, for each listed probe, the accession number of the database sequence that yielded the "Most Similar (top) Hit BLAST E Value", along with the name of the database in which the database sequence is found ("Top Hit Database Source").

Table 4 further provides SEQ ID NOS.

corresponding to the predicted amino acid sequences where they have been determined for the probe and exon nucleotide sequences. These are set out as PEPTIDE SEQ ID NOS.: The peptide sequences for a given exon are predicted as follows: Since each chip exon is a consensus sequence drawn from predictions from various exon finding programs (i.e. Grail, GeneFinder and GenScan), the multiple initial ORFs are first determined in a uniform way according to each prediction. In particular, the reading frame for predicting the first amino acid in the peptide sequence always starts with the first base of any codon and ends with the last base of non-termination codon. Next, for each strand of the exon, initial ORFs are merged into one or more final ORFs in an exhaustive process based on the following criteria: 1) the merging ORFs must be overlapping, and 2) the merging ORFs must be in the same frame.

The Sequence Listing, which is a superset of all of the data presented in Table 4, further includes, for each probe, the most similar hit, with accession number and BLAST E value, from the each of the three queried databases.

Table 4 further lists, for each probe, a portion of the descriptor for the top hit ("Top Hit Descriptor") as provided in the sequence database. For those ORFs that are similar in sequence, but nonidentical to known sequences (e.g., those with BLAST E values between about $1e-05$ and $1e-100$), the descriptor reveals the likely function of the protein encoded by the probe's ORF.

Using BLAST E value cutoffs of $1e-05$ (i.e., 1×10^{-5}) and $1e-100$ (i.e., 1×10^{-100}) as evidence of similarity to sequences known to be expressed is of course arbitrary: in Example 2, *supra*, a BLAST E value of $1e-30$ was used as the boundary when only two classes were to be defined for analysis (unknown, $>1e-30$; known $<1e-30$) (see also FIG. 8).

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Furthermore, even when the "Most Similar (Top) Hit BLAST E Value" is low, *e.g.*, less than about $1e-100$ - which is probative evidence that the query sequence has previously been shown to be expressed - the top hit is highly unlikely
5 exactly to match the probe sequence.

First, such expression entries typically will not have the intronic and/or intergenic sequence present within the single exon probes listed in the Table. Second, even the ORF itself is unlikely in such cases to be present
10 identically in the databases, since most of the EST and mRNA clones in existing databases include multiple exons, without any indication of the location of exon boundaries.

As noted, the data presented in Table 4 represent a proper subset of the data present within the attached
15 sequence listing. For each amplicon probe (SEQ ID NOs.: 1 - 9,980) and probe exon (SEQ ID NOs.: 9,981 - 19,771, respectively), the sequence listing further provides, through iterated annotation fields <220> and <223>:

. . (a) the accession number of the BAC from which
20 the sequence was derived ("MAP TO"), thus providing a link to the chromosomal map location and other information about the genomic milieu of the probe sequence;

(b) the most similar sequence provided by BLAST query of the EST database, with accession number and BLAST
25 E value for the "hit";

(c) the most similar sequence provided by BLAST query of the GenBank NR database, with accession number and BLAST E value for the "hit"; and

(d) the most similar sequence provided by BLASTX
30 query of the SWISSPROT database, with accession number and BLAST E value for the "hit".

EXAMPLE 5

35 Genome-Derived Single Exon Probes Useful For Measuring

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Expression of Genes in Human Heart

Table 4 (413 pages) presents expression, homology, and functional information for the genome-derived single exon probes that are expressed significantly in human heart.

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
442	10386	20209	4.41				
871	10797	20647	17.08				
1028	10847		2.14				
1280	11188	21038	1.97				
1597	11501	21361	1.87				
1818	11523	21381	4.97				
1894	11596	21487	1.01				
1715	11816	21485	0.95				
1721	11822	21481	7.45				
4548	11744	21690	0.98				
1855	11930	21719	3.03				
2118	12005	21807	2.82				
2283	12113	22520	2.34				
3148	13074	22575	3.71				
3405	13320	23121	1.52				
3471	13397	23162	8.97				
3513	13429		0.87				
3507	13521	23506	0.66				
4102	14002	23751	1.71				
4164	14054	23838	5.64				
4184	14084	23855	0.80				
4184	14084	23859	0.80				
4242	14141		1.03				
4730	14616	24402	1.76				
4779	14693		0.78				
4876	14851	24617	5.08				
4888	14893	24629	2.07				
5217	15140	24934	1.92				
5217	15140	24935	1.92				
5328	15248		5				
5436	15359		5.80				
5483	15248		4.9				
5508	15427	25490	2.9				
5988	19451	25978	1.6				

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar Clustal BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5860	15566	25700	1.41				
5863	15769		1.84				
6332	16244	29404	1.61				
6332	16244	29405	1.61				
6967	16577	29769	1.29				
6942	16820	27012	1.3				
7484	17344	27569	3.58				
7894	17634	27758	1.26				
8070	17901		3.7				
8219	18472	26355	2.31				
8390	19246		2.84				
8666	19555	26840	2.91				
8757	17606	26150	1.73				
8757	17606	26151	1.73				
8762	18048		2.18				
8464	19034		1.62				
8760	19230	25220	2.11				
8831	19500	25701	4.31	9.8E+00 AJ259238.1	NT		Homo sapiens LSS gene, partial, exons 15, 16, 17 and 18
8859	19548	26745	1.34	9.8E+00 U32716.1	NT		Haemophilus influenzae Rd section 31 of 183 of the complete genome
7855	17805	28046	1.32	9.8E+00 AF242432.1	NT		Mus musculus Naps1 gene, exon 1; neuronal apoptosis inhibitory protein 1 (Naps1) and general transcription factor 1H polypeptide 2 (Clf2n2) genes, complete cds
7855	17805	28047	1.32	9.8E+00 AF242432.1	NT		Mus musculus Naps1 gene, exon 1; neuronal apoptosis inhibitory protein 1 (Naps1) and general transcription factor 1H polypeptide 2 (Clf2n2) genes, complete cds
2631	12498	22389	2.72	9.4E+00 L11433.1	NT		Dengue virus type 3 membrane protein (pM)/envelope glycoprotein (E) polyprotein mRNA, partial cds
2631	12498	22390	2.72	9.4E+00 L11433.1	NT		Dengue virus type 3 membrane protein (pM)/envelope glycoprotein (E) polyprotein mRNA, partial cds
2663	12820	22612	5.91	9.4E+00 AB04785.1	NT		Mus musculus A13 gene for anthraxin, complete cds
7208	17083	27271	2.97	9.3E+00 P11210	SWISSPROT		IMMEDIATE-EARLY PROTEIN 1 (IE1) (IMMEDIATE-EARLY PHOSPHOPROTEIN PP88)
5239	15163	24832	2.07	9.1E+00 AF096609.1	NT		Leuciscus cephalus ornithalis cytochrome b (cyt b) gene, partial cds; mitochondrial gene for mitochondrial product
5239	15163	24693	2.07	9.1E+00 AF096609.1	NT		Leuciscus cephalus ornithalis cytochrome b (cyt b) gene, partial cds; mitochondrial gene for mitochondrial product
5578	15587	25687	9.51	9.8E+00 BE571006.1	EST HUMAN		001051038T1 NH1 MGCC 81 Homo sapiens cDNA clone IMAGE:383492.3'

Single Exon Probes Expressed in Heart

Probe Seq ID	Exon Seq ID	ORF Seq ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
9848	16754	28871	1.71	8.7E+00	A3010788.1	NT	OmpA pyrophosphatase Cpl32d premature mRNA, partial cds
9848	16754	28872	1.71	8.7E+00	A3010788.1	NT	OmpA2 pyrophosphatase Cpl32c premature mRNA, partial cds
7439	10452	20199	1.78	8.4E+00	S333804.1	NT	Homo sapiens insulin receptor substrate 1 (IRS) mRNA
8599	18381	26842	3.68	8.0E+00	AJ137719.1	NT	Zen mink RNA for influenza virus protein (zeza)
8599	18381	26842	2.31	8.0E+00	P41820	SWISSPROT	BRELF1 A RESISTANCE PROTEIN
8348	10209	26781	2.07	7.9E+00	AL445085.1	NT	Thermococcus acidophilum complete genome, segment 3/5
8698	16747	28840	1.53	7.5E+00	P39341	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
8698	16747	28841	1.53	7.5E+00	P39341	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
5544	14560	26851	2.88	7.4E+00	BF700517.1	EST_HUMAN	HISTONE-RICH GLYCOPROTEIN PRECURSOR
7085	16662	27155	3.83	7.4E+00	P04029	SWISSPROT	HISTONE-RICH GLYCOPROTEIN PRECURSOR
7085	16662	27156	3.83	7.4E+00	P04029	SWISSPROT	Lycopodium obscurum Mill. G1 Phase (SAR2) mRNA, complete cds
2947	12781	22671	4.2	7.2E+00	I22051.1	NT	Lycopodium obscurum Mill. G1 Phase (SAR2) mRNA, complete cds
2947	12781	22672	4.2	7.2E+00	I22051.1	NT	Lycopodium obscurum Mill. G1 Phase (SAR2) mRNA, complete cds
6239	16105	26254	1.3	7.1E+00	P28766	SWISSPROT	ZINC-FINGER PROTEIN 1 (ZINC-FINGER HOMEODOMAIN PROTEIN 1)
6239	16105	26255	1.3	7.1E+00	P28766	SWISSPROT	ZINC-FINGER PROTEIN 1 (ZINC-FINGER HOMEODOMAIN PROTEIN 1)
7536	17386	26256	8.48	7.1E+00	AF16593.2	NT	Arabidopsis thaliana DNA chromosome 4, contig1 fragment No. 81
8690	16877	28890	3.26	7.1E+00	P06850	SWISSPROT	HYPOTHETICAL T7.3 KDA PROTEIN IN MRD4-PHP8 INTERGENIC REGION
8690	16877	28890	2.98	7.0E+00	P44910	SWISSPROT	ARGININE KINASE (AK)
7735	17886	28891	2.98	7.0E+00	P44910	SWISSPROT	WD-40 REPEAT PROTEIN MS33
8575	18443	28892	1.85	7.0E+00	O22469	SWISSPROT	60S RIBOSOMAL PROTEIN L4 (L2)
8818	16997	28897	2.72	6.9E+00	P39579	SWISSPROT	DNA MISMATCH REPAIR PROTEIN MUTS
7925	17757	28015	1.3	6.9E+00	P44834	SWISSPROT	zao7c11.1l Scarsa melanoctyca ZN1HM Homo sapiens cDNA clone IMAGE281800.9'
6014	16464	26980	1.45	6.8E+00	W03412.1	EST_HUMAN	zao7c11.1l Scarsa melanoctyca ZN1HM Homo sapiens cDNA clone IMAGE281800.9'
9514	18464	26981	1.45	6.8E+00	W03412.1	EST_HUMAN	zao7c11.1l Scarsa melanoctyca ZN1H (HEMAGGLUTININ) OUTER LAYER CLONED FROM VP4 [CONTAINS: OUTER CAPSID PROTEIN VP4 AND VP8]
7277	17713	27057	1.47	6.8E+00	P06387	SWISSPROT	OUTER CAPSID PROTEINS VP8 AND VP8
7863	17163	27057	3.82	6.8E+00	P06387	SWISSPROT	HYPOTHETICAL 157.0 KDA PROTEIN CB8C10.5 IN CHROMOSOME III
7796	17646	27881	2.1	6.9E+00	Q9Z570	SWISSPROT	URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE)
7796	17646	27882	2.1	6.9E+00	Q9Z570	SWISSPROT	URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE)
8471	18334	27882	2.17	6.9E+00	Q10309	SWISSPROT	PROBABILE CATION-TRANSPORT ATPASE C9C3.04C
7290	17172	27372	8.32	6.9E+00	P03374	SWISSPROT	ENY POLYPROTEIN [CONTAINS: COAT PROTEIN GP92; COAT PROTEIN GP90]
7016	17497	27686	1.44	6.2E+00	A1010501.1	NT	Enchyrtidium commune unknown mRNA
5928	13933	25956	7.16	5.9E+00	AF195142.1	NT	Mus musculus ribbed leucine kinase 3 (MLK3) and two pore domain K ⁺ channel subunit (Kcnltb) genes, complete cds
3479	13595	27881	0.81	5.9E+00	AF195142.1	NT	Homo sapiens DESCT1 protein (DESCT1), mRNA

Table 4

Probe SEQ ID NO:	Even SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Signal	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
6617	16497	26834	2.95	4.1E+00	U67523.1	NT	Pan. troglodytes novel repetitive solo LTR element in the RNUI2 locus
7676	17427	27041	2.31	4.1E+00	BE554263.1	EST_HUMAN	002476508F NIH_MGC_42 Homo sapiens cDNA clone IMAGE:433209.9
8359	18139		2.59	4.1E+00	P08716	SWISSPROT	HYPOPHYSICAL PROTEIN HVJ/ET
8359	18216		12.46	4.1E+00	EE63580.1	EST_HUMAN	601607507F NIH_MGC_71 Homo sapiens cDNA clone IMAGE:500851.9
8672	19231	25341	1.86	4.1E+00	P47378	SWISSPROT	INDUCIBLE GROWTH FACTOR BINDING PROTEIN 1 PRECURSOR (IGFBP-1) (IGF- binding protein 1)
8260	16731	20265	1.37	4.0E+00	Q53310	SWISSPROT	CELL DIVISION PROTEIN FISY/HOMOLG
8768	17817	28104	2.17	4.0E+00	P14848	SWISSPROT	CYTOSOLIC CONDENSE POLYPEPTIDE II
8885	16648	26864	3.34	4.0E+00	P07864	SWISSPROT	GENOME POLYPROTEIN CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE GLYCOPROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)
8885	16648	26865	3.34	4.0E+00	P07864	SWISSPROT	GENOME POLYPROTEIN CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE GLYCOPROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)
3459	13375	23181	3.89	3.9E+00	X64518.1	NT	N. laibacensis terminal vesicle secretory protein 96 (MSVSP96) gene, promoter region
4226	14124		0.86	3.9E+00	AF056460.1	NT	Mus musculus seminal vesicle secretory protein 96 (MSVSP96) gene, promoter region
5471	16391	25454	2.47	3.9E+00	BE514397.1	EST_HUMAN	MR0-BN0070-300050-028-05 BN0070 Homo sapiens cDNA
5471	16391	25454	2.47	3.9E+00	BE514397.1	EST_HUMAN	MR0-BN0070-300050-028-05 BN0070 Homo sapiens cDNA
9108	16021	25140	4.46	3.9E+00	P23207	SWISSPROT	HYPOPHYSICAL TRANSCRIPTIONAL REGULATOR IN ADIR-RPSF INTERGENIC REGION
9355	16218	25379	4.68	3.9E+00	V23007.1	NT	HYPOPHYSICAL TRANSCRIPTIONAL REGULATOR IN ADIR-RPSF INTERGENIC REGION
8940	17619	26913	2.32	3.9E+00	X65605.1	NT	X-lewis mRNA for M4 mucosacillar receptor
8995	17679	28120	3.05	3.9E+00	Y18000.1	NT	Homo sapiens NF2 gene
8715	16532	26816	5.86	3.9E+00	A4661489.1	EST_HUMAN	hBact2.51 NCL CGAP_Ewt Homo sapiens cDNA clone IMAGE:169318 similar to gpA10415
2588	12459		2.4	3.9E+00	AE001682.1	NT	METALLOPROTEINASE INHIBITOR 1 PRECURSOR (HUMAN); Helicodactyl pyroly, strain J69 section 123 of 132 of the complete genome
09411	16769	25982	1.18	3.9E+00	CA4725.1	EST_HUMAN	Helicodactyl pyroly, strain J69 section 123 of 132 of the complete genome
3908	13545	23822	10.99	3.7E+00	AL161539.2	EST_HUMAN	Auribaculopsis thalassica DNA chromosomes 4, contig fragment No. 39
8720	18580	28872	2.06	3.7E+00	BF698278.1	EST_HUMAN	002120051F NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4277746.9
8720	18580	28872	2.13	3.7E+00	BF698278.1	EST_HUMAN	002120051F NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4277746.9
8731	18596	28873	2.13	3.9E+00	AV781055.1	EST_HUMAN	PA071055F Homo sapiens cDNA clone M35BUE10.5
878	15015	20322	2.1	3.9E+00	AE004447.1	EST_HUMAN	Pseudomonas aeruginosa PA01, section 6 of 529 of the complete genome
7022	18559	27091	3.86	3.9E+00	AE004447.1	NT	Pseudomonas aeruginosa PA01, section 6 of 529 of the complete genome
7022	18559	27091	3.86	3.9E+00	AE004447.1	NT	Pseudomonas aeruginosa PA01, section 6 of 529 of the complete genome

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF/SEQ ID NO:	Expression Signal	Mean Similar (Clustal W) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8228	18110		3.76	3.6E-000	M69765.1	NT	Escherichia coli glycerophosphate dehydrogenase (gpd) gene, partial cds, and the translation start site has been verified (gptE), the translation start site has been verified (gptO), and repressor protein (gptR) genes, complete cds
3209	13133	22934	1.04	3.5E-000	AF221533.1	NT	Cryptosporidium falci heat shock protein 70 (HSP70) gene, partial cds
1496	11400	21200	3.57	3.4E-000	AF261677.1	NT	Brucella melitensis RP258 mRNA, complete cds
2532	12408	22268	1.02	3.4E-000	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
6354	18217	29378	2.41	3.4E-000	P04092	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT
7889	17759	27982	3.17	3.4E-000	AF013167.1	NT	Saccharomyces cerevisiae MSS1 gene, complete cds
8919	19831	28919	1.92	3.4E-000	L77570.1	NT	Homo sapiens DGeorge syndrome critical region, centromeric and
5036	14908	24570	1.41	3.3E-000	7682195	NT	Homo sapiens KIAA0480 gene product (KIAA0480), mRNA
5036	14908	24690	1.41	3.3E-000	7682195	NT	Homo sapiens KIAA0480 gene product (KIAA0480), mRNA
462	10435	20248	1.39	3.2E-000	X96422.1	NT	D. rerio 2p-50 POU gene
3883	10435	20248	0.79	3.2E-000	X96422.1	NT	D. rerio 2p-50 POU gene
5439	19356	25415	2.65	3.2E-000	P12783	SWISSPROT	PHOSPHOGLYCERATE KINASE, CYTOSOLIC
5439	19356	25415	2.65	3.2E-000	P12783	SWISSPROT	PHOSPHOGLYCERATE KINASE, CYTOSOLIC
5903	15713	25925	2.08	3.2E-000	P10931	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
5903	15713	25925	2.08	3.2E-000	P10931	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
5906	15427	26006	2.93	3.2E-000	V10653.1	NT	Chlamydomonas reinhardtii chloroplast DNA for psbA, psbB, psbC, psbD, psbE, psbF, psbG, psbH, psbI, psbJ, psbK, psbL, psbM, psbN, psbO, psbP, psbQ, psbR, psbS, psbT, psbU, psbV, psbW, psbX, psbY, psbZ, psb1, psb2, psb3, psb4, psb5, psb6, psb7, psb8, psb9, psb10, psb11, psb12, psb13, psb14, psb15, psb16, psb17, psb18, psb19, psb20, psb21, psb22, psb23, psb24, psb25, psb26, psb27, psb28, psb29, psb30, psb31, psb32, psb33, psb34, psb35, psb36, psb37, psb38, psb39, psb40, psb41, psb42, psb43, psb44, psb45, psb46, psb47, psb48, psb49, psb50, psb51, psb52, psb53, psb54, psb55, psb56, psb57, psb58, psb59, psb60, psb61, psb62, psb63, psb64, psb65, psb66, psb67, psb68, psb69, psb70, psb71, psb72, psb73, psb74, psb75, psb76, psb77, psb78, psb79, psb80, psb81, psb82, psb83, psb84, psb85, psb86, psb87, psb88, psb89, psb90, psb91, psb92, psb93, psb94, psb95, psb96, psb97, psb98, psb99, psb100, psb101, psb102, psb103, psb104, psb105, psb106, psb107, psb108, 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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (19p) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2607	12737	22635	1.06	3.0E-00	6023084	NT	Homo sapiens hypothetical protein PRO389 (PRO389), mRNA
6275	19195	24970	1.63	3.0E-00	X55036.1	NT	S. aureus gene encoding SaeB1 DNA methyltransferase and SaeB1 restriction endonuclease
6245	18111	24970	0.5	3.0E-00	P18406	NT	CYB51 PROTEIN PRECURSOR (CYB51)
7164	17041		1.45	3.0E-00	X67838.1	NT	S. aureus DNA for myofibrinase
							RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLYL CYCLASE 2F, RETINAL (RETGC-2) (ROD OUTER SEGMENT MEMBRANE GUANYLYL CYCLASE 2) (ROS-GC2) (GUANYLYL CYCLASE F) (GC-F)
8374	18291	26501	6.51	3.0E-00	P51842	SWISSPROT	RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLYL CYCLASE 2F, RETINAL (RETGC-2) (ROD OUTER SEGMENT MEMBRANE GUANYLYL CYCLASE 2) (ROS-GC2) (GUANYLYL CYCLASE F) (GC-F)
8374	18291	26502	6.51	3.0E-00	P51842	SWISSPROT	RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLYL CYCLASE 2F, RETINAL (RETGC-2) (ROD OUTER SEGMENT MEMBRANE GUANYLYL CYCLASE 2) (ROS-GC2) (GUANYLYL CYCLASE F) (GC-F)
1864	11858	21747	2.56	2.9E-00	AE002232.2	NT	Chlamydia pneumoniae AR30, section 53 of 54 of the complete genome
8129	19978	26112	1.63	2.9E-00	X26879.1	NT	F. aridulipes odcP-A gene for P-protein of the shikimate cleavage system
5282	18146	26300	4.47	2.9E-00	O14514	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 1 PRECURSOR
5282	18146	26300	4.47	2.9E-00	O14514	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 1 PRECURSOR
8410	18271	26433	5.19	2.9E-00	P46559	SWISSPROT	ADHERENCE FACTOR (ADHESION AND AGGREGATION-MEDIATING SURFACE ANTIGEN)
1441	11348	21212	5.73	2.8E-00	AF153583.1	NT	Stromal keratinin matrilin 2 (matk) gene, partial cds; chloroplast gene for chloroplast product
1615	11519	26340	3.13	2.8E-00	AL161552.2	NT	Aradiploids thalassia DNA chromosome 4, contig fragment No. 52
6325	18198	26340	4.78	2.8E-00	603724	NT	Mus musculus endothelin (LOC55423), mRNA
230	10196	20012	4.68	2.7E-00	867306	NT	Mus musculus perlecanin repeat gene 3 (Perle3), mRNA
5406	15327	25377	4.63	2.7E-00	6079306	NT	Mus musculus perlecanin repeat gene 3 (Perle3), mRNA
7165	17002		2.21	2.7E-00	L14033.1	NT	Homo sapiens epb polymorphism Kynop IV gene, exons 1 and 2
7895	17846	24253	2.16	2.7E-00	AL10459.1	EST HUMAN	Scp1a-clone scp1a.Tc cDNA library under conditions of riboprim depletion
4578	14467	24253	4.35	2.6E-00	BC035827.1	NT	GM-510381-03 (199-087-H4 B10281) Homo sapiens cDNA
5405	15324	25373	1.97	2.6E-00	AF067481.1	NT	Mus musculus spermatogenesis kinase (SPK16), complete cds
5405	15324	25374	1.97	2.6E-00	6755601	NT	Mus musculus SRY-Box containing gene 13 (Box13), mRNA
							Mus musculus SRY-Box containing gene 13 (Box13), mRNA
6533	16891		5.42	2.6E-00	AF235502.1	NT	Mus musculus SH2-containing inositol 5-phosphatase (Shp) gene, exons 16 through 27, and complete cds
6606	16576	26767	1.2	2.6E-00	AJ132160.1	NT	Mus musculus yelows virus C2-EG gene, isolate Egyptian EV-193
6606	16576	26768	1.2	2.6E-00	AJ132160.1	NT	Mus musculus yelows virus C2-EG gene, isolate Egyptian EV-193
7567	17418	27354	2.95	2.6E-00	AL161540.2	NT	Aradiploids thalassia DNA chromosome 4, contig fragment No. 40
7627	17777		1.52	2.6E-00	6055163	NT	Mus musculus cleavage and polyadenylation specificity factor 3 (Cpsf3), mRNA
9711	19946		2.31	2.6E-00	11410220	NT	Homo sapiens ATP-binding cassette, sub-family B (MDR/TPA), member 4 (ABCB4), mRNA
1448	11353	21216	2.06	2.5E-00	AJ271844.1	NT	Aspergillus nidulans roqQ gene for DNA helicase, exons 1-4

Table 4

Probe SEQ ID NO.	Even SEQ ID NO.	ORF SEQ ID NO.	Expression	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Databases Source	Top Hit Description
1446	11593	21217	2.08	2.5E-00	AJ271844.1	NT	Aspergillus nidulans recQ gene for DNA helicase, exons 1-4
5562	15468	26537	2.93	2.5E-00	P13485	SWISSPROT	TECHOLIC ACID BIOSYNTHESIS PROTEIN F
5562	15468	26537	2.93	2.5E-00	P13485	SWISSPROT	TECHOLIC ACID BIOSYNTHESIS PROTEIN F
5562	15468	26537	1.71	2.5E-00	P13485	SWISSPROT	TECHOLIC ACID BIOSYNTHESIS PROTEIN F
8690	15468	26537	1.71	2.5E-00	P13485	SWISSPROT	TECHOLIC ACID BIOSYNTHESIS PROTEIN F
8690	15468	26537	1.71	2.5E-00	P13485	SWISSPROT	TECHOLIC ACID BIOSYNTHESIS PROTEIN F
5591	16419	25996	1.34	2.5E-00	AF049478.1	EST_HUMAN	GHAF-P0005-PT0000-206-007 PT0000 Homo sapiens cDNA
7264	17414	27334	1.78	2.5E-00	D03007.1	NT	Plus DNA for alkalase C-1, complete cds
9080	18881	---	2.20	2.5E-00	A039603.1	NT	Mus musculus EFH41 gene, partial cds; LMX1 gene, complete cds; and ELN gene, partial cds
2980	12807	22707	0.86	2.4E-00	M04932.1	NT	Chicken alpha-3 collagen type V Mr100k, 3' and
4816	14099	24465	7.02	2.4E-00	4903592	NT	Homo sapiens double C2-like domains, alpha (D0C2A) mRNA
5057	15059	25994	4.19	2.4E-00	P02842	SWISSPROT	VITELLOGENIN PRECURSOR (YOLK PROTEIN 1)
6733	16813	26802	2.14	2.4E-00	P26842	SWISSPROT	CD22L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD22) (T14)
6733	16813	26803	2.14	2.4E-00	P26842	SWISSPROT	CD22L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD22) (T14)
6760	16659	---	2.83	2.4E-00	AE001466.1	EST_HUMAN	Helicobacter pylori, strain J99, section 47 of 132 of the complete genome
7026	16903	---	1.71	2.4E-00	AF037512.1	EST_HUMAN	RC2P-P0004-051299-011-d05 PT0004 Homo sapiens cDNA
7771	17621	27953	9.45	2.4E-00	P24049	SWISSPROT	ENDOCHITINASE B PRECURSOR (CHN-B)
7771	17621	27954	2.5	2.4E-00	P13873	SWISSPROT	SKIN GRANULE PROTEIN PRECURSOR
7820	17770	27911	2.18	2.4E-00	X92511.1	NT	H. sapiens CTGF gene and promoter region
7681	17781	---	0.49	2.4E-00	P06099	SWISSPROT	XYLULOSE KINASE (XYLUKINASE)
7914	17784	28002	1.87	2.4E-00	BE320702.1	EST_HUMAN	hMG80.x1 NC1 CGAP_K4711 Homo sapiens cDNA, clone IMAGE:3133187 3'
7914	17784	28003	1.67	2.4E-00	BE320702.1	EST_HUMAN	hMG80.x1 NC1 CGAP_K4711 Homo sapiens cDNA, clone IMAGE:3133187 3'
8428	18302	28558	1.77	2.4E-00	Y14079.1	NT	Bacillus subtilis chromosomal DNA, region 76 degrees: gfpRPO operon and downstream
8695	18554	28639	2.52	2.4E-00	AF198652.2	NT	Fraxinus x americana cytosolic ascorbate peroxidase (APxSC) gene, APxSC-c allele, complete cts
1233	11410	20992	9.95	2.3E-00	A407424.1	NT	G domesticus artificial single chain antibody gene (L3)
4031	16259	23431	1.28	2.3E-00	AJ401081.1	NT	Bacillus subtilis cyb gene for cytochrome b
5406	16269	23431	2.22	2.3E-00	6978564	NT	Rattus norvegicus ATPase, Ca++ transporting, ubiquitous (Atp2a3), mRNA
9479	17065	---	2.3	2.3E-00	P00790	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CEMP-B)
9573	18431	23613	1.53	2.3E-00	X02955.1	NT	Human Atk and dnaJ genes homologues coding for DnaK and DnaJ
7269	17165	27394	1.81	2.3E-00	Q11127	SWISSPROT	(FUCOSYL)TRANSFERASE (GALACTOSIDE 3,4'-FUCOSYLTRANSFERASE)
8960	18793	23063	2.9	2.3E-00	BF541987.1	EST_HUMAN	902009121F1 NIH_MSC_39 Homo sapiens cDNA, clone IMAGE:4068173 5'
9068	18793	23064	2.6	2.3E-00	BF541987.1	EST_HUMAN	902009121F1 NIH_MSC_39 Homo sapiens cDNA, clone IMAGE:4068173 5'
9068	18793	23064	2.6	2.3E-00	BF541987.1	EST_HUMAN	902009121F1 NIH_MSC_39 Homo sapiens cDNA, clone IMAGE:4068173 5'

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9304	13002	28333	4	2.3E-00	BE65237.1	EST_HUMAN	901433672F1 NIH_XGCC_72 Homo sapiens cDNA clone IMAGE:3018643 5'
9306	13405		1.37	2.3E-00	AF281962.1	NT	Neutrophin alpha 3 protein alpha subunit GNA-3 (gna-3) gene, complete cds
4216	14114	23951	3.92	2.2E-00	D57071.1	NT	Rat gene for regulatory, exont (non-coding exon)
4216	14114	23952	3.92	2.2E-00	D57071.1	NT	Rat gene for regulatory, exont (non-coding exon)
							SORTLIN-RELATED RECEPTOR PRECURSOR (SORTING PROTEIN-RELATED RECEPTOR CONTAINING LDLR CLASS A REPEATS) (NSORLA) (SORLA-1) (LOW-DENSITY LIPOPROTEIN RECEPTOR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LDLR RELATIVE WITH 11 LIGAND- BINDING REPEATS) (LR11) (>
5276	15198	24973	10.08	2.2E-00	O95307	SWISSPROT	SORTLIN-RELATED RECEPTOR PRECURSOR (SORTING PROTEIN-RELATED RECEPTOR CONTAINING LDLR CLASS A REPEATS) (NSORLA) (SORLA-1) (LOW-DENSITY LIPOPROTEIN RECEPTOR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LDLR RELATIVE WITH 11 LIGAND- BINDING REPEATS) (LR11) (>
5276	15198	24974	10.08	2.2E-00	O95307	SWISSPROT	SORTLIN-RELATED RECEPTOR PRECURSOR (SORTING PROTEIN-RELATED RECEPTOR CONTAINING LDLR CLASS A REPEATS) (NSORLA) (SORLA-1) (LOW-DENSITY LIPOPROTEIN RECEPTOR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LDLR RELATIVE WITH 11 LIGAND- BINDING REPEATS) (LR11) (>
5995	15905	25707	9.05	2.2E-00	BE250353.1	EST_HUMAN	300843401T1 NIH_XGCC_17 Homo sapiens cDNA clone IMAGE:2659777 3'
5935	15741	25953	3.3	2.2E-00	D05343	SWISSPROT	MINOR VIRION STRUCTURAL PROTEIN NU2
5979	15932	26005	2.89	2.2E-00	P01459	SWISSPROT	INSULIN-LIKE GROWTH FACTOR II PRECURSOR (IGF-II) (SOMATOMEDIN A)
6155	15113		3.14	2.2E-00	AA594574.1	EST_HUMAN	265952.31 NCI_GCAP_Cell Homo sapiens cDNA clone IMAGE:105379 3'
6490	16244	26514	81.58	2.2E-00	AA449013.1	EST_HUMAN	250510171 Swissprot, full, beta, N204F8, 9v: Homo sapiens cDNA clone IMAGE:789534 5'
7381	17230		11.89	2.2E-00	BE14876.1	EST_HUMAN	901594735F1 NIH_XGCC_9 Homo sapiens cDNA clone IMAGE:3945561 5'
7315	13455		2.1	2.2E-00	D04708	SWISSPROT	TRANSPORIN TY1 PROTEIN A
							9105403.1 Swissprot, fibroblast, fibroblast, 21N4P24010 Homo sapiens cDNA clone IMAGE:1933955 3'
7783	17633	27855	1.56	2.2E-00	A230373.1	EST_HUMAN	similar to pY00403 GLUTATHIONE PEROXIDASE (HUMAN)
7783	17633	27856	1.56	2.2E-00	A230373.1	EST_HUMAN	similar to pY00403 GLUTATHIONE PEROXIDASE (HUMAN)
7812	17652	27902	2.28	2.2E-00	BF24762.1	EST_HUMAN	similar to pY00403 GLUTATHIONE PEROXIDASE (HUMAN)
7975	17658	28098	2.88	2.2E-00	AF183416.1	NT	Homo sapiens ovarian granulosa cell 13.0 RNA for protein IGR74 homolog mRNA, complete cds
9759	17658	28132	4.15	2.2E-00	P07911	SWISSPROT	UROKOLIN PRECURSOR (TAMM-HORSFALL URINARY GLYCOPROTEIN) (THP)
9889	19700	28995	4.97	2.2E-00	P10407	SWISSPROT	EARLY E1A 28 KD PROTEIN
857	12670	20034	6.81	2.2E-00	AF132612.2	NT	Mito nuclear pore-1 cell receptor alpha gene, enhancer region and upstream region
3539	13455		1.19	2.1E-00	AAV44906.1	EST_HUMAN	UHH-3B-akt-c-040-UI at NCI_GCAP_S105 Homo sapiens cDNA clone IMAGE:2734550 3'
6074	16057	28206	3.72	2.1E-00	OT0169	SWISSPROT	ALPHA-2HS-GLYCOPROTEIN PRECURSOR (FETUIN-A)
							Y08910.1 Swissprot, rat, 2N01-H Homo sapiens cDNA clone IMAGE:270618 3' similar to gb-M6554
6195	15958	28087	4.7	2.1E-00	N26576.1	EST_HUMAN	TRANSCRIPTION INITIATION FACTOR TIFID (HUMAN)
6948	16926		1.99	2.1E-00	AU12039.1	EST_HUMAN	AUT2850 NT295M2 Homo sapiens cDNA clone NT292006871 5'
1178	11059	20934	1.23	2.0E-00	AF180527.1	NT	Homo sapiens p22-oidel (DOK10EL) mRNA, complete cds

Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Even SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
1178	11986	20355	1.23	2.0E+00	AF160527.1	NT	Homo sapiens C22d4dd4 (C22DDEL) mRNA, complete cds
1313	11219	21070	1.43	2.0E+00	AF204827.1	NT	Oxyphagus catenatus Var.-X-ATPase beta 1 subunit mRNA, complete cds
1657	11462		3.13	2.0E+00	PJ25682	SWISSPROT	PUTATIVE RNA ME PHL TRANSFERASE SP581
2102	11991	21890	4.6	2.0E+00	Z78279.1	NT	Rnongegus mieia for collagen alpha1 type I
2102	11991	21891	4.6	2.0E+00	Z78279.1	NT	Rnongegus mieia for collagen alpha1 type I
4011	13817	23962	2.09	2.0E+00	AU684466.1	EST_HUMAN	NR3065.X1 NC1 CGAP_GUT Homo sapiens cDNA clone IMAGE:2972198.3 similar to gp-X01677
4011	13817	23963	2.09	2.0E+00	AU684466.1	EST_HUMAN	NR3065.X1 NC1 CGAP_GUT Homo sapiens cDNA clone IMAGE:2972198.3 similar to gp-X01677
6978	16558	20751	3.8	2.0E+00	A5008976.1	EST_HUMAN	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN); Escherichia coli O157 DNA, map position at 46 min., complete cds
6978	16558	20752	3.8	2.0E+00	A5008976.1	NT	Escherichia coli O157 DNA, map position at 46 min., complete cds
6978	16558	20753	3.8	2.0E+00	A5008976.1	NT	Escherichia coli O157 DNA, map position at 46 min., complete cds
7170	17047	217237	3.3	2.0E+00	F31500.1	EST_HUMAN	HSPD27703 HM3 Homo sapiens cDNA clone s4001717308
9629	19033	24098	5.81	2.0E+00	5834948	NT	Gallus gallus mitochondrion, complete genome
5437	15357	25412	4.87	1.9E+00	6754369	NT	Mus musculus isolectal 1,4,5-triphosphate receptor 1 (lpr1), mRNA
5437	15357	25413	4.87	1.9E+00	6754369	NT	Mus musculus isolectal 1,4,5-triphosphate receptor 1 (lpr1), mRNA
6047	15950		2.27	1.9E+00	Q63927	SWISSPROT	GTP-BINDING SR-LIKE PROTEIN R243
8927	18959	29899	2.58	1.9E+00	P02467	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
8927	18959	27000	2.58	1.9E+00	P02467	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
7022	16905		3.36	1.9E+00	BF5902308.1	EST_HUMAN	CBP-MT01143(0900-323-112.MT114) Homo sapiens cDNA
7195	17033		1.80	1.9E+00	O33161	SWISSPROT	ARGININE DEIMINASE (ADI) (ARGININE DIHYDROLASE) (AD)
3034	12681	22773	1.71	1.8E+00	P21004	SWISSPROT	PROTEIN B6 PRECURSOR
3082	13009	22799	4.48	1.9E+00	U04356.1	NT	Synchoecoccus sp. PC07942 copper transporting P-ATPase (cuaA) and ATP synthase epsilon subunit (epsilon) genes, complete cds
3082	13009	22800	4.48	1.9E+00	U04356.1	NT	Synchoecoccus sp. PC07942 copper transporting P-ATPase (cuaA) and ATP synthase epsilon subunit (epsilon) genes, complete cds
5577	15402		2.22	1.8E+00	P18102	SWISSPROT	HEDGEHOG RECEPTOR (PATCHED PROTEIN)
5712	16540	25723	1.9	1.8E+00	BF331699.1	EST_HUMAN	801897949FT NH IMGIC_19 Homo sapiens cDNA clone IMAGE:472964.5
0043	46629	20078	1.3	1.8E+00	BF330692.1	EST_HUMAN	801897949FT NH IMGIC_17 Homo sapiens cDNA clone IMAGE:47139039.5
7140	17017	27210	2.09	1.8E+00	O43281	SWISSPROT	EMBRYONAL FYN-ASSOCIATED SUBSTRATE (EFES)
7293	17109	27309	1.21	1.8E+00	R31402.1	EST_HUMAN	pY208.1 Scores plasmid N62pF Homo sapiens cDNA clone IMAGE:135278.6
7899	17749		3.29	1.8E+00	AF111849.1	NT	Homo sapiens PR00530 mRNA, complete cds
8908	18787		3.78	1.8E+00	P36062	SWISSPROT	HYPOTHEICAL T6.5 KD PROTEIN IN SDHI-CMIM/TAY3 INTERGENIC REGION

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9426	19384		4.01	1.8E+00/AF134254.1	NT		Chlamydomonas reinhardtii alternative oxidase 1 (AOX1) gene, nuclear gene encoding mitochondrial protein
9504	19119		2.4	1.8E+00	9506404	EST	Rattus norvegicus Adren-related protein complex 1b (Arpc1b), mRNA
9696	19429		1.34	1.8E+00/BF16903.1	EST_HUMAN		601903009F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:419589.5
1092	11008	20949	1.92	1.7E+00/Q60114	SWISSPROT		LEVANSUORASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE) (SUCROSE 6-FRUCTOSYL TRANSFERASE)
2225	12110	22013	3.25	1.7E+00/AL163260.2	NT		Homo sapiens chromosome 21 segment HS21C80
2321	12202	22101	1.02	1.7E+00/AI141067.1	EST_HUMAN		cc3305.x1 Scores: NIH_MPC_31 Homo sapiens cDNA clone IMAGE:1676137.3
4356	14252	24037	0.84	1.7E+00/Q60114	SWISSPROT		LEVANSUORASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE) (SUCROSE 6-FRUCTOSYL TRANSFERASE)
5448	15369	25424	1.48	1.7E+00/BE03346.1	EST_HUMAN		CMO-BT0282-171269-127+03 BT0282 Homo sapiens cDNA
5448	15369	25425	1.48	1.7E+00/BE03346.1	EST_HUMAN		CMO-BT0282-171269-127+05 BT0282 Homo sapiens cDNA
5684	15575	25673	3.58	1.7E+00/G91748	SWISSPROT		COUP TRANSCRIPTION FACTOR 1 (COUP-1F1) (COUP-1F1)
7014	16891		1.29	1.7E+00/BF30000.1	EST_HUMAN		601894255F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4140084.5
7282	19467	27355	2.15	1.7E+00/Q6479	SWISSPROT		HOMEODOMAIN PROTEIN DLX3
7282	19467	27355	2.15	1.7E+00/Q6479	SWISSPROT		HOMEODOMAIN PROTEIN DLX3
7282	19467	27355	2.15	1.7E+00/Q6479	SWISSPROT		HOMEODOMAIN PROTEIN DLX3
8374	18686	28077	1.78	1.7E+00/W22424.1	EST_HUMAN		6767 Homo telina cDNA, Tsp4501-cleaved auxiliary Homo sapiens cDNA, not directional
8384	19044	25306	1.37	1.7E+00/A878443.1	EST_HUMAN		482407.v1 NC1 COAP_Gest4 Homo sapiens cDNA clone IMAGE:2257540.3 similar to contains MSR1.11 MSR1 (residue absent)
9880	12851	25185	2.26	1.7E+00/A106573.1	EST_HUMAN		470301.v1 Scores: beta3, NHT Homo sapiens cDNA clone IMAGE:1753417.3 similar to contains L1.L1 L1
9880	12851	25185	2.26	1.7E+00/A106573.1	EST_HUMAN		beta3, NHT Homo sapiens cDNA clone IMAGE:1753417.3 similar to contains L1.L1 L1
1080	11832	21773	16.73	1.8E+00/AF196330.1	NT		Homo sapiens beta-actin-derived growth factor gene, alternatively spliced, complete cds
1997	11891	21783	3.61	1.8E+00/AF077374.1	NT		Homo sapiens small proline-rich protein (S-PRI) gene, exons 1, 2, and 3 and complete cds
2003	11895	21785	1.96	1.8E+00/Y11344.1	NT		Homo sapiens S100calAa11 gene, exon 2
2238	12122		1.48	1.8E+00/Q6873.1	NT		B-haplo gene encoding encephalomyelination
2891	12958	22956	2.92	1.8E+00/W59426.1	EST_HUMAN		252301.v1 Scores: 10d1, heart, NHT_H10W Homo sapiens cDNA clone IMAGE:341899.5 similar to
3949	13954		0.14	1.8E+00/BF570077.1	EST_HUMAN		961226965 NAGE-TL1CAGE-SYNTHASE 3 (NAGE-SYNTHASE 3) (HUMAN)
4255	14154	23628	1.44	1.8E+00/AF158827.1	NT		602168051T1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4510591.3
4255	14154	23629	1.44	1.8E+00/AF158827.1	NT		Homo sapiens proliferation-associated SNF2-like protein (SNARCA6) mRNA, complete cds
5010	14890	24657	3.14	1.8E+00/Y11344.1	NT		Homo sapiens proliferation-associated SNF2-like protein (SNARCA6) mRNA, complete cds
5019	14890	24658	3.14	1.8E+00/Y11344.1	NT		Mus musculus S100calAa11 gene, exon 2
5558	15474	25549	2.19	1.8E+00/D04068.1	NT		Mus musculus S100calAa11 gene, exon 2
6290	16160	26317	2.64	1.8E+00/BE697267.1	EST_HUMAN		BCR-CTD415-200709-032-c10 CTD415 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Mean Similarity (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6881	16651		1.21	1.6E+00 Q4378		SWISSPROT	VIRULENCE FACTOR M/VIN HOMOLOG
6881	16780	29568	3.55	1.6E+00 AJ297131.1		NT	Mus musculus SL MAP_17_CYP_a, SOL_c, CYP_b genes
7444	19485	29646	1.3	1.6E+00 X52046.1		NT	Mus musculus COL3A1 gene for collagen alpha1
7444	19495	29647	1.3	1.6E+00 X52046.1		NT	Mus musculus COL3A1 gene for collagen alpha1
7611	17452	27679	1.29	1.6E+00 T41290.1		EST_HUMAN	phf86_191TV Outback Alp-paired hncDNA library Homo sapiens cDNA clone phf86_191TV
7852	17702	27946	1.25	1.6E+00 AW835644.1		EST_HUMAN	QV4L10016-090200-100-207 LT0016 Homo sapiens cDNA
8217	17520	27947	1.25	1.6E+00 AW835644.1		EST_HUMAN	QV4L10016-090200-100-207 LT0016 Homo sapiens cDNA
8217	17520	29501	5.86	1.6E+00 AF005631.1		NT	Homo sapiens transglutaminase type 1 (I-gel) gene, promoter region
8944	18722	29047	3.25	1.6E+00 AF104313.1		NT	Homo sapiens unknown mRNA
8902	19378	29047	1.65	1.6E+00 AF104313.1		EST_HUMAN	AV76043 MOS Homo sapiens cDNA clone MOSDAH08.5
30	10017	19812	4.29	1.6E+00 U83449.1		NT	Rattus norvegicus Jan demetabolism protein 2 (Jdp-2) mRNA, complete cds
231	10200	20014	1.76	1.6E+00 AE022012		NT	Chlamydomonas reinhardtii AFR39, section 32 of 84 of the complete genome
605	10541		1.79	1.5E+00	6752661	NT	Mus musculus a disintegrin and metalloproteinas domain (ADAM) 15 (metaglinin) (Adam15), mRNA
2959	12239	22135	2.46	1.5E+00 AJ131402.1		NT	Potamo virus A RNA complete genomes, isolate U
2468	12444	22237	2.02	1.5E+00	6678360	NT	Mus musculus T-cell lymphoma invasion and metastasis 1 (Tiam1), mRNA
3026	12239	22135	2.22	1.5E+00 AJ131402.1		NT	Potamo virus A RNA complete genomes, isolate U
3129	13246	23634	0.82	1.5E+00 AE001846.1		NT	Dinococcus redobulatus R1 section 82 of 229 of the complete chromosome 1
8835	19752	29850	2.71	1.5E+00 R17879.1		EST_HUMAN	910487497 NIH, NMJ, 68 Homo sapiens cDNA clone IMAGE:381559.5
8230	19036		1.42	1.5E+00 BC162386.1		EST_HUMAN	910487497 NIH, NMJ, 68 Homo sapiens cDNA clone IMAGE:381559.5
6250	19116	25368	29.13	1.5E+00 P47179		SWISSPROT	HYPOHECTICAL T18.4 KD PROTEIN IN BAT2-DOLTS INTERGENIC REGION PRECURSOR
6250	19116	25369	29.13	1.5E+00 P47179		SWISSPROT	HYPOHECTICAL T18.4 KD PROTEIN IN BAT2-DOLTS INTERGENIC REGION PRECURSOR
7671	17521	27477	7.56	1.5E+00 BF376754.1		EST_HUMAN	ROB-100078-15900-034-g05 T180078 Homo sapiens cDNA
7782	17652		1.71	1.5E+00 BF376754.1		EST_HUMAN	ROB-100078-15900-034-g05 T180078 Homo sapiens cDNA
7656	17706	27651	1.96	1.5E+00 AA017689.1		EST_HUMAN	920357711 NC1, CGAP, Bm64 Homo sapiens cDNA clone IMAGE:183885.5
7656	17706	27652	1.96	1.5E+00 AA017689.1		EST_HUMAN	920357711 NC1, CGAP, Bm64 Homo sapiens cDNA clone IMAGE:183885.5
8702	18520	29802	3.91	1.5E+00 AA017689.1		EST_HUMAN	263949.01 Soares retina N2b4-HR Homo sapiens cDNA clone IMAGE:361309.5
8708	18541		10.73	1.5E+00 X07390.1		EST_HUMAN	DKFZ74547P243.1 #1 847 (synonym: ttfb1) Homo sapiens cDNA clone DKFZ74547P243.3
8223	18946		1.15	1.5E+00	6753287	NT	Mus musculus caseinase 8 associated protein 2 (Casep2), mRNA
9596	19178		2.89	1.5E+00 AL445065.1		NT	Mus musculus caseinase 8 associated protein 2 (Casep2), mRNA
9650	19243	19908	1.28	1.4E+00	6978462	NT	Thermoplasma acidophilum complete genomes, segment 3/6
27	10014		1.28	1.4E+00	7691685	NT	Rattus norvegicus 8 - Lipoxygenase (Alox5), mRNA
27	10014	19909	1.28	1.4E+00	7691685	NT	Rattus norvegicus 8 - Lipoxygenase (Alox5), mRNA
2231	12116		0.95	1.4E+00 AF053557.1		NT	Homo sapiens DKFZP989M0122 protein (DKFZP989M0122), mRNA
2231	12116		0.95	1.4E+00 AF053557.1		NT	Homo sapiens DKFZP989M0122 protein (DKFZP989M0122), mRNA
2231	12116		0.95	1.4E+00 AF053557.1		NT	Helicobacter pylori glutamine synthetase (glnA) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2286	12109		9.38	1.4E+00	U97622.1	NT	Osteo arles prion protein gene, complete cds
2634	12201	22394	1.63	1.4E+00	X74463.1	NT	Human papillomavirus type 7 genomic DNA
2746	12608	22500	3.29	1.4E+00	AF04564.2	NT	Fugu ubiquitin proteasomalubos type 1 (N1F1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds
2746	12608	22501	3.29	1.4E+00	AF04564.2	NT	Fugu ubiquitin proteasomalubos type 1 (N1F1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds
3034	12682	22766	1.01	1.4E+00	AE002324.2	NT	Chlamydia muridarum, section 65 of 86 of the complete genome
3034	12682	22766	1.01	1.4E+00	AE002324.2	NT	Chlamydia muridarum, section 65 of 86 of the complete genome
3291	13213		0.97	1.4E+00	AF453733	EST	Human sapiens: 1437000-295406 NN1005 Homo sapiens cDNA
4162	14062	23636	1.06	1.4E+00	AF020465.1	EST	Homo sapiens: 1437000-295406 NN1005 Homo sapiens cDNA
4162	14062	23636	1.06	1.4E+00	AF020465.1	EST	Homo sapiens: 1437000-295406 NN1005 Homo sapiens cDNA
4637	14378		1.33	1.4E+00	BF061547.1	EST	Homo sapiens: 1437000-295406 NN1005 Homo sapiens cDNA
4637	14378		1.33	1.4E+00	BF061547.1	EST	Homo sapiens: 1437000-295406 NN1005 Homo sapiens cDNA
5301	15222	26026	1.81	1.4E+00	AF005487.6	EST	PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (PPAR-ALPHA)
5301	15222	26026	1.81	1.4E+00	AF005487.6	EST	PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (PPAR-ALPHA)
5394	15313		5.17	1.4E+00	AB002386.1	NT	Wt5907-21 NCI C636-Pan1 Homo sapiens cDNA clone IMAGE:2810460.3
5394	15313		5.17	1.4E+00	AB002386.1	NT	Wt5907-21 NCI C636-Pan1 Homo sapiens cDNA clone IMAGE:2810460.3
5760	16022	26812	2.39	1.4E+00	U134372	SWISSPROT	DNA TOPOISOMERASE III ALPHA
5760	16022	26812	2.39	1.4E+00	AB002712.1	NT	Homo sapiens mRNA for KIAA0905 protein, complete cds
5802	16766		4.9	1.4E+00	Q92777	SWISSPROT	SYNAPSIN II
5802	16766		4.9	1.4E+00	Q92777	SWISSPROT	SYNAPSIN II
5980	15766	25984	2.71	1.4E+00	Q92777	SWISSPROT	Homo sapiens scawelin-1/2 locus, Contig1, D7S622, genes CANV2 (exons 1, 2a, and 2b), CANV1 (exons 1 and 2)
5980	15766	25984	2.71	1.4E+00	Q92777	SWISSPROT	Homo sapiens scawelin-1/2 locus, Contig1, D7S622, genes CANV2 (exons 1, 2a, and 2b), CANV1 (exons 1 and 2)
6316	16181	26341	1.06	1.4E+00	AJ133269.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
6316	16181	26341	1.06	1.4E+00	AJ133269.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
7107	16994		5.21	1.4E+00	U217756.1	EST	Y63H12.11 Source: infant brain TNE Homo sapiens cDNA clone IMAGE:34345.5
7256	17353	27325	1.88	1.4E+00	R20459.1	EST	Homo sapiens: 1437000-295406 NN1005 Homo sapiens cDNA
7303	17179	27381	3.37	1.4E+00	BE044667.1	EST	Homo sapiens: 1437000-295406 NN1005 Homo sapiens cDNA
8420	18294	29548	1.94	1.4E+00	AF195528.1	EST	Homo sapiens: 1437000-295406 NN1005 Homo sapiens cDNA
8420	18294	29548	1.94	1.4E+00	AF195528.1	EST	Homo sapiens: 1437000-295406 NN1005 Homo sapiens cDNA
8560	18326	28395	4.97	1.4E+00	AB006882.1	NT	Homo sapiens: 1437000-295406 NN1005 Homo sapiens cDNA
8560	18326	28395	4.97	1.4E+00	AB006882.1	NT	Homo sapiens: 1437000-295406 NN1005 Homo sapiens cDNA
8769	18626	28609	3.15	1.4E+00	BE02107.2	EST	Homo sapiens: 1437000-295406 NN1005 Homo sapiens cDNA
8769	18626	28609	3.15	1.4E+00	BE02107.2	EST	Homo sapiens: 1437000-295406 NN1005 Homo sapiens cDNA
8769	18626	28609	3.15	1.4E+00	BE02107.2	EST	Homo sapiens: 1437000-295406 NN1005 Homo sapiens cDNA
8769	18626	28609	3.15	1.4E+00	BE02107.2	EST	Homo sapiens: 1437000-295406 NN1005 Homo sapiens cDNA
8727	18933	28687	2.89	1.4E+00	U30790.1	NT	Pneumocystis carinii f. sp. ratii guanine nucleotide binding protein alpha subunit (pgp1) gene, complete cds
8727	18933	28687	2.89	1.4E+00	U30790.1	NT	Pneumocystis carinii f. sp. ratii guanine nucleotide binding protein alpha subunit (pgp1) gene, complete cds
9221	19804		1.34	1.4E+00	AL161500.2	NT	Asiatick Italiane DNA chromosome 4, contig fragment No. 12

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
558	10486		1.67	1.3E+00/27340.1	NT		Mucedo gene encoding 4-Dihydroxyethyl-thiopyranose dehydrogenase
884	10810	20659	2.74	1.3E+00/AL271102.1	NT		Cardifilins sp. partial 26S rRNA gene, isolate Thet
1113	11028		16.5	1.3E+00/119213.1	NT		Homo sapiens putative partial beta pseudogene for hair keratin, exons 2 to 7
1275	11183	21033	10.9	1.3E+00/4607898	NT		Homo sapiens zinc finger protein 167 (ZF167) mRNA
1276	11183	21034	10.9	1.3E+00/4607898	NT		Homo sapiens zinc finger protein 167 (ZF167) mRNA
1334	11241		1.62	1.3E+00/187130.2	NT		Cox lacyrma-jb1 dihydrodipicolinate synthase (dapA) gene, complete cds
1893	11497		2.09	1.3E+00/AE02338.2	NT		Chlamydia muridarum, section 66 of 85 of the complete genome
							Cytrus carpis MRP6 and MASP6 genes for mannose-binding lectin-associated serine protease (MASP) and MASP-related protein, complete cds
2106	12093		2.1	1.3E+00/AB030447.1	NT		601691233R1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE3918546 3'
2503	12378		2.19	1.3E+00/BE66735.2	EST_HUMAN		Mus musculus alpha-spectrin 1, cytochalasin (Spect1), mRNA
2509	12635	22632	1.12	1.3E+00/6759621	NT		Fugu nucleoside gamma-aminobutyric acid receptor beta subunit gene, partial cds; 55kd cytochrome membrane protein (P65), synaptic vesicle-associated integral membrane protein (VAMP-1), procollagen C-proteinase enhancer protein (PCOLCE) genes, complete cds
3547	13463	23268	1.03	1.3E+00/AF016494.1	NT		Mus musculus alpha-spectrin 1, cytochalasin (Spect1), mRNA
4802	13933	22932	0.82	1.3E+00/AL252087.1	NT		Pterodromus ruficollis partial 83/AMA-1 gene for apical membrane antigen 1
4984	14539	24807	0.88	1.3E+00/AL252087.1	NT		Pterodromus ruficollis partial 83/AMA-1 gene for apical membrane antigen 1
4984	14539	24809	0.88	1.3E+00/AL252087.1	NT		Pterodromus ruficollis partial 83/AMA-1 gene for apical membrane antigen 1
5665	15576	25674	7.76	1.3E+00/AV326934.1	EST_HUMAN		PMD-CT0298-201 (98-04-04-08 CT0298) Homo sapiens cDNA
5665	15576	25675	7.76	1.3E+00/AV326934.1	EST_HUMAN		PMD-CT0298-201 (98-04-04-08 CT0298) Homo sapiens cDNA
5884	15710	23869	1.33	1.3E+00/133406.1	NT		Drosophila melanogaster roach-laminin A gene product, complete cds
8828	16707	26901	1.25	1.3E+00/AL069112.1	NT		Sus scrofa p16 gene
6917	16795	26985	3.05	1.3E+00/BE66735.2	EST_HUMAN		601691745R1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE3856105 3'
7054	16931		1.56	1.3E+00/9810247	NT		Homo sapiens GLO1 protein (GLO1), mRNA
7480	17350		5.44	1.3E+00/AF042884.1	NT		Homo sapiens heparan glucosaminyl N-acetyltransferase-2 gene, complete cds
7487	17357	27560	2.31	1.3E+00/X72019.1	NT		S. alba p16-1 mRNA for protease
7487	17357	27561	2.31	1.3E+00/X72019.1	NT		S. alba p16-1 mRNA for protease
7674	17426	27639	1.46	1.3E+00/000754	SWISSPROT		LYSOSOMAL ALPHA-MANNOSIDASE PRECURSOR (MANNOSIDASE, ALPHA B) (LYSOSOMAL ACID
7620	17471	27680	1.27	1.3E+00/AB07659.1	EST_HUMAN		w085407.X1 NC_004947 Homo sapiens cDNA clone IMAGE242100 3'
7675	17526	27761	4.9	1.3E+00/BE66376.2	EST_HUMAN		601691745R1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE3856105 3'
7666	17716	27967	1.6	1.3E+00/AE04392.1	NT		Vitre chondria chromosome II, section 49 of 85 of the complete chromosome
7814	17724	27968	1.39	1.3E+00/020603.1	NT		Campylodactylus jenui karyomycin phosphotransferase (dhpA-7) gene, complete cds
8078	17969		4.3	1.3E+00/014117	SWISSPROT		HYDROXYMETHYLASE (DHAPASE) (HYDANTONINASE) (DHP)
8277	18157	28386	2.34	1.3E+00/1P26286	SWISSPROT		MYRNA 3'-END PROCESSING PROTEIN RNAI5

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8296	18178	28424	2.23	1.3E+00/1.6922.2	NT	NT	Mus musculus desmin gene
8646	18610		1.81	1.3E+00/AW17797.1	EST_HUMAN	XP009533.1	NT
8628	18639	25923	2.82	1.3E+00/A2942.1	NT	Human mRNA for GGAAP_HNR Homo sapiens cDNA clone IMAGE:2738868.3	
8695	18705	26999	2.71	1.3E+00/256992.1	NT	Bacillus subtilis genomic DNA 23.9kb fragment	
9502	19033		2.35	1.3E+00/167973.1	NT	Cavia porcellus inward-rectifying potassium channel K2.2 (KCNJ12) gene, complete cds	
9533	19139	25203	3.24	1.3E+00/BF348043.1	EST_HUMAN	6020231.65F1	NT
9544	19496		2.68	1.3E+00/333464	SWISSPROT	ET GLYCOPROTEIN PRECURSOR (MATRIX GLYCOPROTEIN) (MEMBRANE GLYCOPROTEIN)	
884	10671	20384	8.14	1.2E+00/A676246.1	EST_HUMAN	452200.3	NT
806	10733	20578	1.33	1.2E+00/P56228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-II)	
806	10735	20579	1.33	1.2E+00/P56228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-II)	
806	10736	20580	1.33	1.2E+00/P56228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-II)	
860	10763		2.19	1.2E+00/8924234	NT	Homo sapiens hypoxanthine phosphoribosyl transferase PRO3077 (PRO3077), mRNA	
1145	11058	20901	5.63	1.2E+00/A5960245.2	NT	Elleisidella asquithensis synthase mRNA, complete cds	
1187	11097	20943	1.77	1.2E+00/AJ252342.1	NT	pda seed-borne mosaic virus complete genome	
1187	11097	20943	1.77	1.2E+00/AJ252342.1	NT	pda seed-borne mosaic virus complete genome	
1383	11897	21746	1.05	1.2E+00/AF140035.1	NT	Homo sapiens G-protein coupled receptor 14 (GPR14) gene, complete cds	
3072	12858	22789	0.95	1.2E+00/A502081.1	NT	Homo sapiens mRNA for GUA40574 protein, partial cds	
3128	13053	22851	5.41	1.2E+00/AL161653.2	NT	Aluadapet thalassa DNA chromosome 4, contig fragment No. 63	
3128	13053	22852	5.41	1.2E+00/AL161653.2	NT	Aluadapet thalassa DNA chromosome 4, contig fragment No. 63	
3249	13172		2.9	1.2E+00/P54970	SWISSPROT	CONJUGAL TRANSFER PROTEIN INDE PRECURSOR	
3311	13232	22638	0.78	1.2E+00/AF165740.1	NT	Homo sapiens LH33 gene, intron 2	
3312	13233		0.69	1.2E+00/M81779.1	NT	Gallus T-cadherin mRNA, complete cds	
3550	13564	23390	7.28	1.2E+00/U75602.1	NT	Mus musculus subtilisin-like serine protease LPC (PC2) gene, exons 1 to 8, partial cds	
3504	13814	23598	1.49	1.2E+00/BF373570.1	EST_HUMAN	MR3-F10175-05090-203.g05_1 F10175 Homo sapiens cDNA	
4201	13232	23038	1.09	1.2E+00/AF188740.1	NT	Homo sapiens LH33 gene, intron 2	
4298	14195	23881	1.39	1.2E+00/6860051	NT	Rattus norvegicus glycine receptor alpha 2 subunit (glycine receptor, neuronal) (GluR2), mRNA	
4371	14267		1.64	1.2E+00/M81060.1	NT	Rattus norvegicus A23 gene, exons 1, 23	
4421	14316	24102	1.26	1.2E+00/AL161800.2	NT	Arabisopsis thaliana DNA chromosome 4, contig fragment No. 21	
4400	14384	24148	1.82	1.2E+00/AF189465.1	NT	Homo sapiens post-synaptic density 95 (DLG4) gene, complete cds	
4495	14379		5.44	1.2E+00/109200.1	NT	T. pinhalum chloroplast 16S rDNA, partial cds	
4584	13233		0.94	1.2E+00/M81779.1	NT	Gallus T-cadherin mRNA, complete cds	
5409	15329	25379	1.66	1.2E+00/AW181327.1	EST_HUMAN	MR3-S10191-140200-913-c05 S10191 Homo sapiens cDNA	
5739	15647	25753	2.47	1.2E+00/X74883.1	NT	D. hyalae syl repeat cluster DNA, fragment D	
5760	15679	25783	3.28	1.2E+00/BE003113.1	EST_HUMAN	QIV4-EN0090-270400-190-403 BN0090 Homo sapiens cDNA	

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORE SEQ ID NO:	Expression Signal	Mask Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5766	15704	25815	1.87	1.2E+00/260984.1	NT	NT	C.gilanicum pla gene and actA gene
5768	15704	25816	1.87	1.2E+00/260984.1	NT	NT	C.gilanicum pla gene and actA gene
5823	15729	25841	32.83	1.2E+00/AL195254.1	EST_HUMAN	EST_HUMAN	alga-1g12.1 Soares, testis, NIH Homo sapiens cDNA clone 1322374 3'
5916	15823	25946	1.82	1.2E+00/AW813276.1	EST_HUMAN	EST_HUMAN	MR3-S10191-140200-013-03 S10191 Homo sapiens cDNA
6136	15699	26121	2.65	1.2E+00/AJ002144.1	NT	NT	Mus musculus DSPP gene
6306	15463	26392	1.9	1.2E+00/AV734655.1	EST_HUMAN	EST_HUMAN	AV734655 cda Homo sapiens cDNA clone cDAAPH03 5'
6608	16367	26544	2.4	1.2E+00/74207.1	NT	NT	Licids pvd and pvt genes
6684	16861	27055	3.45	1.2E+00/AB033303.1	NT	NT	Homo sapiens mRNA for KIAA1204 protein, partial cds
7216	17065	27265	1.74	1.2E+00/AW37210.1	EST_HUMAN	EST_HUMAN	MR2-C10222-207099-001-407 C10222 Homo sapiens cDNA
7407	17274	27460	3.08	1.2E+00/233955.1	NT	NT	R communis gene for pyrophosphate-dependent phosphofructokinase beta subunit
7540	17391	27760	1.8	1.2E+00/11745.1	EST_HUMAN	EST_HUMAN	HUMH001A01 Liver HepG2 cell line, Homo sapiens cDNA clone hmd1401
7711	17861	27766	3.28	1.2E+00/269923.1	NT	NT	H sapiens ENO3 gene for muscle specific enolase
8563	18432	28026	2.03	1.2E+00/AV617617.1	EST_HUMAN	EST_HUMAN	PMO-S10264-16108-001-401 S10264 Homo sapiens cDNA
8563	18576	28026	23.27	1.2E+00/BE_40761.1	EST_HUMAN	EST_HUMAN	PMH110422-160200-007-910 HT0422 Homo sapiens cDNA
8722	17851	28145	4.87	1.2E+00/150147.1	NT	NT	Galus congensis synapsin-associated protein 103 mRNA, complete cds
9114	15871	28767	2.9	1.2E+00/JF055958.1	NT	NT	Mus musculus 60 kDa fibronectin protein SS1/60 gene, complete cds
9520	15972	29367	15.4	1.2E+00/AL163203.2	NT	NT	Homo sapiens chromosome 21 segment HS210203
9548	16025	29367	1.48	1.2E+00/JF051915.1	NT	NT	Escherichia coli HsdR gene, partial cds
456	10400	20217	1.73	1.1E+00/069960.1	NT	NT	Human mRNA for KIAA0227 gene, partial cds
1726	1627	21466	1.39	1.1E+00/AW695953.1	EST_HUMAN	EST_HUMAN	QV05N0042-170300-163-917 BN0042 Homo sapiens cDNA
1657	11753	21528	0.62	1.1E+00/AW67699.1	EST_HUMAN	EST_HUMAN	UHFH-BR05-48142-02-U161 NHF1M62 52 Homo sapiens cDNA clone IMAGE3074834 3'
3268	13209	23006	6.61	1.1E+00/AL163213.2	NT	NT	Homo sapiens chromosome 21 segment HS210213
3268	13209	23010	6.61	1.1E+00/AL163213.2	NT	NT	Homo sapiens chromosome 21 segment HS210213
3441	13356	23105	0.53	1.1E+00/892264.1	NT	NT	Homo sapiens hypothetical protein FLJ10746 (FLJ10746), mRNA
3510	13426		1.26	1.1E+00/892267.3	NT	NT	Homo sapiens hypothetical protein FLJ11280 (FLJ11280), mRNA
3531	13447	23244			EST_HUMAN	EST_HUMAN	wf54611.1 Soares, NFL_1_GBC_S1 Homo sapiens cDNA clone IMAGE2359461 3' similar to
3557	13571	23357	0.66	1.1E+00/AB083000.1	EST_HUMAN	EST_HUMAN	SWP7951 HUMAN C12868 P53-BINDING PROTEIN 53BP1 ;
3557	13571	23357	1.16	1.1E+00/AE003896.1	NT	NT	Xylella fastidiosa, section 32 of 229 of the complete genome
3557	13571	23356	1.16	1.1E+00/AE003896.1	NT	NT	Xylella fastidiosa, section 32 of 229 of the complete genome
3676	13592	23376	17.81	1.1E+00/5729757.1	NT	NT	Homo sapiens calpain 9 (nCL-4) (CAPN9) mRNA
3682	13378	23365	0.66	1.1E+00/692264.1	NT	NT	Homo sapiens hypothetical protein FLJ10746 (FLJ10746), mRNA
4122	14022		5.85	1.1E+00/5835331.1	NT	NT	Ruricola complete mitochondrial genome
4850	14740	24520	1.16	1.1E+00/23195.1	NT	NT	Drosophila melanogaster cytoplasmic dynein heavy chain mRNA, complete cds
4821	14800	24573	2.92	1.1E+00/181465.1	NT	NT	African swine fever virus, complete genome

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4999	14874	24638	1.16	1.1E+00/78425.1	NT	NT	E facialis p307 gene
5246	15172	24645	1.57	1.1E+00	6978530	EST	Rattus norvegicus Aquaporin 4 (Aqp4), mRNA
6446	15370	25426	12.04	1.1E+00/BE607184.1	NT	EST_HUMAN	6916527/ERR1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3029335 3'
5460	15390	25440	1.29	1.1E+00/H138582.1	EST	EST_HUMAN	q485c05.x1 Soares, Ilesia, NIH Homo sapiens cDNA clone IMAGE:1792600 3'
6422	16293	25444	1.93	1.1E+00/772338.1	NT	NT	Herpes simplex virus type 1 (strain KOS) UL41 gene
6422	16293	25444	1.93	1.1E+00/772338.1	NT	NT	Herpes simplex virus type 1 (strain KOS) UL41 gene
6435	16286	25458	7.63	1.1E+00/AL161880.2	NT	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
6728	16908	26799	3.22	1.1E+00/AF036965.1	EST	EST_HUMAN	602082932.F1 NIH_MGC_31 Homo sapiens cDNA clone IMAGE:4246028 5'
7658	17508	27793	1.65	1.1E+00/AB023151.1	NT	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
7719	17568	27791	4.39	1.1E+00/AL161916.2	NT	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
7744	17594	27813	20.08	1.1E+00	6754021	NT	Homo sapiens KIA00369 gene product (KIA00369), mRNA
8043	17934	28182	2.66	1.1E+00	11067364	NT	Klebsiella pneumoniae glycerol oxidase subunit 2 (cox2) gene, mitochondrial gene encoding mitochondrial protein, partial cds
8090	17981		3.41	1.1E+00/AF068942.1	NT	NT	Homo sapiens hypoxanthine phosphoribosyl transferase 1 (HGPRT1) mRNA, complete cds
8447	13426		5.73	1.1E+00	6022973	NT	Homo sapiens hypoxanthine phosphoribosyl transferase 1 (HGPRT1) mRNA, complete cds
8450	18928	28581	4.41	1.1E+00/AF012892.1	NT	NT	Petrocaltium citreum cytosolic glucose-6-phosphate dehydrogenase 1 (G6PDH1) mRNA, complete cds
8450	18928	28582	4.41	1.1E+00/AF012892.1	NT	NT	Petrocaltium citreum cytosolic glucose-6-phosphate dehydrogenase 1 (G6PDH1) mRNA, complete cds
8682	18851	28835	4.73	1.1E+00/AB036965.1	EST	EST_HUMAN	q78511.x1 Soares, NIH_MGC_31 Homo sapiens cDNA clone IMAGE:2561543 3'
9300	19069		4	1.1E+00/P07066	SWISSPROT	SWISSPROT	LOW TEMPERATURE ESSENTIAL PROTEIN
9402	19056	25510	2.13	1.1E+00/AF210696.1	NT	NT	Tamias californicus immunoglobulin protein T3/0 mRNA, partial cds
9523	19570		1.54	1.1E+00/AF224169.1	NT	NT	Deoxyribose dephosphorylating pyrophosphatase isomerase (Dpi) mRNA, complete cds
92	10077		3.49	1.0E+00/22908.1	NT	NT	Xenopus laevis ribosomal gene, complete cds
108	10089	19604	1.14	1.0E+00/084428.1	NT	NT	Cavia cobaya mRNA for aspartate kinase, complete cds
412	10359		2.16	1.0E+00/AB021594.1	NT	NT	Marchantia polymorpha genes for 26S rRNA, 5S rRNA, 18S rRNA, 5.8S rRNA and 26S rRNA
552	10502	20306	1.14	1.0E+00/AF210696.1	NT	NT	Marchantia polymorpha genes for 26S rRNA, 5S rRNA, 18S rRNA, 5.8S rRNA and 26S rRNA
691	10956	20413	4.51	1.0E+00/AL163218.2	NT	NT	Giardia lamblia mRNA for homodimer transcription factor (to gene)
693	10957		0.95	1.0E+00/AF25684.1	NT	NT	Homo sapiens chromosome 21 segment HS21C018
1364	12692		1.04	1.0E+00/X80416.1	NT	NT	Ades aegypti much-like protein MUC1 mRNA, complete cds
1722	11623	21462	1.82	1.0E+00/AF006831.1	NT	NT	V. carterii Algal CCM mRNA
2435	12312	22208	1.4	1.0E+00/P48356	SWISSPROT	SWISSPROT	Pisalia stali intestine virus RNA for nonstructural polyprotein, capsid protein precursor, complete cds
2435	12312	22206	1.4	1.0E+00/P48356	SWISSPROT	SWISSPROT	DNA GYRASE SUBUNIT B
2435	12312	22206	1.4	1.0E+00/P48356	SWISSPROT	SWISSPROT	DNA GYRASE SUBUNIT B

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Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Meat Similar (Top) HR BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6691	16740	26932	2.7	1.0E+00	Q02207	SWISSPROT	PEROXISOMAL HYDROXYASE-DEHYDROGENASE-EPIMERASE (HDE) (MULTIFUNCTIONAL BETA-OXIDATION PROTEIN) (MFP) [INCLUDES: 2-ENOYL-COA HYDRATASE ; D-3-HYDROXYACYL COA DEHYDROGENASE]
6691	16740	26933	2.7	1.0E+00	Q02207	SWISSPROT	PEROXISOMAL HYDROXYASE-DEHYDROGENASE-EPIMERASE (HDE) (MULTIFUNCTIONAL BETA-OXIDATION PROTEIN) (MFP) [INCLUDES: 2-ENOYL-COA HYDRATASE ; D-3-HYDROXYACYL COA DEHYDROGENASE]
6697	19466		2.01	1.0E+00	BEI47331.1	EST_HUMAN	RC3H10229-161099-011-c08 HT0228 Homo sapiens cDNA
7064	16941	27133	1.9	1.0E+00	U34327.1	NT	Human immunodeficiency virus type 1 (HIV-1), isolate SF33,
7339	17207	27405	1.76	1.0E+00	BE007592.1	EST_HUMAN	601497281F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3890421 5'
7460	17320	27326	1.28	1.0E+00	6759439	NT	Mus musculus chloride channel calcium activated 1 (Clcat) mRNA
7460	17320	27327	1.28	1.0E+00	6759439	NT	Mus musculus chloride channel calcium activated 1 (Clcat) mRNA
7544	17395	27907	2.03	1.0E+00	AV6939554.1	EST_HUMAN	AV6939554 KGC Homo sapiens cDNA clone GICCYA11 5'
7546	17397	27909	1.2	1.0E+00	U44952.1	NT	Xenopus laevis zona pellucida C glycoprotein precursor (MZPC) mRNA, complete cds
7546	17397	27910	1.2	1.0E+00	U44952.1	NT	Xenopus laevis zona pellucida C glycoprotein precursor (MZPC) mRNA, complete cds
7616	17769	28005	2.83	1.0E+00	AV7699253.1	EST_HUMAN	AV7699253 BM Homo sapiens cDNA clone BMAFW C01 5'
7693	17835	28073	17.08	1.0E+00	U4004932.1	EST_HUMAN	2044c27.1 Scars, fetal liver, spleen, INFLS, S1 Homo sapiens cDNA clone IMAGE:428608 5'
7693	17835	28078	17.08	1.0E+00	U4004932.1	EST_HUMAN	2044c27.1 Scars, fetal liver, spleen, INFLS, S1 Homo sapiens cDNA clone IMAGE:428608 5'
9163	18028		2.05	1.0E+00	P15306	SWISSPROT	THROMBOMODULIN PRECURSOR (TETOMODULIN) (TM)
9513	19128		1.51	1.0E+00	AV0797184.1	EST_HUMAN	EST1389293 IMAGE resource, MAGN Homo sapiens cDNA
9569	19330		1.87	1.0E+00	U040290.1	NT	Homo sapiens mRNA for RUA1517 protein, partial cds
1253	11438	21318	0.84	9.8E-01	AF245453.1	NT	Drosophila melanogaster regulator of G-protein signaling LOC10 in mRNA, complete cds
1253	11438	21318	0.84	9.8E-01	AF245453.1	NT	Drosophila melanogaster regulator of G-protein signaling LOC10 in mRNA, complete cds
2596	12467	22590	0.9	9.8E-01	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
3553	13468		1.18	9.8E-01	AF174355.1	NT	Apple medusa virus RNA 2 putative polymerase gene, complete cds
5481	13381	25441	9.22	9.8E-01	P49667	SWISSPROT	SERINE/THREONINE PROTEIN KINASE MINIPROTEIN
7338	17204		1.38	9.8E-01	U06967.1	NT	Lycopodium obscurum putative MIT copy 1 nematode resistance gene
7510	17298		2.43	9.8E-01	U2894.2	SWISSPROT	BC2 BRADYKININ RECEPTOR (BK-2 RECEPTOR)
5097	17968	28237	2.82	9.8E-01	AJ005029.1	NT	Danio rerio mRNA for Eph-like receptor tyrosine kinase rdb
512	10454	20265	2.32	9.8E-01	P22967	SWISSPROT	AMINO-ACID ACETYLTRANSFERASE (NAOETYL-GLUTAMATE SYNTHASE) (AGS) (NAGS)
3732	13844	23429	0.82	9.8E-01	BE057439.2	EST_HUMAN	601603933R2 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3839461 3'
3732	13844	23430	0.82	9.8E-01	BE057439.2	EST_HUMAN	601603933R2 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3839461 3'
6272	16137	26292	4.61	9.8E-01	AJ302136.1	NT	Enterobacteriaceae sp. JM103 partial groES gene for GroES-like protein and partial groEL gene for GroEL-like protein, isolate JM683

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar Cloned EST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6272	16137	26293	4.61	9.6E-01	A302158.1	NT	Enterobacteriaceae sp. JM983 partial <i>groES</i> gene for GroES-like protein and partial <i>groEL</i> gene for GroEL-like protein, isolate JM983
8362	18239	28487	4.43	9.6E-01	BE285705.1	EST_HUMAN	601110258F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350750 5'
8362	18239	28488	4.43	9.6E-01	BE285705.1	EST_HUMAN	601110258F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350750 5'
9408	19061		1.62	9.6E-01	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Cdc-2/Catenin-dependent protein kinase 1 (CAK1), creatine transporter (CRT1), COM protein (COM), adenosine diphosphate synthase >
5100	14974		1.01	9.7E-01	A1600384.1	EST_HUMAN	W62504.X1 Soares Thyms NHFTH Homo sapiens cDNA clone IMAGE:234594.3'
9248	16114	26266	2.37	9.7E-01	U26716.1	NT	Triticum aestivum stb1 rat resistance protein Yr10 (Yr10) gene, complete cds
6882	16800	27023	1.86	9.7E-01	AF149112.1	NT	Salmonella typhimurium adenine-methyltransferase (msd) and restriction endonuclease (rep)
6584	16832	27025	1.74	9.7E-01	N60544.1	NT	U18B14-ss-a7-0.0113 NGL CGAP_Sus8 Homo sapiens cDNA clone IMAGE:3085740 3'
8510	18382		4.62	9.7E-01	BE511209.1	EST_HUMAN	Bop1a cDNA clone T4 cDNA library under conditions of nitrogen deprivation
9956	19419		1.39	9.7E-01	AL114381.1	NT	Bromus tectorum putative cytosolic phosphoglucomutase (pgm1) mRNA, complete cds
4337	14234	24016	6.8	9.6E-01	AF107925.1	NT	Bromus tectorum putative cytosolic phosphoglucomutase (pgm1) mRNA, complete cds
4337	14234	24017	6.8	9.6E-01	AF107925.1	NT	Bromus tectorum putative cytosolic phosphoglucomutase (pgm1) mRNA, complete cds
4355	14231	24035	1.3	9.6E-01	AF178874.1	EST_HUMAN	PM2:U18035-240305-305-412 U18035 Homo sapiens cDNA
5083	14953	24728	0.82	9.6E-01	7852378	NT	Homo sapiens KIA00911 gene product (KIA00911), mRNA
5517	15435	25486	3.46	9.6E-01	Z70555.1	NT	Parvovirus B19 DNA, patient C, genome position 2445-2584
5517	15435	25498	3.46	9.6E-01	Z70555.1	NT	Parvovirus B19 DNA, patient C, genome position 2445-2584
6580	16769		1.37	9.6E-01	X63276.1	NT	P factorium complete gene map of flanked-like DNA (FCA)
8608	18622	28912	4.19	9.6E-01	AU752905.1	EST_HUMAN	AU752905 NPD Homo sapiens cDNA clone NPDAC08 6'
8608	18622	28913	4.19	9.6E-01	AU752905.1	EST_HUMAN	AU752905 NPD Homo sapiens cDNA clone NPDAC08 6'
9709	19646	24989	1.62	9.6E-01	U04423.1	NT	Shyenne NADH dehydrogenase subunit 2 (NADH2) gene, mitochondrial gene encoding mitochondrial
3715	13027	23410	1.6	9.5E-01	BE902340.1	EST_HUMAN	601675539F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:398473 5'
3715	13027	23411	1.6	9.5E-01	BE902340.1	EST_HUMAN	601675539F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:398473 5'
7260	17143	27359	1.17	9.5E-01	AW961102.1	EST_HUMAN	RG1-CT02955-2411594-011-502 CT02955 Homo sapiens cDNA
3165	13090		3.67	9.4E-01	AF165960.1	NT	Bartonia clausenensis RNA polymerase beta subunit (rpb2) gene, partial cds
3181	13106		1.37	9.4E-01	AF069056.1	NT	Pimpinella brachycarpa zinc finger protein (ZFP1) mRNA, complete cds
8354	18029		1.84	9.4E-01	BE181251.1	EST_HUMAN	601496703F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3989929 5'
9708	19654		1.43	9.4E-01	11419657	NT	Homo sapiens epithelial growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog) (EGFR), mRNA
1700	11901		1.11	9.3E-01	AF242382.1	NT	Homo sapiens phytyl-CoA hydroxylase (PHYH) gene, exon 5

Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Expn SEQ ID NO.	ORF SEQ ID NO.	Expression Signal Value	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2654	13464	23267	1.18	9.3E-01	BE071172.1	EST_HUMAN	RGS-17/503-271/190-01/1-801 BT0503 Homo sapiens cDNA
3046	13857	23630	0.92	9.3E-01	N02019.1	NT	Bohrin pacificum/bohrin type 2, complete genome
3048	13857	23631	0.92	9.3E-01	N02019.1	NT	Bohrin pacificum/bohrin type 2, complete genome
3150	15027	23631	1.34	9.3E-01	AF073515.1	NT	Equisetum arvense microsatellite LE2013
5454	15354	25410	1.62	0.0E+00	AF210384.1	NT	Human sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
5462	15402	25465	3.84	9.3E-01	L36189.1	EST_HUMAN	Staphylococcus Epidermidis multidrug-resistant hydrophobic dehydrogenase mRNA, complete cds
5701	16581	28771	1.83	9.3E-01	AF47040.1	EST_HUMAN	6008003.1 NC CGAP CGAP CGAP Homo sapiens cDNA clone IMAGE:383537
5822	16828	28771	1.38	9.3E-01	AF271207.1	NT	Aedes triseriatus putative large adult rostrum protein pL34 mRNA, complete cds
9954	19418	27688	1.38	9.3E-01	U02871.2	NT	Human sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2a), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2b), melanoma antigen family A3 (MAGEA3), cathectin (CALT), MAGEA12 dehydrogenase-like protein (MAGEA12), and LIP
3301	13725	22830	3.04	9.2E-01	BF67986.1	EST_HUMAN	601461133T1 NH JMC-72 Homo sapiens cDNA clone IMAGE:3976184.3
6543	16556	25648	4.23	9.2E-01	6671677	EST_HUMAN	601461133T1 NH JMC-72 Homo sapiens cDNA clone IMAGE:3976184.3
7810	17469	27688	1.38	9.2E-01	6671677	EST_HUMAN	601461133T1 NH JMC-72 Homo sapiens cDNA clone IMAGE:3976184.3
7887	17680	27688	3.83	9.2E-01	11430903	NT	Human sapiens histosomal apyrase-like protein 1 (LALPL1), mRNA
7952	17802	28041	1.73	9.2E-01	BF664251.1	EST_HUMAN	763806.01 NCI-GAP K1G1 Homo sapiens cDNA clone IMAGE:3878219.3 similar to SWNU5M_TTVB8
8980	18767	29059	1.85	9.2E-01	BF74202.1	EST_HUMAN	763806.01 NCI-GAP K1G1 Homo sapiens cDNA clone IMAGE:3878219.3 similar to SWNU5M_TTVB8
9006	18869	29101	2.01	9.2E-01	BF690047.1	EST_HUMAN	602163729T1 NH JMC-93 Homo sapiens cDNA clone IMAGE:4052018.6
2077	11957		1.43	6.1E-01	8623066	NT	Human sapiens hypophyseal protein FL20048 (FL20048), mRNA
3165	13094	22889	0.87	9.1E-01	T26418.1	EST_HUMAN	AB200GBR Infant brain, L1LN array of Dr. M. Soares IN1B Homo sapiens cDNA clone L1A200GB 5'
3166	13094	22889	0.87	9.1E-01	T26418.1	EST_HUMAN	AB200GBR Infant brain, L1LN array of Dr. M. Soares IN1B Homo sapiens cDNA clone L1A200GB 5'
4310	14207	23891	0.86	9.1E-01	U26418.1	EST_HUMAN	AB200GBR Infant brain, L1LN array of Dr. M. Soares IN1B Homo sapiens cDNA clone L1A200GB 5'
5919	15524	24950	2.92	9.1E-01	Q61704	SWISSPROT	INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H3 PRECURSOR (ITI-HEAVY CHAIN H3)
6472	16331	28498	15.99	9.1E-01	A0406623.1	EST_HUMAN	dbTg08.51 NC CGAP CGAP CGAP Homo sapiens cDNA clone IMAGE:1336822.3
6591	16409	26587	2.2	9.1E-01	AF20965.1	EST_HUMAN	dbTg08.51 NC CGAP CGAP CGAP Homo sapiens cDNA clone IMAGE:1336822.3
8446	19441		30.05	9.1E-01	U706013.1	NT	Human sapiens uncoupling protein-3 (UCP3) gene, complete cds
3700	13085	22900	0.89	9.0E-01	7661625	NT	Human sapiens neurotensin II-alpha gene, partial cds
4321	14161	23859	2.27	9.0E-01	AF069810.1	EST_HUMAN	Human sapiens DNF-276M42/292 protein (DNF276M42/292), mRNA
4946	14821	24689	0.82	9.0E-01	AF071726.1	EST_HUMAN	Oryzlatagus caricularis Raut51 (RAU51) mRNA, complete cds
8338	16250		1.45	9.0E-01	D03661.1	NT	Xenopus laevis genes for aldolase, complete cds

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (100%) Hit EST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5494	15413	25476	2.08	8.9E-01/AF026198.1	NT		Fugu ribunpes neutral cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds, putative protein 1 (PUT1) gene, partial cds, mitosis-specific chromosome segregation protein SMC1 homolog (SMC1) gene, complete cds, and calcium channel alpha-1 subunit
5760	15592			8.9E-01/X00986.1	NT		Rabbit MHC fragment RLA-DF DNA
8890	18794	29085	1.32	8.9E-01/AE03944.1	NT		Xyella fastidiosa, section 9A of the complete genome
9285	18987	29085	3.47	8.9E-01/AE02186.2	NT		Gliemaphysalis punctum AFS39, section 21 of 84 of the complete genome
4442	14336	24120	3.28	8.9E-01/O26330	SWISSPROT		PUTATIVE F420-DEPENDENT NADP REDUCTASE
8430	18304	28560	2.98	8.9E-01/O26337.1	NT		M.aeruginosa (HUB 5-2-4) DNA from plasmid PMA1
9108	18722		1.75	8.9E-01/O60911.1	NT		Synecocystis sp. PCC-5803 complete genome, 13,27, 15/5592-17/10643
457	10401	20218	1.84	8.7E-01/AF06953.2	NT		Homo sapiens SOST (SOST) gene, partial cds
2393	12233	22130	1.09	8.7E-01/5901833	NT		Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA
2845	12773	22560	4.64	8.7E-01/A469963.1	EST_HUMAN		hm05f11.s1 NC1, CGAP_P4.1 Homo sapiens cDNA clone IMAGE:1078377
4938	14816		2.51	8.7E-01/AF121070.1	NT		Pseudomonas aeruginosa P-40, suddenly XXVIIA (steroid 27-hydroxylase, cerebrotendinous xenotomatus), polyprotein 1 (C1P27A1b) mRNA
7013	17464	27681	1.45	8.7E-01/AE04993.1	NT		Pseudomonas aeruginosa PA01, section 124 of 129 of the complete genome
8306	18900	28243	5.47	8.7E-01/BF039710.1	EST_HUMAN		OV0.NN1021-103800.337-c03 NN1021 Homo sapiens cDNA
8570	18778	28067	4.18	8.7E-01/BF07894.1	EST_HUMAN		60182359461 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043564.3'
8570	18778	28068	4.18	8.7E-01/BF07894.1	EST_HUMAN		60182359461 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043564.3'
9488	18334		2.78	8.7E-01/AF01688.1	EST_HUMAN		XV661898 GLC Homo sapiens cDNA clone SLOC3(807.3)
466	10409		1.66	8.6E-01/AT01712.1	NT		Rat ORF1 gene for insulin-like growth factor 1
840	10767	20618	3.62	8.6E-01/W60488.1	EST_HUMAN		2844403.11 Source: "fetal heart (F04H107) Homo sapiens cDNA clone IMAGE:343515.5"
2224	12109	22012	1.01	8.6E-01/4903210	NT		Xenotomatus, polyprotein 1 (C1P27A1b) mRNA
3568	13482	23273	0.81	8.6E-01/AL161955.2	NT		Aradipos thaliana DNA chromosome 4, coding fragment No. 65
3730	13642	23427	1.29	8.6E-01/467294.1	NT		Drosophila melanogaster morph (Omerit) mRNA, complete cds
5595	15509	25590	11.82	8.6E-01/X00547.1	NT		Chicken lipoprotein lipase gene
5595	15509	25587	11.82	8.6E-01/X00547.1	NT		Chicken lipoprotein lipase gene
6030	15934	26065	2.14	8.6E-01/AF143732.1	NT		Grus canadensis recombinant activating protein 1 (RAG-1) gene, partial cds
6030	15934	26066	2.14	8.6E-01/AF143732.1	NT		Grus canadensis recombinant activating protein 1 (RAG-1) gene, partial cds
6626	16906		1.92	8.6E-01/AP001618.1	NT		Bacillus halodurans genomic DNA, section 12/14
6443	16904	26168	2.75	8.5E-01/BE42612.1	EST_HUMAN		6010697107F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3463505.5'
7824	17774	28013	1.36	8.5E-01/AB00769.1	NT		Cyrenidium ciliatum gene for Sgc, complete cds
7824	17774	28014	1.36	8.5E-01/AB00769.1	NT		Cyrenidium ciliatum gene for Sgc, complete cds

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Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9430	19649		2.92	8.5E-01	11418543	NT	Homo sapiens human immunodeficiency virus type 1 enhancer-binding protein 1 (HIVBP1), mRNA
9436	19075		2.03	8.5E-01	9507008	NT	Rattus norvegicus protein tyrosine phosphatase, non-receptor type 5 (Ptpn5), mRNA
9683	19238	25243	1.29	8.5E-01	AB030816.1	NT	Mus musculus mper gene for period1, complete cds
4108	14008	23785	0.84	8.4E-01	AF143508.1	NT	Mus musculus NK cell receptor 2B4 gene, promoter region and partial cds
5378	19443	25145	2.7	8.4E-01	76726.1	NT	Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 7
5378	19443	25145	2.7	8.4E-01	76726.1	NT	Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 7
7721	17571		3.13	8.4E-01	A248287.1	NT	Pyrococcus aloyes complete genomic segment 5/8
724	10566	20498	2.31	8.3E-01	A248287.1	NT	Thermus thermophilus cyclochrome c-552 (cycA) and CycB (cycB) genes, complete cds
3006	12883	22774	2.64	8.3E-01	AL161066.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 18
3738	13651	23494	1	8.3E-01	AB010579.1	NT	Nicotiana glauca mRNA for chloroplast ribosomal protein L10, complete cds
3830	13839	23618	3.11	8.3E-01	U19177.1	NT	Streptomyces antibioticus polyketide biosynthetic gene cluster
4817	14769	24570	1.12	8.3E-01	U49918.1	NT	Gene families MHC DLA Class II DRB pseudogene DR32
4517	14769	24571	1.12	8.3E-01	U49918.1	NT	Gene families MHC DLA Class II DRB pseudogene DR32
5171	14769	24570	0.95	8.3E-01	U49918.1	NT	Gene families MHC DLA Class II DRB pseudogene DR32
5171	14769	24571	0.95	8.3E-01	U49918.1	NT	Gene families MHC DLA Class II DRB pseudogene DR32
5222	15143	24939	2.13	8.3E-01	AL161540.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 49
7873	17424		4.2	8.3E-01	AF191982.1	EST_HUMAN	hMO17L2.6 NO1_G04P_C08 Homo sapiens cDNA clone IMAGE:1076465 5' similar to contains THR11 THR12 repeat element
7823	17672	27914	1.23	8.3E-01	AF198070.1	NT	Drosophila melanogaster Ust homolog mRNA, complete cds
7897	17717	27992	3.1	8.3E-01	AF108135.1	NT	Mus musculus neuro-44 gene, exons 3 through 12 and partial cds
8602	17953	28204	2.49	8.3E-01	AE000003.1	NT	Methanobacterium thermoautotrophicum from basar 1270510 to 1283409 (section 109 of 148) of the complete genome
8676	17997		2.48	8.3E-01	7212472	NT	Phycophthora infestans mitochondrial, complete genome
8623	18488	28700	2.03	8.3E-01	AF102053.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (PHIT) gene, exon 5
2005	11898	21789	2.89	8.2E-01	AB000488.1	NT	Rattus norvegicus mRNA for RHPO-1, complete cds
2043	11934		1.51	8.2E-01	AF14559.1	NT	Mus musculus trophobin (Ttn) gene, complete cds
2646	12813		1.14	8.2E-01	AF375989.1	EST_HUMAN	IL3-C1021B-101199-403-C08 CT0219 Homo sapiens cDNA
5045	14917	24991	1	8.2E-01	AB000488.1	NT	Rattus norvegicus mRNA for RHPO-1, complete cds
6122	10019	26154	3.26	8.2E-01	AF197433.1	EST_HUMAN	GMA-H10243-081199-037-407 H10243 Homo sapiens cDNA
6309	19462	20330	3.58	8.2E-01	Z12126.1	NT	S.cerevisiae MET4 and POL1 genes encoding MET4 protein, alpha-isopropylmalate (alpha-IPM) synthetase (partial), and DNA polymerase alpha (partial)
7788	17938	27871	1.53	8.2E-01	AF106259.1	NT	Homo sapiens threosol-related protein mRNA, complete cds
7837	17787	28028	6.09	8.2E-01	G81070	SWISSPROT	BACKUSICK-KALIFMANBARDEAR-BEDL SYNDROMES PUTATIVE CHAPERONIN

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7987	17787	26026	6.66	8.2E-01 Q6J70	SWISSPROT	NT	MOCKUSCKKAUFMANBARDEI BLED SYNDRONES PUTATIVE CHAPERONIN
8909	18717	29011	2.81	8.2E-01 L10327.1	NT	NT	Motacilla contagium Mus type 1 ORF1 and ORF2 DNA
8998	18777	29004	6	8.2E-01 P10383	SWISSPROT	NT	OVARY TUMOR LOCUS PROTEIN
8971	18777	29009	6.85	8.2E-01 H67388.1	EST_HUMAN	NT	YV14002.1 Soares, placenta, 3x6weeks, 2Ndr#86cW Homo sapiens cDNA clone IMAGE:282195 5' similar to gp.M5072.605 RIGOSOMAL PROTEIN L7A (HUMAN);
9451	19083	25284	1.73	8.2E-01 AJ001261.1	EST_HUMAN	NT	Mus musculus mRNA for NIFSNAP2 protein
2731	12329	22130	1.26	8.1E-01 AF194839.1	NT	NT	Mus musculus TANK binding kinase TBK1 (TBK1) mRNA, complete cds
3412	13326	23130	2.81	8.1E-01 AF050596.1	NT	NT	Mus musculus MHC class 1 region
3412	13326	23121	2.81	8.1E-01 AF050596.1	NT	NT	Homo sapiens MHC class 1 region
5992	16897	20020	2.49	8.1E-01 Q13149	SWISSPROT	NT	Homo sapiens MHC class 1 region
5992	16897	20020	2.49	8.1E-01 Q13149	SWISSPROT	NT	NEURONAL MEMBRANE GLYCOPROTEIN NG2-B
8775	18392	28679	1.94	8.1E-01 BE634958.1	EST_HUMAN	NT	NEURONAL MEMBRANE GLYCOPROTEIN NG2-B
8775	18392	28680	1.94	8.1E-01 BE634958.1	EST_HUMAN	NT	ROD-TN0080-220080-025-d10 TN0080 Homo sapiens cDNA
8775	18392	28680	1.94	8.1E-01 BE634958.1	EST_HUMAN	NT	ROD-TN0080-220080-025-d10 TN0080 Homo sapiens cDNA
9168	18590	25543	1.84	8.1E-01 AE201711.1	NT	NT	Thermogaia maritima section 23 of 135 of the complete genome
170	10142	10142	3.02	8.0E-01 AJ271510.1	NT	NT	Staphylococcus aureus partial pla gene for phosphate acetyltransferase allele 15
285	10250	20070	3.76	8.0E-01 AJ132772.1	EST_HUMAN	NT	Bos taurus tub and rrlf genes
1960	11884	20070	1.83	8.0E-01 BF530982.1	EST_HUMAN	NT	ROD72473P1 NCI COAP Bm67 Homo sapiens cDNA clone IMAGE:4215099 5'
9309	12867	22781	2.73	8.0E-01 AF179897.1	NT	NT	Samol. boliviensis olfactory receptor (SB023) gene, partial cds
3273	13354	22993	1.18	8.0E-01 AE001693.1	NT	NT	Mus musculus gene for cytochrome P450 2A9, complete cds
3434	13587	23943	1.4	8.0E-01 AL162758.2	NT	NT	Nesitene meningialis oligodendrocyte group A strain Z249T complete genome, segment 7/7
4452	14327	24115	5.65	8.0E-01 X63730.2	NT	NT	G.gallus mRNA for nicotinic acetylcholine receptor (nAChR) beta 3 subunit
6951	16541	20211	2.84	8.0E-01 AW091489.1	EST_HUMAN	NT	ROD-N10172-270300-021-H05 N101012 Homo sapiens cDNA
668	10030	20211	3.78	7.9E-01 D11476.1	NT	NT	Lymantria dispar nuclear polyhedrales virus gene for DNA polymerase, complete cds
668	10030	20211	3.78	7.9E-01 D11476.1	NT	NT	Unspliced nascent section 31 of 59 of the complete genome
1587	11491	18571	65.97	7.9E-01 AB010885.1	NT	NT	Homo sapiens mRNA for KIAA1452 protein, partial cds
1587	11491	18571	65.97	7.9E-01 U32739.1	NT	NT	Haemophilus influenzae Rd section 54 of 163 of the complete genome
2216	12102	22006	5.24	7.9E-01 AF004815.1	NT	NT	Oryzylagus curticulus mRNA for mitsugumiin28, complete cds
2217	12103	22007	2.26	7.9E-01 AF130459.1	NT	NT	Danio rerio TPA-associated protein 1 (Tpa1) (tapa1) mRNA, complete cds
3472	13368	23163	2.75	7.9E-01 AF226964.1	NT	NT	Gallus gallus SOX8 transcription factor (SOX8) mRNA, complete cds
4204	14103	24103	0.82	7.9E-01 BE263912.1	EST_HUMAN	NT	90119203P1 NIH LMOC_7 Homo sapiens cDNA clone IMAGE:395786 5'
4508	14401	24180	1.02	7.9E-01	NT	NT	Mus musculus embryo (Emb), mRNA
4508	14401	24180	1.02	7.9E-01	NT	NT	Mus musculus embryo (Emb), mRNA
5075	14845	24721	0.84	7.9E-01 Z47210.1	NT	NT	S.pneumoniae tdc3, cap3A, cap3B and cap3C genes and orfs
5075	14845	24721	0.84	7.9E-01 Z47210.1	NT	NT	S.pneumoniae tdc3, cap3A, cap3B and cap3C genes and orfs

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5084	14954		1.01	7.6E-01	M2660.1	NT	Human insulin receptor (allele 2) (gene, exons 14, 15, 16 and 17
6721	16001	20790	2.43	7.6E-01	X06966.1	NT	P sodium GR gene
7504	17973	27582	4.78	7.6E-01	U01912.1	NT	Gardia lamella variant-specific surface protein G3MB (vsg3MB-B) mRNA, partial cds
7781	17631	27864	3.95	7.6E-01	P19719	SWISSPROT	SMALL HYDROPHOBIC PROTEIN
8372	18249		2.93	7.6E-01	7002471	NT	Homo sapiens KIAA1072 protein (KIAA1072) mRNA
8543	18415	26982	2.48	7.6E-01	P19022	SWISSPROT	NEURAL CADHERIN PRECURSOR (NCADHERIN)
858	10784		1.75	7.6E-01	Z43785.1	EST_HUMAN	HSC1H4041 normalized infant brain cDNA Homo sapiens cDNA clone c-1h404
2229	12114	22016	3.2	7.6E-01	AW056507.1	EST_HUMAN	HS1271637 MAGC resequences, MAGF Homo sapiens cDNA
4603	14497	24278	0.79	7.6E-01	U87305.1	NT	Rattus norvegicus transmembrane receptor Unc5H1 mRNA, complete cds
5698	15607	25709	2.32	7.6E-01	AF115858.1	NT	Sphonodon punctatus alpha enolase mRNA, partial cds
7323	17198	27588	1.27	7.6E-01	U01561.1	NT	D discoideum rec2AP gene
8424	18623		1.42	7.6E-01	U2060.1	NT	Arabidopsis thaliana L-termeo-L-cyclopropanecarboxylate synthase (ACS5) (gene, complete cds
138	10112	19832	6.93	7.7E-01	AF194345.1	NT	Lycopodium obscurum ADP-glucose pyrophosphorylase large subunit (AGP-L1) mRNA, complete cds
709	10841		1.85	7.7E-01	AF050187.1	NT	Mus musculus major histocompatibility locus class II region major histocompatibility protein class II alpha chain (H2alpha) and major histocompatibility protein class II beta chain (H2beta) genes, complete cds, butyrophilin-like (NIG3), butyrophilin-1b
2680	12545	22435	2.8	7.7E-01	Q33913	SWISSPROT	CITRATE SYNTHASE
3213	13234		0.8	7.7E-01	8930408	NT	Homo sapiens UDP-N-acetylglucosyl-6-phosphate D-glucosylamine polypyrrolidase N-acetylglucosylamine transferase 7 (GNA4C-T7) (GNA4C-T7) cDNA
3540	13661	23285	4.43	7.7E-01	AF118035.1	NT	Homo sapiens PRO1675 mRNA, complete cds
4297	14193	23779	2.88	7.7E-01	AF159483.1	NT	Calumic columnia japonica sub-species japonica beta-actin mRNA, partial cds
4297	14195	23960	2.88	7.7E-01	AF159488.1	NT	Calumic columnia japonica sub-species japonica beta-actin mRNA, partial cds
5415	13533	25986	1.44	7.7E-01	P10653	SWISSPROT	RAFFINOSE INVERTASE (INVERTASE)
5415	13533	25987	1.44	7.7E-01	P10653	SWISSPROT	RAFFINOSE INVERTASE (INVERTASE)
5626	15541	25930	1.95	7.7E-01	R08900.1	EST_HUMAN	Y624022.1 Soares testis liver antigen INFLS Homo sapiens cDNA clone IMAGE:277653
9212	10112	19832	2.8	7.7E-01	AF194345.1	NT	Lycopodium obscurum ADP-glucose pyrophosphorylase large subunit (AGP-L1) mRNA, complete cds
9311	13904		6.14	7.7E-01	11497621	NT	Archaeoglobus fulgidus, complete genome
5710	15618	25720	4.04	7.6E-01	AF069510.1	NT	Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase non-biotinylated subunit (MCCB) mRNA, complete cds
5710	15618	25721	4.04	7.6E-01	AF069510.1	NT	Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase non-biotinylated subunit (MCCB) mRNA, complete cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Distance Score	Top Hit Descriptor
6689	16579	26770	1.41	7.8E-01	AF146793.2	NT	Mouse musculus neuromedin U precursor (Nmu) gene, partial cds; (PNU) gene, partial cds; CLOCK (Clock) gene, complete cds; PTTZ (Pttz) gene, complete cds; and HSNR (Hsnr) gene, complete cds
6726	16590	29756	2.04	7.8E-01	683762	NT	Mouse musculus actin (Acta-penrig), mRNA
6730	16601	29767	2.04	7.8E-01	683762	NT	Mouse musculus actin (Acta-penrig), mRNA
7184	17061	27252	1.28	7.8E-01	673557	NT	Mouse musculus cytochrome P-450, 28a pseudosubtil inducible, type a (Cyp28a), mRNA
7347	17215	27414	7.62	7.8E-01	673372	SWISSPROT	MUSCARNIC ACETYLCHOLINE RECEPTOR M2
7347	17215	27414	7.62	7.8E-01	P03072	SWISSPROT	MUSCARNIC ACETYLCHOLINE RECEPTOR M2
8664	18353	28837	2.31	7.8E-01	X98347.1	NT	H. sapiens mRNA for neurofilament NF70
8664	18353	28838	2.31	7.8E-01	X98347.1	NT	H. sapiens mRNA for neurofilament NF70
8948	18785	28838	4.81	7.8E-01	AL161562.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 88
9073	18850		2.74	7.8E-01	AE020702.1	NT	Human sapiens mRNA for KIA00935 protein, partial cds
602	10444		1.92	7.8E-01	AL163301.2	NT	Human sapiens chromosome 21 segment HS21C101
569	16058	20315	2.23	7.8E-01	AF405003.1	NT	Human sapiens FRAXB common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
3315	13236	23040	0.88	7.8E-01	C14203.1	EST_HUMAN	C14203 Clontech human actin pcDNA+ mRNA (68572) Homo sapiens cDNA clone GEM-037E11.5
4573	10083	19900	13.92	7.8E-01	8922072	NT	Human sapiens hypothetical protein FLJ107932 (FLJ10793), mRNA
9381	19042		3.57	7.8E-01	AF16314.1	NT	Human sapiens dentin sialophosphoprotein precursor (DSPP) gene, complete cds
8528	19329	23209	1.87	7.8E-01	D09007.1	NT	Synchaetococcus sp. PC06803 complete genome, 9/27, 1094647.1168885
8984	19366	25190	1.42	7.8E-01	AE000823.1	NT	Methanobacillus thermoautotrophicum from basus 317350 to 328762 (section 29 of 149) of the complete genome
1114	11029	20866	1.23	7.4E-01	A1569146.1	EST_HUMAN	h14009.x1 NCL CGAP_Bm25 Homo sapiens cDNA clone IMAGE216797.3 similar to contains Au repetitive element/containing element MIR repetitive element;
2295	12177	22076	0.97	7.4E-01	AB011108.1	NT	Human sapiens mRNA for KIA00834 protein, partial cds
3205	13579	23366	1.22	7.4E-01	AF112538.1	NT	Malva pusilla actin (Act1) mRNA, complete cds
4013	14111	23860	4.43	7.4E-01	AL163246.2	EST_HUMAN	Human sapiens chromosome 21 segment HS21C046
7256	17135	27328	7.23	7.4E-01	BE175603.1	EST_HUMAN	80157520XHF1 NIH_M9C_9 Homo sapiens cDNA clone IMAGE383474.5
9041	18326		3.28	7.4E-01	0735217	NT	h1301.x1 NCL CGAP_Lym5 Homo sapiens cDNA clone IMAGE2059685.3
9150	18701		1.99	7.4E-01	A1472841.1	EST_HUMAN	Human sapiens chromosome 21 segment HS21C046
14515	14008	24194	0.95	7.3E-01	AF2041108.1	NT	Mus musculus complement component 1 inhibitor (C1inh)
4602	14490	24277	4.76	7.3E-01	AF225421.1	NT	Borrelia burgdorferi Lyme5 Homo sapiens cDNA clone IMAGE2059685.3
5127	14894		1.17	7.3E-01	AF225421.1	NT	Human sapiens growth arrest-specific 7 (GAS7), transcript variant b, mRNA
5984	15889	29011	5.61	7.3E-01	33402211	NT	Human sapiens H10717 mRNA, complete cds
5984	15889	29011	5.61	7.3E-01	33572.1	NT	Human sapiens growth arrest-specific 7 (GAS7), transcript variant b, mRNA
5984	15889	29011	5.61	7.3E-01	33572.1	NT	Mus musculus antigen (G372) gene

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6454	13515	26460	7.42	7.3E-01	M26511.1	NT	V. alginolyticus surface (scb) gene, complete cds
6454	13515	26461	7.42	7.3E-01	M26511.1	NT	V. alginolyticus surface (scb) gene, complete cds
8728	18255	28670	3.29	7.3E-01	X1678018.1	EST_HUMAN	223508.31 Sources, full [ref_seq]_N16L5_31 Homo sapiens cDNA clone IMAGE:431799.3
8728	18255	28671	3.29	7.3E-01	X1678018.1	EST_HUMAN	223508.31 Sources, full [ref_seq]_N16L5_31 Homo sapiens cDNA clone IMAGE:431799.3
1414	-10742		2.34	7.2E-01	X32921.1	NT	Rattus norvegicus insulin-like-2 kinase (IR-2a) mRNA, complete cds
1914	11809	21687	3.88	7.2E-01	X37440.1	NT	R. laevis non-muscle myosin heavy chain 2-1 mRNA
2412	12259	22168	1.48	7.2E-01	A03069003.1	EST_HUMAN	Gallus gallus gene for melanocortin 2-receptor, complete cds
3028	12259	22748	1.16	7.2E-01	AF198100.1	NT	Fowlpox virus, complete genome
3408	13323	23124	2.14	7.2E-01	AF066908.1	NT	Glutathione S-transferase pi-1 (GSTP1) gene, complete cds
3795	13707	23464	1.31	7.2E-01	BF193350.1	EST_HUMAN	U135559.07 NCBI CGAP: Bm64 Homo sapiens cDNA clone IMAGE:418322.5
4860	14848	24335	2.41	7.2E-01	D00314.1	NT	L-mimosine-inducible gene for arabinose phosphotransferase (EC 2.1.1.7)
6064	14834	24706	1.16	7.2E-01	AF198779.1	NT	Homo sapiens transcription factor (GSM) enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A44 differentiation-dependent protein, triple LIM domain protein 6, and synapophysin genes, complete cds, and L-type calcium channel α
6094	14834	24707	1.16	7.2E-01	AF198779.1	NT	Homo sapiens transcription factor (GSM) enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A44 differentiation-dependent protein, triple LIM domain protein 6, and synapophysin genes, complete cds, and L-type calcium channel α
6823	16801	28984	1.21	7.2E-01	AF230681.1	NT	Ornithine decarboxylase (ODC) gene, complete cds
7922	17172	28011	2.22	7.2E-01	BF970081.1	EST_HUMAN	902115381.FT NIH_MGC_36 Homo sapiens cDNA clone IMAGE:427581.9
8121	18009	28256	4.78	7.2E-01	U26232.1	NT	Rattus norvegicus cyclo-oxygenase mRNA, complete cds
8570	19100		4.08	7.2E-01	AF000003.1	NT	Aeropyrum pernix genomic DNA, section 87
677	10810	20431	10.38	7.1E-01	D21070.1	NT	Rana celsae-like mRNA for buffering skeletal muscle calcium release channel (ryanodine receptor) alpha isoform (RYR1), complete cds
3024	12562	23745	10.8	7.1E-01	AJ27077.1	NT	Homo sapiens partial TCF-4 gene for T-cell transcription factor-4, exons 15-18
4114	14014	23763	2.93	7.1E-01	T395350	NT	Mus musculus atropisin (Atop), mRNA
4114	14014	23764	2.93	7.1E-01	T395350	NT	Mus musculus atropisin (Atop), mRNA
5923	15538	25675	1.86	7.1E-01	BF481034.1	EST_HUMAN	902155438.FT NIH_MGC_83 Homo sapiens cDNA clone IMAGE:426834.5
5923	15538	25676	1.86	7.1E-01	BF481034.1	EST_HUMAN	902155438.FT NIH_MGC_83 Homo sapiens cDNA clone IMAGE:426834.5
6149	16022	28162	1.97	7.1E-01	U09323.1	NT	Oncoprotein melanogaster 6-pyruvate/hydroxypyruvate synthase (crt) gene, complete cds
7747	17745	27445	2.25	7.1E-01	BE904405.1	EST_HUMAN	901490331.FT NIH_MGC_70 Homo sapiens cDNA clone IMAGE:359495.5
7659	17550		1.61	7.1E-01	AF044149.1	EST_HUMAN	003811.1 Sources, testis, NHT Homo sapiens cDNA clone IMAGE:731109.3
8353	18519		1.04	7.0E-01	AB014514.1	EST_HUMAN	Homo sapiens mRNA for KIAA0814 protein, partial cds
1209	11118	20966	1.04	7.0E-01	AB014514.1	EST_HUMAN	Homo sapiens mRNA for KIAA0814 protein, partial cds
1209	11118	20967	1.04	7.0E-01	AB014514.1	EST_HUMAN	Homo sapiens mRNA for KIAA0814 protein, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2399	12277	22173	1.4	7.0E-01	N62412.1	EST_HUMAN	y23607.s1 Scores: multiple, adenosine, 2_NHMGSP Homo sapiens cDNA clone IMAGE:288708 3' similar to contains Alu repetitive element;
2399	12277	22174	1.4	7.0E-01	N62412.1	EST_HUMAN	y23607.s1 Scores: multiple, adenosine, 2_NHMGSP Homo sapiens cDNA clone IMAGE:288708 3' similar to contains Alu repetitive element;
4899	14984	169301	1.96	7.0E-01	AJ169301.2	NT	Human chromosome 21 segment HS21C101
6890	14984	169301	8.1	7.0E-01	A5000233.1	NT	Escherichia coli K-12 MG1695 section 148 of 400 of the complete genome
8483	18336	20599	2	7.0E-01	AF1769342.1	EST_HUMAN	AF1769342 MDS Homo sapiens cDNA clone MDSCHG4.5
8483	18336	20599	2	7.0E-01	AF1769342.1	EST_HUMAN	AF1769342 MDS Homo sapiens cDNA clone MDSCHG4.5
954	10878	20725	15.73	6.9E-01	U69574.1	NT	Candida albicans squelone apodase (CAERG1) gene, complete cds and translational regulator gene, partial cds
954	10878	20726	15.73	6.9E-01	U69574.1	NT	Candida albicans squelone apodase (CAERG1) gene, complete cds and translational regulator gene, partial cds
1268	11160	21049	2.21	6.9E-01	A5003520.1	EST_HUMAN	CH249203.s1 NQ_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1085778 3'
3399	13317	22611	1.83	6.9E-01	A500222.1	EST_HUMAN	Chlamydia muridarum, section 3 of 85 of the complete genome
6652	16523	23726	0.95	6.9E-01	Y17373.1	NT	Mus musculus mRNA for immunoglobulin gamma heavy chain variable region, isolate PC 2B11
6652	16523	23726	2.73	6.9E-01	AF161573.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69
6852	18523	26727	2.73	6.9E-01	AF161573.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69
8582	18450	26729	3.96	6.9E-01	D06013.1	NT	Homo sapiens DNA gene, complete cds
8582	18450	26729	3.96	6.9E-01	D06013.1	NT	Homo sapiens DNA gene, complete cds
9016	16543		2.37	6.9E-01	Q09698	SWISSPROT	FOURHEAD BOX PROTEIN C2 (FOURHEAD-RELATED PROTEIN FKH14) (MESENCHYME FORK HEAD PROTEIN 1) (MFI-1 PROTEIN) TRANSCRIPTION FACTOR FRH-14
9411	10566	20713	1.03	6.9E-01	AF0171784.1	NT	Shred intestinalis cuticularinase mouse gene, complete cds
2639	12566		1.16	6.9E-01	D06917.1	NT	Synectochytrid sp. Q06803 complete genome, Z1727.31 18565-3573470
2798	11920	21962	1.98	6.8E-01	AJ0644475.1	EST_HUMAN	476616.s1 Scores: Parathyroid, Unim, NRP4, Homo sapiens cDNA clone IMAGE:1402566 3' similar to gc365941.1, mat ALCOHOL DEHYDROGENASE CLASS II P1 (CHAMANE);
4499	14393	21453	1.26	6.8E-01	J00762.1	NT	Rat(hooded) protein gene: exon II and flanks
4748	14634	24420	0.83	6.8E-01	A5003706.1	NT	Homo sapiens thurin (HEVIN) mRNA
7658	17407	27622	1.52	6.8E-01	A5003706.1	NT	Homo sapiens thurin (HEVIN) mRNA
8437	18311	20566	2.34	6.8E-01	AJ276975.1	NT	Stagonopora avenue biffi gene for beta-glucosidase, exons 1-4
8437	18311	20567	2.34	6.8E-01	AJ276975.1	NT	Stagonopora avenue biffi gene for beta-glucosidase, exons 1-4
8489	18331	20562	2.80	6.8E-01	AF176930.1	NT	Mus musculus zinc finger protein (Peg3) mRNA, complete cds
8489	18331	20562	2.80	6.8E-01	AF176930.1	NT	Mus musculus zinc finger protein (Peg3) mRNA, complete cds
8450	18331	20564	2.69	6.8E-01	AF176930.1	NT	Anopheles gambiae anfr M2 translation initiation factor (4C) (eIF-4C) mRNA, complete cds
9819	18495	20767	1.79	6.8E-01	AF164119.1	NT	Anopheles gambiae anfr M2 translation initiation factor (4C) (eIF-4C) mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	QF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
295	10256	20080	26.34	6.7E-01	AF21384.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFkB1) gene, complete cds
338	10255	20110	19.53	6.7E-01	AF21384.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFkB1) gene, complete cds
2100	11989	21887	1.57	6.7E-01	AA451954.1	EST_HUMAN	z11212.1 Soares, total_fetus_1b22HF8_3w Homo sapiens cDNA clone IMAGE760310 3' similar to contains element TAR1 repetitive element
2120	12713	21908	3.59	6.7E-01	AF18073.1	NT	Drosophila melanogaster MatB5C gene, complete cds; NMDMC isoform (Nmdmc) gene, complete cds, alternatively spliced; and transcription factor (Rakt) gene, complete cds, alternatively spliced
2966	12853	22652	3.7	6.7E-01	6578580	NT	Mus musculus Winkler-Aldrich syndrome protein (Wasp), mRNA
4350	12426	24032	0.94	6.7E-01	X74241.1	NT	S. tuberosum mRNA for glucose-6-phosphate dehydrogenase
4881	14792	24539	0.85	6.7E-01	AY07910.1	EST_HUMAN	x65911.2 X1 NC1 CCNP_Cx17 Homo sapiens cDNA clone IMAGE:2574858 3'
6182	15046	24811	0.89	6.7E-01	AJ25242.1	NT	Dendrobium imbricatum mRNA for phosphoenolpyruvate carboxylase, partial
5927	15542	25631	1.62	6.7E-01	AE001486.1	NT	Helicobacter pylori, strain J99, section 47 of 132 of the complete genome
5817	15723	25836	1.42	6.7E-01	9635035	NT	Gaillard herpesvirus 2, complete genome
5817	15723	25837	1.42	6.7E-01	9635035	NT	Gaillard herpesvirus 2, complete genome
6329	16192	26397	3.98	6.7E-01	AE004906.1	NT	Pseudomonas aeruginosa PAO1, section 157 of 526 of the complete genome
6342	16205	26397	1.48	6.7E-01	AE004906.1	NT	Helicobacter pylori, strain J99, section 47 of 132 of the complete genome
8323	18200	26149	2.23	6.7E-01	BF55446.1	EST_HUMAN	OM3-HT0766-010600-197-403 HT0769 Homo sapiens cDNA
8754	17603	26147	3.69	6.7E-01	014337	SWISSPROT	N-ACETYL-GLUCOSAMINYL-PHOSPHATIDYLINOSITOL BIOSYNTHETIC PROTEIN GPI
21462	12339	22227	0.87	6.8E-01	AF075240.1	NT	Homo sapiens SLIT1 protein (SLIT2) mRNA, partial cds
2887	12532	22422	1.26	6.8E-01	AF165336.1	NT	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds
3445	13552	23168	1.04	6.8E-01	4505880	NT	Homo sapiens same domain, seven thymospondin repeats (Dps 1 and type 1-5e), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5a (SEMA5A) mRNA
3508	13552	23310	3.05	6.8E-01	U07969.1	NT	Callosin random DNA marker, 262bp
4020	13924			6.8E-01	U61328.1	NT	Human hereditary hemochromatosis region, histone 2A-like protein gene, hereditary hemochromatosis (H-H) gene, NRC3 gene, and sodium phosphate transporter (NPT3) gene, complete cds
5822	15728	25840	0.87	6.8E-01	6089577	NT	Nucleoside monophosphate kinase 2 (NCK2), mRNA
6525	15394	25953	3.63	6.8E-01	AY66506.1	EST_HUMAN	AY66506.6 Glc-Homo sapiens cDNA clone G1C6104 3'
7971	17422		2.41	6.8E-01	AL163278.2	NT	Homo sapiens chromosome 21 segment H52C078
9819	19197	25298	1.35	6.8E-01	AE004982.1	NT	Yargo chromosome chromosome 21 segment H52C078
808	10544	20352	1.37	6.8E-01	M75140.1	NT	H. vulgatus Na,K-ATPase alpha subunit mRNA, complete cds
808	10544	20353	1.37	6.8E-01	M75140.1	NT	H. vulgatus Na,K-ATPase alpha subunit mRNA, complete cds

Table 4

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
3388	13304	23104	5.1	6.05-01	A804125.1	NT	Mus musculus gene for Taz2, complete cds
3391	13356	23633	1.08	6.05-01	4904832	NT	Homo sapiens intracellular 10 receptor, alpha (IL (R5A)) mRNA
4185	14095	23860	4.17	6.05-01	AJ272285.1	NT	Homo sapiens SPZ2 gene for secreted phospholipase 24 precursor, exons 1-8
4216	14113	23850	0.88	6.05-01	AB11536.2	NT	Ancient hominid DNA chromosome 4, contig fragment No. 39
4984	14899	24632	2.27	6.05-01	U98921.1	NT	Phaeolectus vulgaris ATPase gamma subunit mRNA, nuclear gene encoding mitochondrial protein, partial cds
5176	16041		0.68	6.05-01	U97598.1	NT	Acetabularia lythium putative ATP binding protein delta-AcAb gene, partial cds, and GDP-mannose co-localized phospholipase alpha-mannosyltransferase gene, complete cds
6008	16593	26071	1.38	6.05-01	D88348.1	NT	Chicken mRNA for 115-40a melanosomal matrix protein, complete cds
7916	17916	28008	2	6.05-01	AJ115076.1	NT	Mus musculus small GTP-binding protein RAB29 (Rab29) gene, complete cds
8030	17922	28168	3.24	6.05-01	H67593.1	EST_HUMAN	HY706c.1 Soares placenta, 806weeks, 2NHP8369W Homo sapiens cDNA, clone IMAGE:253516 5'
8073	17964	28215	4.03	6.05-01	AJ001287.1	EST_HUMAN	nt5037 at NCBI: CGAP Phet1 Homo sapiens cDNA, clone IMAGE:1100748 3'
8170	18089		4.27	6.05-01	AJ138078.1	EST_HUMAN	AUT38078 PLACE1 Homo sapiens cDNA, clone PLACE10078 5'
8877	18880	23881	2.3	6.05-01	AF014115.1	NT	Plasmodium berghei cytochrome c oxidase subunit III, cytochrome c oxidase subunit I, and cytochrome b genes, mitochondrial genes encoding mitochondrial proteins, complete cds
9415	19060		2.78	6.05-01	BE49530.1	EST_HUMAN	h741010.41 NC1: CGAP L224 Homo sapiens cDNA, clone IMAGE:3178130 3'
9951	19459		1.69	6.05-01	Z714145.1	NT	S.cerevisiae chromosome IV reading frame ORF YOL097c
282	10218	20035	5.4	6.04-01	U48848.1	NT	Drosophila melanogaster 8ld dyshen light chain mRNA, complete cds
3410	13327	23128	2.45	6.04-01	U48854.2	NT	Mus musculus dyctaloykcan 1 (DAG) 1 gene, exons 1 and 2, and complete cds
3365	13697	23464	1.34	6.04-01	AB048627.1	NT	Homo sapiens mRNA for KIAA1997 protein, partial cds
4789	14251	24069	0.94	6.04-01	Y12488.1	NT	M.musculus wtn gene
4350	14295	24067	0.84	6.04-01	Y12488.1	NT	M.musculus wtn gene
7007	18834	27016	1.78	6.04-01	AJ501247.1	NT	Trepionema pallidum section 63 of 67 of the complete genome
7807	17657	27805	13.62	6.04-01	U63238.1	NT	Homo sapiens axonin 2/melanofieldin (ATM) genes, complete cds
7818	17958	27963	1.44	6.04-01	BF670405.1	EST_HUMAN	002160289Ft NH_1M5C_81 Homo sapiens cDNA, clone IMAGE:328129 5'
9521	19135		6.34	6.04-01	AV178921.1	EST_HUMAN	HY76912.1 MDS Homo sapiens cDNA, clone MDS30039 5'
9581	19583		1.65	6.04-01	9845300	NT	Rat cytomagallotus Massinetti, complete genome
427	10372	20169	4.41	6.03-01	P06528	SWISSPROT	HISTONE-RICH PROTEIN PRECURSOR (CLONE PHR-III)
524	10460	20277	2.15	6.03-01	U02693.1	NT	Haemophilus influenzae Rd section 4 of 193 of the complete genome
2156	12005	21903	3.87	6.03-01	U81136.1	NT	Shigella flexneri multi-antigenic resistance locus
2514	12065	22300	3.89	6.03-01	Y75331.1	NT	Gallus gallus bone morphogenetic protein 1 (BMP1) mRNA, partial cds
2524	12408	22301	3.93	6.03-01	Y75331.1	NT	Gallus gallus bone morphogenetic protein 1 (BMP1) mRNA, partial cds
2983	12811		0.99	6.03-01	Y17275.1	NT	Lycopodium obscurum p65a gene, complete CDS

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3985	13922	23069	1.38	6.3E-01	596873.1	NT	D.melanogaster mRNA for metabotropic glutamate receptor
6599	16937	28791	3.17	6.3E-01	BE02044.1	EST_HUMAN	601676989.F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3960361 5'
7150	17027	27223	1.67	6.3E-01	S52927.1	NT	glycoprotein IIIa (JAI 1 and 3 fusion junction) [human, Genomic Mutant, 300 nt]
7421	17289	27495	2.72	6.3E-01	9627521	NT	Varicella virus, complete genome
7421	17289	27495	2.72	6.3E-01	9627521	NT	Varicella virus, complete genome
8024	17854	28095	1.4	6.3E-01	AE00313.1	NT	Escherichia coli K-12 MG1685 section_203 of 400 of the complete genome
8413	18298	28543	2.27	6.3E-01	MA87715.1	EST_HUMAN	nm00606.s1 NC1_QCAP_Co10 Homo sapiens cDNA clone IMAGE:1161371 5' similar to TR0023919 Q02916
8647	18311	28791	11.72	6.3E-01	A1804180.1	EST_HUMAN	HLARL :
8728	18391	28953	1.94	6.3E-01	P47003	SWISSPROT	Q01743-002299-048 BT043 Homo sapiens cDNA
8965	18650	28948	1.98	6.3E-01	P36073	SWISSPROT	HYPOHETICAL 15.3 KD PROTEIN IN INO1-H832 INTERGENIC REGION
9128	18697	24569	0.21	6.3E-01	5910293	NT	Homo sapiens keratin complex 2, gene Bc (K12-59)
9220	18844	24569	1.54	6.3E-01	AF105227.1	NT	Homo sapiens 3'-phosphoadenine 5'-phosphatransferase (PAPS) mRNA, complete cds
9405	19619	25069	1.69	6.3E-01	X83528.1	NT	G.lintulae pcdO gene
9578	19203	25069	3.02	6.3E-01	Q10135	SWISSPROT	HYPOHETICAL 142.5 KD PROTEIN C28E2.02 IN CHRO10-50A1
9626	19287	25069	5.09	6.3E-01	AF02283.1	NT	Mus musculus calcium-sensing receptor related protein 1 (CaSR-34) mRNA, partial cds
9631	19710	28933	5.45	6.3E-01	NT2253.1	EST_HUMAN	3901693.s1 Scans fold filter, Homo sapiens cDNA clone IMAGE:13542 3'
7435	18448	28638	1.71	6.2E-01	BE020387.1	EST_HUMAN	6013361-46F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:365010 5'
7476	17336	27462	2.86	6.2E-01	M24461.1	NT	Human pulmonary surfactant-associated protein SP-B (SP-TP3) mRNA, complete cds
7789	17949	27585	7.14	6.2E-01	AF161311.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 23
8007	17857	28099	5.02	6.2E-01	P27410	SWISSPROT	NON-STRUCTURAL POLYPROTEIN CONTAINS: RNA-DIRECTED RNA POLYMERASE ; THIOL PROTEINASE PC; HELICASE (2C LIKE PROTEIN); COAT PROTEIN
8007	17857	28100	5.02	6.2E-01	P27410	SWISSPROT	NON-STRUCTURAL POLYPROTEIN CONTAINS: RNA-DIRECTED RNA POLYMERASE ; THIOL PROTEINASE PC; HELICASE (2C LIKE PROTEIN); COAT PROTEIN
2348	12225	24677	4.5	6.1E-01	8678076	NT	Mus musculus secreted acidic cysteine rich glycoprotein (Sparc) mRNA
4931	14809	24677	0.89	6.1E-01	U20427.1	NT	Rattus norvegicus dihydropyrimidinase-related protein 1 (DPRP1) mRNA, complete cds
4931	14809	24678	0.89	6.1E-01	U20427.1	NT	Rattus norvegicus dihydropyrimidinase-related protein 1 (DPRP1) mRNA, complete cds
6104	15998	26134	3.78	6.1E-01	M84733.1	NT	Rat TRPM2 gene, complete cds
6104	15998	26135	3.78	6.1E-01	M84733.1	NT	Rat TRPM2 gene, complete cds
6792	16871	25963	3.72	6.1E-01	AF038353.1	NT	Arabidopsis thaliana putative zinc transporter (ZPT1) mRNA, complete cds
7108	16935	27176	1.76	6.1E-01	11431065	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 4 (MAP4K4), mRNA
7108	16935	27176	1.76	6.1E-01	11431065	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 4 (MAP4K4), mRNA
7419	17286	27462	19.47	6.1E-01	AF236117.1	NT	Homo sapiens G-protein coupled receptor EDG-7 mRNA, complete cds
7419	17286	27463	19.47	6.1E-01	AF236117.1	NT	Homo sapiens G-protein coupled receptor EDG-7 mRNA, complete cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7778	17038	27860	1.69	6.1E-01 AF110917.1	NT	NT	Homo sapiens oxparazine transporter (SLC6A3) gene, complete cds
4468	10240	20243	0.92	6.0E-01 D07075.1	NT	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
549	10460		2.84	6.0E-01	5802599	NT	Homo sapiens epsilon-related protein complex 3, mem 2 subunit (CL230) mRNA
3391	17245	21103	1.78	6.0E-01 AF068233.1	NT	NT	Homo sapiens respiratory syncytial virus strain CH-69-53b, attachment protein (G) gene, complete cds
3744	13065	24336	1.02	6.0E-01 AJ223306.1	NT	NT	<i>Vibrio anguillarum</i> epsilon-antitoxin genes N, P, M, G, W, L genes, French strain 07-71
92271	15131	24978	1.36	6.0E-01 F20283	SWISSPROT	SWISSPROT	CHDOPALIN RECEPTOR
5339	15260	25068	2.38	6.0E-01 AW139713.1	EST_HUMAN	EST_HUMAN	UHL-BF1-64b-5-100-1.5/1 NCL_CGAP_Suid3 Homo sapiens cDNA clone IMAGE:2718619.3
5940	15845	25868	2.61	6.0E-01 U38913.1	NT	NT	Musca domestica insecticide-susceptible strain voltage-sensitive sodium channel mRNA, complete cds
6350	16743	23675	6.2	6.0E-01 AJ277661.1	NT	NT	Homo sapiens partial LXR1 gene for LXR domain only 1 protein, exon 1
6725	16905	26764	4.19	6.0E-01 P02835	SWISSPROT	SWISSPROT	SEGMENTATION PROTEIN FUSH TARAZU
6726	16905	26766	4.19	6.0E-01 P02835	SWISSPROT	SWISSPROT	SEGMENTATION PROTEIN FUSH TARAZU
7653	17803	27727	1.69	6.0E-01 AE006193.1	NT	NT	Homo sapiens genes for leucotriens B4 receptor BLT2, leucotriens B4 receptor BLT1, complete cds
7894	17744		1.43	6.0E-01 Q01467	SWISSPROT	SWISSPROT	PEROXISOMAL MEMBRANE PROTEIN PERO (PEPX-N3)
8411	18286	26841	1.78	6.0E-01 AJ131892.1	NT	NT	Gallus gallus mRNA for tyrosin protein, 419 kb isoform
8411	18286	26842	1.78	6.0E-01 AJ131892.1	NT	NT	08007.x1 NCL_CGAP_P228 Homo sapiens cDNA, clone IMAGE:2098291.3
8838	18651	28039	2.74	6.0E-01 AJ426623.1	EST_HUMAN	EST_HUMAN	Homo sapiens nuclear factor (erythroid-derived 2-like 3) (NFE2L3), mRNA
9500	19115	25291	1.64	6.0E-01 11421693	NT	NT	Homo sapiens cAMP-inhibited phosphodiesterase (Pde3a), mRNA
9787	19881	24065	2.1	6.0E-01 905503	NT	NT	Homo sapiens nuclear factor (erythroid-derived 2-like 3) (NFE2L3), mRNA
9809	19484		2.18	6.0E-01 BE117617.1	EST_HUMAN	EST_HUMAN	RO-H1-0375-030500-015-c3 HT63.Homo sapiens cDNA
9841	20071	20762	1.26	5.9E-01 U37201.1	NT	NT	Haemophilus influenzae Rd section 16 of 163 of the complete genome
3232	33160	22364	4.85	5.9E-01 AJL193267.2	NT	NT	Homo sapiens chromosome 21 segment HS21C067
3232	33160	22365	4.85	5.9E-01 AJL193267.2	NT	NT	Homo sapiens chromosome 21 segment HS21C067
4129	14020		4.12	5.9E-01 AF162756.1	NT	NT	Rattus norvegicus cavinin 2 mRNA, partial cds
5880	15705	25017	2.1	5.9E-01 AF055140.2	NT	NT	Homo sapiens low density lipoprotein receptor-related protein II (LRP2) genes, exon 1 and partial cds
8061	17952	26033	2.97	5.9E-01 Q0303	SWISSPROT	SWISSPROT	THYMIDYLATE KINASE (DTMP KINASE)
8328	18205	28454	3.1	5.9E-01 AW037175.1	EST_HUMAN	EST_HUMAN	PWH-DT0041-190105-002-H03 DT0041 Homo sapiens cDNA
8520	18401	28569	2.36	5.9E-01 AF094625.1	NT	NT	Mus musculus strain SPRET/Ev CD48 antigen (CD48) genes, partial cds
9165	18008	25342	1.91	5.9E-01 L42320.1	NT	NT	Oryzlatyca culiculus alpha 1 anti-tyrosin (alpha 1.7) gene, promoter region
9404	19057		2.18	5.9E-01 A3017705.1	NT	NT	Apagallus cyzine pyrG gene for oridine-5-phosphate deacetylase, complete cds
9614	19193		4.15	5.9E-01 P44072	SWISSPROT	SWISSPROT	MICROTUBULE-ASSOCIATED PROTEIN 1A [CONTAINS MAP1 LIGHT CHAIN L2]
1887	17163	21637	1.44	5.9E-01 P44072	SWISSPROT	SWISSPROT	SIM1 PROTEIN

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Max Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
3902	13812	23566	0.96	5.9E-01	BF96738.1	EST_HUMAN	60182547MT NIH_MGC 56 Homo sapiens cDNA clone IMAGE:4076131 5'
4413	14307	24090	2.81	5.9E-01	AF000077.1	NT	Vigna radiata mRNA for protein pyrophosphatase, complete cds
4690	14876	24881	1.04	5.9E-01	AF110846.1	NT	Megalin sciatix sex-differential homolog (Megs3) gene, partial cds, alternatively spliced products
5753	15601	25768	1.29	5.9E-01	DT96059.1	EST_HUMAN	HLM50205068 Homo placenta poly(A ⁺) (Tfrijlware) Homo sapiens cDNA clone GEX-500603 5'
6077	16000		2.3	5.9E-01	SG5091.1	NT	cyclic AMP-regulated phosphoprotein (cra, mRNA, 1030 nt)
6904	16484		2.62	5.9E-01	H41571.1	EST_HUMAN	W61003 s1 Soares adult brain N262HB357 Homo sapiens cDNA clone IMAGE:172757 3' similar to
6764	15643	26830	2.23	5.9E-01	P14328	SW/SSPROT	96-578187 M-PHASE INDUCER PHOSPHATASE 2 (HUMAN)
6764	15643	26831	2.23	5.9E-01	P14328	SW/SSPROT	SPORE COAT PROTEIN SP98
7163	17030	27224	8.64	5.9E-01	AJ270774.1	NT	Homo sapiens partial TGF-4 gene for T-cell transcription factor-4, exon 6-11
8358	18265	29463	8.47	5.9E-01	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exon 2 to 5
8396	18272		3.23	5.9E-01	BF700092.1	EST_HUMAN	602127577F1 NIH_MGC 56 Homo sapiens cDNA clone IMAGE:4284403 5'
8462	18355		1.76	5.9E-01	BF700092.1	EST_HUMAN	602127577F1 NIH_MGC 56 Homo sapiens cDNA clone IMAGE:4284403 5'
3186	13111	22915	1.48	5.7E-01	Q9W1L2	SW/SSPROT	PUTATIVE TRANSCRIPTION FACTOR OVO-LIKE 1 (NOVO1) (NOVO1A)
3460	13378		2.43	5.7E-01	AB033503.1	NT	Populus satuminiana pecca-2 mRNA for 1-aminocyclopropane-1-carboxylate synthase, complete cds
3829	13741	23533	1.65	5.7E-01	AF011581.1	NT	Homo sapiens T cell receptor beta chain (BV557-2.6.11S1) mRNA, partial cds
5201	15054	24977	2.24	5.7E-01	U76517.1	NT	Rattus norvegicus cAMP-regulated guanine nucleotide exchange factor II (cAMP-GEFII) mRNA, partial cds
5838	15742	26554	3.72	5.7E-01	BF036413.1	EST_HUMAN	601545058F1 NIH_MGC 68 Homo sapiens cDNA clone IMAGE:385650 5'
6100	15710	24874	1.41	5.7E-01	AF111440.1	NT	Isotricha cincta subunit T4 cDNA library under conditions of nitrogen deprivation
6504	16422	26863	2.12	5.7E-01	P03073	SW/SSPROT	PYRROLINE-5-CARBOXYLATE REDUCTASE (PCR) (PCR REDUCTASE)
9124	16883		0.88	5.7E-01	BE170551.1	EST_HUMAN	943410705-190700-003-002 HT07933 Homo sapiens cDNA
3318	13259	23043	1.21	5.9E-01	AB126832.2	NT	Homo sapiens mRNA for KIA00749 protein, partial cds
3318	13259	23044	1.21	5.9E-01	AB126832.2	NT	Homo sapiens mRNA for KIA00749 protein, partial cds
3808	13720	23609	0.83	5.9E-01	AF10501.2	NT	Aradipipis italiana DNA chromosome 4, coding fragment No. 13
4146	14046	23818	0.83	5.9E-01	D83135.1	NT	Oxidized TBR gene, exon8, complete cds
7111	15988	27180	4.18	5.9E-01	AY958703.1	EST_HUMAN	AY058703 GRC Homo sapiens cDNA clone GKC/S106 5'
7111	15988	27181	4.18	5.9E-01	AY958703.1	EST_HUMAN	AY058703 GRC Homo sapiens cDNA clone GKC/S106 5'
9023	15871		2.49	5.9E-01	BE986280.1	EST_HUMAN	001514001F01 NIH_MGC 71 Homo sapiens cDNA clone IMAGE:39154857 5'
							ng/500 to 1000 CGAP 710 Homo sapiens cDNA clone IMAGE:450074 similar to contains element PTR7
							regulatory element:
9137	18693	28794	1.73	5.9E-01	AA464835.1	EST_HUMAN	H02132028F1 NIH_MGC 81 Homo sapiens cDNA clone IMAGE:4271834 5'
9524	19193		1.32	5.9E-01	P05005	SW/SSPROT	HIGH AFFINITY POTASSIUM TRANSPORTER
9919	19362		3.09	5.9E-01	BF575829.1	EST_HUMAN	602132028F1 NIH_MGC 81 Homo sapiens cDNA clone IMAGE:4271834 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1193	11103	20949	1.09	5.5E-01	8303912	NT	Rattus norvegicus Protoporphyrin Coenzyme X carboxylase, beta polypeptide (Pob), mRNA
2686	12533	22423	2.88	5.5E-01	P03341	SWISSPROT	GAG POLYPROTEIN (CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P16; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10)
2686	12533	22424	2.88	5.5E-01	P03341	SWISSPROT	GAG POLYPROTEIN (CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P16; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10)
2888	12815	22908	1.34	5.5E-01	5902045	NT	Homo sapiens superfamily viral-like activity 2 (S. carboxylase homolog-like (SKVZL), mRNA
3027	12955	22926	1.39	5.5E-01	AF227240.1	EST_HUMAN	ye18101 at Sources adult brain N25SH9557 Homo sapiens cDNA clone IMAGE:76269 3'
3106	13121	23226	3.1	5.5E-01	AF227240.1	NT	Rabbit oral papillomavirus, complete genome
3634	13548	23335	1.20	5.5E-01	P48755	SWISSPROT	FOS-RELATED ANTIGEN-1
139	10113	19033	3.74	5.4E-01	7657296	NT	Homo sapiens KIAA0929 protein Max2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
139	10113	19634	3.74	5.4E-01	7657296	NT	Homo sapiens KIAA0929 protein Max2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
570	10509	20316	2.61	5.4E-01	AF232005.1	NT	Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and GsaA (gsaA) genes, complete cds; and unknown genes
570	10509	20317	2.61	5.4E-01	AF232005.1	NT	Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and GsaA (gsaA) genes, complete cds; and unknown genes
4250	11157	21065	2.24	5.4E-01	AF164093.1	EST_HUMAN	OV14NN0040-0704500-101-cd1 NN0040 Homo sapiens cDNA
2050	11949	21067	2.76	5.4E-01	AF202347.2	NT	Chlamydomonas reinhardtii preproinsulin mRNA for 15.15 beta carboxylase cleavage (beta-cdx gene)
2208	12005	21068	2.23	5.4E-01	AJ276982.1	NT	Gracilaria tikvahiae preproinsulin mRNA for 15.15 beta carboxylase cleavage (beta-cdx gene)
7708	17388	21069	2.01	5.4E-01	BF572383.1	EST_HUMAN	Gracilaria tikvahiae preproinsulin mRNA for 15.15 beta carboxylase cleavage (beta-cdx gene)
8421	18301	28557	2.87	5.4E-01	P39858	SWISSPROT	Gracilaria tikvahiae preproinsulin mRNA for 15.15 beta carboxylase cleavage (beta-cdx gene)
8862	18702	28966	4.51	5.4E-01	Q36675	SWISSPROT	Gracilaria tikvahiae preproinsulin mRNA for 15.15 beta carboxylase cleavage (beta-cdx gene)
8862	18702	28967	4.51	5.4E-01	Q36675	SWISSPROT	Gracilaria tikvahiae preproinsulin mRNA for 15.15 beta carboxylase cleavage (beta-cdx gene)
9087	18862		2.12	5.4E-01	AJ863308.1	EST_HUMAN	Gracilaria tikvahiae preproinsulin mRNA for 15.15 beta carboxylase cleavage (beta-cdx gene)
505	10447	20260	2.02	5.3E-01	AF1019413.1	NT	Homo sapiens HLA class III region containing lensculin X (hensculin-X) gene, partial cds; cyclochrome P450 21B1 (CYP21B), complement component C4 (C4B) G11, hellease (SKZW), RD, complement factor B1 (fB), and complement component C2 (C2) genes>
2093	11962	21677	0.91	5.3E-01	AF113919.1	NT	Fraxinus alba var. capitata phosphatase D2 (P.D2) gene, complete cds
2093	11962	21678	0.91	5.3E-01	AF113919.1	NT	Fraxinus alba var. capitata phosphatase D2 (P.D2) gene, complete cds
2755	12817	22508	8.24	5.3E-01	4506328	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA
2755	12817	22509	8.24	5.3E-01	4506328	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA
3205	13129	22931	2.92	5.3E-01	AF067953.1	NT	Homo sapiens secreted C-type lectin precursor (SLC1) gene, complete cds

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Meet Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
772	10702	20541	1.80	4.9E-01	BF171462.1	EST_HUMAN	602076949F1 NIH_MGC_52 Homo sapiens cDNA clone IMAGE:4243860 5'
1984	11760	21834	1.30	4.9E-01	LA0669.1	NT	Cavie proclule pulmonary surfactant protein A (SP-A) mRNA, complete cds
5979	15388	25988	2.46	4.9E-01	AF102093.1	NT	Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 10
5679	15398	25989	2.46	4.9E-01	AF102093.1	NT	Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 10
6406	16267	26428	1.76	4.9E-01	AB040051.1	NT	Oryza sativa subcap. japonica NEEF-G mRNA for mitochondrial elongation factor G, complete cds
7197	17074		1.41	4.9E-01	BF109791.1	EST_HUMAN	601874694F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4102693 5'
7356	19769		2.2	4.9E-01	10946803	NT	Maia musculus unc113 homolog (C. elegans) 1 (Unc113), mRNA
6065	18848		1.43	4.9E-01	AF176912.1	NT	Homo sapiens neurotrophin-1B-cell stimulating factor-3 gene, complete cds
6065	19733		3.95	4.9E-01	AA613562.1	EST_HUMAN	nc22911.1 nt1 NC1 CGAP Cor10 Homo sapiens cDNA clone IMAGE:1144852 3'
							Homo sapiens potassium channel, subfamily K, member 5 (TASK-2) (KCNK5) mRNA, and translated products
4377	14136		1.12	4.9E-01	4304680	NT	Secotiarymyces cerevisiae) sporulation protein (SPO11) gene required for meiotic recombination, complete cds
5381	15300	25153	8.94	4.9E-01	AB2987.1	NT	nc85603.1 nt1 CGAP_AVI Homo sapiens cDNA clone IMAGE:1217813
6018	15622		3.94	4.9E-01	14456578.1	EST_HUMAN	Homo sapiens reproduction 8 (DRS2268E) mRNA
6330	16193		1.96	4.9E-01	5031660	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4
6563	16421	26901	3.32	4.9E-01	AL161462.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4
6563	16421	26902	3.32	4.9E-01	AL161462.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4
6913	16469	26979	1.16	4.9E-01	AB20744.1	EST_HUMAN	W7710.45 Scores breast 2Ab-HB1 Homo sapiens cDNA clone IMAGE:154796 5' similar to contains element MER8, positive element
8111	18007		2.04	4.9E-01	AB33902.1	NT	Scapularis OREFs from chromosome X
8266	18511		2.92	4.9E-01	AF227855.1	NT	Topoisomerase coud tyrosopase VIP II SRE repeat region
8670	19359		2.26	4.9E-01	BE176032.1	EST_HUMAN	601860324F1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3043606 5'
5525	15830	25953	8.36	4.7E-01	BF17173.1	EST_HUMAN	601863569F1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:4058387 5'
8221	18103		5.77	4.7E-01	AF102573.1	NT	Influenza A virus isolate Hc10297 hemagglutinin (HA) gene, partial cds
8434	18308	26564	2.06	4.7E-01	AF1008.1	NT	Human collagen alpha2(X) (COL1A2) gene, exons 6 through 10, and partial cds
8682	18370	26955	2.43	4.7E-01	AW168446.1	EST_HUMAN	RC3-N1 0229-24040-011 E08 NT1023 Homo sapiens cDNA
9374	19048		1.36	4.7E-01	AW341861.1	EST_HUMAN	Ref1tab.X1 Scorec, NIH_MGC_31 Homo sapiens cDNA clone IMAGE:2609168 3'
9374	19048	23375	1.27	4.6E-01	AF161658.1	EST_HUMAN	Ref1tab.X1 Scorec, NIH_MGC_31 Homo sapiens cDNA clone IMAGE:4245681 5'
3683	13957	23393	1.28	4.6E-01	BF063300.1	EST_HUMAN	602038103F1 NIH_MGC_31 Homo sapiens cDNA clone IMAGE:4245681 5'
3683	13957	23394	1.28	4.6E-01	BF063300.1	EST_HUMAN	602038103F1 NIH_MGC_31 Homo sapiens cDNA clone IMAGE:4245681 5'
5087	14957		0.97	4.6E-01	AF11267.1	NT	Bovine steroid 21-hydroxylase gene (C-450-421) gene, complete cds
5560	15280	25111	3.38	4.6E-01	AB00643	SWISSPROT	INTERFERON REGULATORY FACTOR 3 (IRF-3)
5390	15280	25112	3.38	4.6E-01	AB00643	SWISSPROT	INTERFERON REGULATORY FACTOR 3 (IRF-3)
5404	15323	25372	1.78	4.6E-01	BE134781.1	EST_HUMAN	601580755F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843937 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5414	15334	25384	3.20	4.6E-01	A1247676.1	EST_HUMAN	qf59h02.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1846011 3' similar to TR-015938 015338 BUTYROPHELIN ;
5414	15334	25385	3.20	4.6E-01	A1247678.1	EST_HUMAN	qf59h02.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1846011 3' similar to TR-015938 015338 BUTYROPHELIN ;
5418	15339	25393	1.86	4.6E-01	P20560	SWISSPROT	MEIOSIS SPECIFIC PROTEIN HOP1
6057	16040	29181	1.47	4.6E-01	U02332.1	NT	Emetella nidulans NEMPA (nemA) gene, mitochondrial gene encoding putative mitochondrial protein, complete cds
6057	16040	29182	1.47	4.6E-01	U02332.1	NT	Emetella nidulans NEMPA (nemA) gene, mitochondrial gene encoding putative mitochondrial protein, complete cds
6043	16722	29919	13.49	4.6E-01	BF067966.1	EST_HUMAN	602330653.P1 NIH_MGC_36 Homo sapiens cDNA clone IMAGE:4267623 5'
7363	17220	27430	26.49	4.6E-01	P55202	SWISSPROT	ATRIAL NATRIURETIC PEPTIDE RECEPTOR B PRECURSOR (ANP-B) (ANPRB) (GC-B) (GUANYLATE CYCLASE)
7363	17230	27431	26.49	4.6E-01	P55202	SWISSPROT	ATRIAL NATRIURETIC PEPTIDE RECEPTOR B PRECURSOR (ANP-B) (ANPRB) (GC-B) (GUANYLATE CYCLASE)
7730	17590	27902	1.33	4.6E-01	A015634.1	EST_HUMAN	wg75412.x1 Soares_NSF_P8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2370765 3'
7730	17590	27903	1.33	4.6E-01	A015634.1	EST_HUMAN	wg75412.x1 Soares_NSF_P8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2370765 3'
8360	18226	27903	2.86	4.6E-01	P08163	SWISSPROT	PUTATIVE VITELLOGENIN RECEPTOR PRECURSOR (VL)
8368	18245	29495	4.78	4.6E-01	BE-05448.1	EST_HUMAN	LG-H10730-100500-075-005 HT0730 Homo sapiens cDNA
8368	18245	29495	4.78	4.6E-01	BE-05448.1	EST_HUMAN	LG-H10730-100500-075-005 HT0730 Homo sapiens cDNA
8766	17916	29190	5.45	4.6E-01	A1501293.1	NT	Human thymidine methyltransferase (TGMT) gene, exon 10 and complete cds
8766	17916	29191	5.45	4.6E-01	A1501293.1	NT	Human thymidine methyltransferase (TGMT) gene, exon 10 and complete cds
9313	19005		1.43	4.6E-01	D35318.1	EST_HUMAN	HU0163F008 Clontech human fetal brain polyA+ mRNA (85835) Homo sapiens cDNA clone GEN-105503 5'
9878	19461		2.21	4.6E-01	A1520134.1	NT	LaminA prolamellar maturation (matK) gene, chloroplast gene encoding chloroplast protein, partial cds
10869	11765	21659	1.73	4.5E-01	A0001931.1	NT	Drosophila melanogaster R1 section 08 of 228 of the complete chromosome 1
10869	11765	21660	1.73	4.5E-01	A0001931.1	NT	Drosophila melanogaster R1 section 08 of 228 of the complete chromosome 1
2841	12769	22558	4.97	4.5E-01	A0470065.1	EST_HUMAN	qf59h02.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1847179 3'
3278	13196	22065	3.97	4.5E-01	U007793	SWISSPROT	BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN PRECURSOR (HS-G) (PERLECAN) (PLC)
3331	13251	23056	1.05	4.5E-01	A1520778.1	NT	Mus musculus DNA polymerase epsilon catalytic subunit (Poi) gene, exons 2 through 12
3942	13850		1.41	4.5E-01	Q23247	SWISSPROT	COLLAGEN ALPHA 3(V) CHAIN
3982	13859	23955	1.1	4.5E-01	A1059008.1	EST_HUMAN	ad64606.x1 Bacterial actin HPLR66 Homo sapiens cDNA clone IMAGE:2535489 3'
4035	15079		4.02	4.5E-01	A1673495.1	EST_HUMAN	h06g02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3041810 3'

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4962	14742	24222	0.94	4.5E-01	BE034452.2	EST_HUMAN	60165722R1 NH_106367 Homo sapiens cDNA clone IMAGE:396023 3'
5406	15326	25376	1.45	4.5E-01	AW03814.1	EST_HUMAN	Q52P70012.140100-031-c08 PT0012 Homo sapiens cDNA
5993	15938		1.47	4.5E-01	U00956	SWISSPROT	COAT PROTEIN
6488	16346	26515	2.49	4.5E-01	AB59849.1	EST_HUMAN	W32902X1 NCL CGAP_U10 Homo sapiens cDNA clone IMAGE:2426818 3' similar to TR_Q02823 Q02823
6997	16778	26970	3.14	4.5E-01	AG48966.1	EST_HUMAN	SW1902F1 NCL CGAP_U10 KDA SUBUNIT 1
7100	16977		1.84	4.5E-01	11444788	EST_HUMAN	125641.1 x1 NCL CGAP_Ox45 Homo sapiens cDNA clone IMAGE:2262844 3'
7991	17841	26932	25.03	4.5E-01	U05006.1	EST_HUMAN	Homo sapiens hypothetical protein DKFZ547G183 (DKFZ547G183), mRNA
7991	17841	26933	25.03	4.5E-01	U05006.1	EST_HUMAN	Homo sapiens hypothetical protein DKFZ547G183 (DKFZ547G183), mRNA
8237	18117	26960	2.42	4.5E-01	AV1501271.1	EST_HUMAN	ES102531 Fetal brain, Striatum (G18393203) Homo sapiens cDNA clone HFE017
8338	19724		2.26	4.5E-01	BE371461.1	EST_HUMAN	x14901.1 NCL CGAP_U10 Homo sapiens cDNA clone IMAGE:2703865 3' similar to SW:INT6_MOUSE
8684	19245		1.44	4.5E-01	BF337351.1	EST_HUMAN	09146201F1 NH_106367 Homo sapiens cDNA clone IMAGE:3452661 5'
9763	19263		2.15	4.5E-01	11422068	EST_HUMAN	80203327F1 NCL CGAP_Bm24 Homo sapiens cDNA clone IMAGE:3132200 5'
9874	19552	24937	1.83	4.5E-01	AF338234.2	EST_HUMAN	Homo sapiens beta-actin-specific kinase 2 (TESK2), mRNA
1991	19585		2.47	4.4E-01	6850603	NT	Homo sapiens histone H4 protein (H4), partial cds
						NT	Human alpha-1B globulin, diaphanous protein (dia), gene, partial cds
						NT	Mouse muscicula integral membrane-associated protein 1 (limp1), mRNA
2940	12220	22118	3.98	4.4E-01	P49765	SWISSPROT	(VASCULAR ENDOTHELIAL GROWTH FACTOR B PRECURSOR (VEGF-B) (VEGF RELATED FACTOR)
3274	13195	22664	0.96	4.4E-01	AF05700.1	NT	Rattus norvegicus SYNGAP-5, mRNA, complete cds
3274	13195	22665	0.96	4.4E-01	AF05700.1	NT	Rattus norvegicus SYNGAP-5, mRNA, complete cds
3277	13198	22668	1.37	4.4E-01	BF06726.1	EST_HUMAN	791602.57 NCL CGAP_Bm16 Homo sapiens cDNA clone IMAGE:3363796 5'
4141	14041		1.33	4.4E-01	BE37807.1	EST_HUMAN	601237138F1 NCL CGAP_44 Homo sapiens cDNA clone IMAGE:303393 5'
4524	14803		0.93	4.4E-01	BE41396.1	EST_HUMAN	MR6-HT0078-131286-007-g06 HT0078 Homo sapiens cDNA
5326	15246	25050	1.99	4.4E-01	P49429	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
5326	15246	25051	1.99	4.4E-01	P49429	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
5480	15409	25474	1.13	4.4E-01	S56019.1	NT	human fetal, Squalene-Dawley, sulfur-dioxide-treated tracheal epithelium, mRNA, partial, 300 nt
5498	15418	25481	1.98	4.4E-01	AV720408.1	EST_HUMAN	AV720408 GCL Homo sapiens cDNA clone GLOC5C12 5'
						EST_HUMAN	q62011.1 NCL CGAP_Bm23 Homo sapiens cDNA clone IMAGE:1961125 3' similar to TR_Q29768 Q29768
5624	16539	25627	1.6	4.4E-01	A1184413.1	EST_HUMAN	UNKNOWN PROTEIN ;
5624	16539	25628	1.6	4.4E-01	A1184413.1	EST_HUMAN	q62011.1 NCL CGAP_Bm23 Homo sapiens cDNA clone IMAGE:1961125 3' similar to TR_Q29768 Q29768
5782	16588	25798	1.79	4.4E-01	AV000795.1	EST_HUMAN	UNKNOWN PROTEIN ;
5552	16462		10.84	4.4E-01	211670.1	NT	AF1420XN B1-ALDEHYDE REDUCTASE ;
						NT	S. tuberosum mRNA for induced slobin lip protein (partial)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1335	12901	21009	1.04	4.2E-01	Q39102	SWISSPROT	CELL DIVISION PROTEIN FTSH HOMOLOG PRECURSOR
1904	11900		0.80	4.2E-01	AA781853.1	EST_HUMAN	nc24960 at NC1 CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1288068 3'
3558	13469	23263	4.78	4.2E-01	AE003947.1	NT	XylA1a nucleoside, section 93 of 228 of five complete genome
3565	13469	23268	1.05	4.2E-01	AI203338.1	EST_HUMAN	qB4401.x1 Soares_JHMP-91 Homo sapiens cDNA clone IMAGE:1879946 3'
3903	13715	23503	0.96	4.2E-01	AW435627.1	EST_HUMAN	QV04L10015-180200-127-01 L10015 Homo sapiens cDNA
3900	13910	23595	1	4.2E-01	Q04866	SWISSPROT	SOX-8 PROTEIN
4545	14438		3.65	4.2E-01	BE073574.1	EST_HUMAN	RC5-B10559-020300-013.E09 B10559 Homo sapiens cDNA
4559	14487	24273	4.96	4.2E-01	AA834083.1	EST_HUMAN	n69901 at NC1 CGAP_P10 Homo sapiens cDNA clone IMAGE:987777 similar to gb-M33600 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-1 BETA CHAIN (HUMAN);
4671	14557	24350	3.13	4.2E-01	R13467.1	EST_HUMAN	YF77601.1 Soares Infant brain TMB Homo sapiens cDNA clone IMAGE:28278 5'
5503	15422	25494	1.5	4.2E-01	BF240555.1	EST_HUMAN	60187921F1 NH1_MGC_15 Homo sapiens cDNA clone IMAGE:4108468 5'
5503	15460	25618	1.66	4.2E-01	BA094812.1	EST_HUMAN	RC3-GT0254-006400-028-04 CT0254 Homo sapiens cDNA
6151	16024	26164	9.1	4.2E-01	AY158472.1	EST_HUMAN	AU158472 PLACE3 Homo sapiens cDNA clone IMAGE:2000470 3'
6151	16024	26165	9.1	4.2E-01	AY158472.1	EST_HUMAN	AU158472 PLACE3 Homo sapiens cDNA clone IMAGE:2000470 3'
6184	16461	26218	2.1	4.2E-01	BB25904.1	EST_HUMAN	Brcal1 breast cancer gene (rats, VIF spleen, genomic, 419 nt, segment 2 of 2)
6207	16933	26233	5.91	4.2E-01	AI161547.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 47
6503	16543	26739	2.1	4.2E-01	AY057448.1	EST_HUMAN	EST5569413 IMAGE reassurances, IMAGE Homo sapiens cDNA
6563	16543	26740	2.1	4.2E-01	AY057448.1	EST_HUMAN	EST5569413 IMAGE reassurances, IMAGE Homo sapiens cDNA
6776	16955	26844	1.19	4.2E-01	4759309	NT	Homo sapiens cytochrome c oxidase subunit VIc (COX6C), nuclear gene encoding mitochondrial protein, mRNA
7892	17942	26894	1.48	4.2E-01	AW963666.1	EST_HUMAN	MR3-SN0010-280300-053-07 SN0010 Homo sapiens cDNA
8400	18278	28258	2.2	4.2E-01	AA023489.1	NT	Cytosol import OXA2 mRNA for membrane glyoxylate cytochrome, complete cds
9660	18517	28796	1.64	4.2E-01	BE069465.2	EST_HUMAN	AV781615 HTF Homo sapiens cDNA clone IMAGE:3068085 3'
9663	19353		1.68	4.2E-01	AV731815.1	EST_HUMAN	AV781615 HTF Homo sapiens cDNA clone HTF8H08 5'
1078	10994	20835	1.88	4.1E-01	AI005461.1	EST_HUMAN	RC-B1001-210199-142 B1091 Homo sapiens cDNA
1087	11003	20844	2.4	4.1E-01	AY055243.1	EST_HUMAN	AV705243 ADB Homo sapiens cDNA clone ADBAHF08 5'
1087	11003	20845	2.4	4.1E-01	AY055243.1	EST_HUMAN	AV705243 ADB Homo sapiens cDNA clone ADBAHF08 5'
1562	11498	21569	1.03	4.1E-01	AI006949.1	EST_HUMAN	PM4B1103-270499-054 B1103 Homo sapiens cDNA
2878	12543	22434	1.82	4.1E-01	7702883	NT	Homo sapiens amplexipromoting complex subunit 7 (APC7), mRNA
2910	12836	22853	1.76	4.1E-01	AI161932.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36
2910	12836	22854	1.76	4.1E-01	AI161936.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36
3203	13186	22985	1.13	4.1E-01	AA060344.1	EST_HUMAN	qB4408 at Soares_NF1_1_GBC_S1 Homo sapiens cDNA clone IMAGE:1605643 3'
4177	14077	23852	2.90	4.1E-01	AA246207.1	NT	Rhodococcus sp. AD-46 lipoG, lipoI, lipoJ, lipoK, lipoL and lipoF genes
4208	14107		1.07	4.1E-01	AA060257.1	EST_HUMAN	em33602 at Soares_NF1_1_GBC_S1 Homo sapiens cDNA clone IMAGE:1429119 3'

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Probe SEQ ID NO.	Expr SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
2605	12473	22587	3.94	3.9E-01	A0303019.1	NT	Human sapiens mRNA for KIAA1182 protein, partial cds
2673	12538	22527	5.98	3.9E-01	X62032.1	NT	H sapiens Bmyb gene
2673	12538	22528	5.98	3.9E-01	X62032.1	NT	H sapiens Bmyb gene
3058	12583	22776	3.83	3.9E-01	AJ225968.1	NT	Streptococcus meliloti egf_59126_034 genes and cfr3
3968	13856	23672	1.47	3.9E-01	BF62691.1	EST_HUMAN	761001.x1 NC1_CGAP_B10 Homo sapiens cDNA clone IMAGE:3339169.3
3968	13856	23671	1.47	3.9E-01	BF62691.1	EST_HUMAN	80105949487 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3833969.5
4918	16781	24972	1.48	3.9E-01	BF62696.1	EST_HUMAN	80186234025 NIH_MGC_33 Homo sapiens cDNA clone IMAGE:4082049.5
5913	15528	25911	3.93	3.9E-01	BF206036.1	EST_HUMAN	9816604.01 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701391.3 similar to TR094821
7324	17220	27400	1.5	3.9E-01	AW195898.1	EST_HUMAN	C64821 KIAA07191 PROTEIN;
7503	17372	27591	1.4	3.9E-01	A0373397.1	EST_HUMAN	765602.x1 NC1_CGAP_Bn23 Homo sapiens cDNA clone IMAGE:2467658.3 similar to
7680	17520	27785	2.97	3.9E-01	M11979.1	EST_HUMAN	SW-RPMX_HUMAN P48382 BINDING REGULATORY FACTOR.1
8165	18040	2891	2.22	3.9E-01	AJ166593.1	EST_HUMAN	Human clathrin 27 gene, exons 10 and 11, and L1 and AU repeats
9091	18942	3081	1.9E-01	AF304354.1	NT	SWISSPROT	AV09597.4 GKX_Homo sapiens cDNA clone GKCBQ011.5
9209	18940	3209	2.38	3.9E-01	GI61270	NT	Homo sapiens proteoglycan 3 (PRG3) gene, complete cds
9268	18960	23528	1.26	3.9E-01	A030181.1	NT	HomoCBQX PROTEIN HLX1
1154	10128	12436	7.44	3.9E-01	AE001811.1	NT	Thermococcus maritima section 123 of 156 of the complete genome
1827	11284	12286	1.22	3.9E-01	A0503870.1	NT	Human sapiens protein kinase PKIbeta (gribabeta) mRNA
2524	12364	22286	2.44	3.9E-01	AJ214117.1	NT	Xtella fastidiosus, section 16 of 230 of the complete genome
2591	12726	22352	4.41	3.9E-01	Q07802.1	NT	Kanazapagos halophilus putative c-myc-like transcription factor (MYC35-3) mRNA, complete cds
2672	12866	22362	0.82	3.9E-01	AJ205701.1	NT	Mus musculus pulchra family 1, member 6 (Sc146), mRNA
3070	12938	22732	2	3.9E-01	AF043363.1	NT	Human immunodeficiency virus type 1 complete genome (isolate 95SI-MP1219)
3438	13355	23160	7.77	3.9E-01	AF161518.2	NT	Paracoccus aminophilus aminopeptidase N (amp1) gene, partial cds
3494	13410	24061	0.79	3.9E-01	A007216.1	EST_HUMAN	AB088124.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2357665.3
3964	13410	24061	0.91	3.9E-01	A1007219.1	EST_HUMAN	W838124.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2357665.3
3941	13732	23546	0.85	3.9E-01	6754069	NT	Mus musculus general transcription factor II (GH2), mRNA
5946	14818	24902	0.98	3.9E-01	BE544093.1	EST_HUMAN	801074101 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3460154.5
5445	15366	25422	1.62	3.9E-01	Q04498	SWISSPROT	QVQ-310337-271259-049-402 B10537 Homo sapiens cDNA
5964	16059	26023	4.47	3.9E-01	BE072399.1	EST_HUMAN	QVQ-310337-271259-049-402 B10537 Homo sapiens cDNA
6053	16036	26177	3.81	3.9E-01	A0374001.1	EST_HUMAN	sa54H1.x1 Scores_bcd_1beta_M29IF8_3w Homo sapiens cDNA clone IMAGE:2047917.3 similar to
6436	16037	26177	4.83	3.9E-01	X01597.1	NT	containing AU repetitive element
6890	16599	27032	3.07	3.9E-01	A0046861.1	NT	M musculus gene for bullbrain-binding protein
6980	16657	27032	3.07	3.9E-01	A0046861.1	NT	Homo sapiens mRNA for KIAA1331 protein, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7516	17304		4.11	3.8E-01	B6413.1	EST_HUMAN	y63406.1 Soares fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:126539 5' similar to contains
8820	18933		2.82	3.8E-01	BE179129.1	EST_HUMAN	Alu repetitive elementcontaining P1RS repetitive element ;
8839	18747	28041	2.57	3.8E-01	R42550.1	EST_HUMAN	ROCHT0841-04080-032472 HT0841 Homo sapiens cDNA
8939	18747	28042	2.57	3.8E-01	R42550.1	EST_HUMAN	y62911.1 at Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:30289 3'
9297	18997		2.38	3.8E-01	AE001124.1	EST_HUMAN	y62911.1 at Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:30289 3'
9422	18661		1.34	3.8E-01	U94768.1	NT	Borrelia burgdorferi (section 10 of 70) of the complete genome
9530	19137		2.21	3.8E-01	BE232565.1	EST_HUMAN	Human p53 (TP53) gene, complete cds
9617	19938		1.84	3.8E-01	AF291483.1	NT	QV3-E10063-190700-271-c03 E10063 Homo sapiens cDNA
9821	18975	24693	1.37	3.8E-01	T54787.1	EST_HUMAN	y42311.1 at Stragelana fetal spleen (4607205) Homo sapiens cDNA clone IMAGE:73821 3' similar to similar
9837	19406	25180	1.13	3.8E-01	AF164972.1	NT	to gbA06977 SERUM ALBUMIN PRECURSOR (HUMAN)
9870	19430	25151	1.33	3.8E-01	AA776820.1	EST_HUMAN	Mus musculus developmental control protein mRNA, partial cds
2431	12206	22209	0.85	3.7E-01	AB037831.1	NT	Human alpha 1(I) Soret, beta 2, N1IT Homo sapiens cDNA clone 1251657 3' similar to TRCQ15288 Q15288 NO
3414	13331	25133	0.68	3.7E-01	AF055304.1	NT	Homo sapiens mRNA for KIAA1410 protein, partial cds
4138	14038	23912	0.83	3.7E-01	AF121870.1	EST_HUMAN	Danio rerio bone morphogenetic protein 4 precursor (BMP4) gene, complete cds
4225	14123	23964	1.59	3.7E-01	AE027007.1	EST_HUMAN	cd3207.1 at Soares, NSF, F8, 97, 01, PA, P, S1 Homo sapiens cDNA clone IMAGE:1610188 3'
4392	14180	23974	3.32	3.7E-01	AE027007.1	EST_HUMAN	ME3-O10007-083000-104402 Q10007 Homo sapiens cDNA
5235	19101	25260	2.79	3.7E-01	AE027007.1	NT	Nesidioblastoid neuroendocrine group 3, adult MC38, section 50 of 206 of the complete genome
5382	16234	23419	4.31	3.7E-01	BE037343.1	EST_HUMAN	Homo sapiens tumor necrosis factor receptor 7 precursor (TNFR7) cDNA
5392	16234	23419	4.31	3.7E-01	BE037343.1	EST_HUMAN	601433907.F1 N1L1LKC_39 Homo sapiens cDNA clone IMAGE:388562 5'
5548	16727	25921	2.34	3.7E-01	11459739	NT	601433907.F1 N1L1LKC_39 Homo sapiens cDNA clone IMAGE:388562 5'
5548	16727	25922	2.34	3.7E-01	11459739	NT	Homo sapiens chromosome 12 open reading frame 4 (C12ORF4), mRNA
7307	17183	27668	3.93	3.7E-01	AE127198.1	EST_HUMAN	Homo sapiens chromosome 12 open reading frame 4 (C12ORF4), mRNA
7894	17714	27668	3.93	3.7E-01	AE127198.1	EST_HUMAN	Callitrix jacchus mRNA for beta-crystallin 10, 10-dioxygenase (CDO) gene)
8232	18113	25955	1.81	3.7E-01	AE127198.1	EST_HUMAN	Robust mRNA for fast skeletal muscle myosin heavy chain (MYHC)
8392	18208	23518	2.68	3.7E-01	AE127198.1	NT	Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIA0851 gene
8392	18208	23519	2.68	3.7E-01	AE127198.1	NT	Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIA0851 gene
8702	17911	23165	4.23	3.7E-01	AE127198.1	NT	Bovine mRNA for terminal deoxynucleotidyltransferase (TdT) (EC 2.7.7.37)
8879	18784		2.79	3.7E-01	0677078	NT	Mus musculus reelin (RBL1), cDNA
9008	19303		1.87	3.7E-01	004682.1	NT	Human heart-specific muscle ATP1A3P translocator (ANT1) gene, complete cds
9176	18917		1.94	3.7E-01	AE124326.1	NT	Chlamydomonas reinhardtii partial omp1 gene for outer membrane protein 1
9272	18976		2.41	3.7E-01	068976.1	NT	Human mRNA for KIAA0223 gene, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar Top Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9634	16206		2.18	3.7E-01	AL121154.1	EST_HUMAN	DKFp702K07.1 T782 (synonym: tme2) Homo sapiens cDNA clone DKF7262K07.5'
9701	16251	25217	1.52	3.7E-01	Y18000.1	NT	Homo sapiens NF2 gene
9664	16746		1.31	3.7E-01	AL297834.1	NT	Bos taurus partial stat5b gene, exons 2-15 and joined CDS
979	16902		7.17	3.6E-01	169241.1	NT	Human mdr1 gene, partial cds
1392	11189	21054	2.59	3.6E-01	T80255.1	EST_HUMAN	y030305.t1 Scoville infant brain T1N18 Homo sapiens cDNA clone IMAGE:24443.5'
1392	11189	21055	2.59	3.6E-01	T80255.1	EST_HUMAN	y030305.t1 Scoville infant brain T1N18 Homo sapiens cDNA clone IMAGE:24443.5'
1874	11770	21645	6.05	3.6E-01	AW590184.1	EST_HUMAN	h933802.x1 NC1_QOAP_G08 Homo sapiens cDNA clone IMAGE:2947419.3'
1874	11770	21646	6.05	3.6E-01	AW590184.1	EST_HUMAN	h933802.x1 NC1_QOAP_G08 Homo sapiens cDNA clone IMAGE:2947419.3'
1908	11893	21682	6.18	3.6E-01	AF76207.1	NT	Mus musculus ribosomal protein S19 (Rps19) gene, complete cds
2007	11899		1.08	3.6E-01	AF766237.1	NT	Rattus norvegicus repeat element associated with the Rasgrf1 gene
2223	12108		1.04	3.6E-01	AB002324.1	NT	Human mRNA for KIAA0323 gene, partial cds
2341	12221		2.39	3.6E-01	X76725.1	NT	P. trachealis (P3804) gene for actin
2437	12314	22211	1.63	3.6E-01	AW812033.1	EST_HUMAN	RC5-S10171-181095-011-207/510171 Homo sapiens cDNA
2589	12450	22350	2.28	3.6E-01	P24206	SWISSPROT	PROTEIN-ISOASPARTATE O-METHYLTRANSFERASE (PROTEIN-BETA-ASPARTATE METHYLTRANSFERASE) (PMT) (PROTEIN-ISOASPARTYL METHYLTRANSFERASE) (L-ISOASPARTYL PROTEIN CARBOXYL METHYLTRANSFERASE)
2699	15977		8.9	3.6E-01	AF189465.1	NT	Drosophila melanogaster sugar transporter 3 (sug3) mRNA, complete cds
3424	13341	23145	1.65	3.6E-01	X76758.1	NT	H. sapiens proctolin transporter gene, exons 9 and 10
3424	13341	23146	1.65	3.6E-01	X76758.1	NT	H. sapiens proctolin transporter gene, exons 9 and 10
4308	14203	23865	1.79	3.6E-01	EE107583.1	EST_HUMAN	RC1H10545-159003-014-1512-RT03-45 Homo sapiens cDNA
4935	14203	24572	0.85	3.6E-01	AL009099.1	NT	Strasler repus mRNA for MAP-48, aphaz protein
4935	14570	24572	1.23	3.6E-01	AL239237.1	NT	Bacteria from axenic bulk soil TGS RNA gene (strain XB45)
4941	14819	24867	2.01	3.6E-01	AW339393.1	EST_HUMAN	h90294.x1 NC1_QOAP_Lu24 Homo sapiens cDNA clone IMAGE:287566.3'
5599	15805	25228	1.8	3.6E-01	Y10706.1	NT	Homo sapiens PHFEX gene
6228	16104		5.49	3.6E-01	IR94090.1	EST_HUMAN	y74460.t1 Scoville fetal liver spleen T1N13 Homo sapiens cDNA clone IMAGE:276987.5'
6317	16180	26340	1.66	3.6E-01	AW02174.1	EST_HUMAN	W72510.x1 Sources_Myrcus_N1FTH Homo sapiens cDNA clone IMAGE:2613010.3' similar to TR-015117
6816	16955	26866	13.42	3.6E-01	AL161883.2	NT	O15117 FYN BINDING PROTEIN, F11
7305	17082	27269	3.37	3.6E-01	4594696	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 79
7305	17082	27270	3.37	3.6E-01	4594696	NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), transcript variant LAMP2A, mRNA
7302	17178	27380	1.4	3.6E-01	AL163204.2	NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), transcript variant LAMP2A, mRNA
7674	17624	27760	15.34	3.6E-01	G33194	SWISSPROT	Homo sapiens chromosome 21 segment H3Z1C004 PROBABLE PEPTIDE ABC TRANSPORTER-ATP-BINDING PROTEIN Y4T5

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8314	18191	28440	1.94	3.6E-01	BE002990.1	EST_HUMAN	6016764181 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3936887 5'
8453	18326	28595	3.89	3.6E-01	AE004293.1	NT	Arabidopsis thaliana mRNA for SUG, complete cds
8711	17890	28134	3.56	3.6E-01	AE000855.1	NT	Methanobacterium thermoautotrophicum from basins 702375 to 714311 (section 62 of 148) of the complete genome
9044	19761		1.81	3.6E-01	Y19210.1	NT	Homo sapiens HB55 gene for hair keratin, isoform 1 to 9
9127	18889		3.05	3.6E-01	AE000353.1	NT	Escherichia coli K-12 MG1655 section 225 of 400 of the complete genome
9281	18983		3.03	3.6E-01	U06888.1	NT	Mus musculus Emr1 mRNA, complete cds
9889	19704						x80411.x1 NOI_OGAP_Parv1 Homo sapiens cDNA clone IMAGE:2979118 3' similar to gb:K00558 TUBULIN ALPHA-1 CHAIN (HUMAN);
202	10174	18990	1.58	3.6E-01	AW190229.1	EST_HUMAN	Mus musculus mannose receptor, C type 2 (Mrc2), mRNA
692	10590	20414	0.97	3.5E-01	AL161581.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 77
479	10840	20465	1.24	3.5E-01	7709138	NT	Homo sapiens GAP-like protein (LOC51305), mRNA
708	10840	20467	1.24	3.5E-01	7709138	NT	Homo sapiens GAP-like protein (LOC51305), mRNA
763	10824	20351	3.17	3.5E-01	BF129785.1	EST_HUMAN	501811058R1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4033951 3'
1603	11508	21370	1.17	3.5E-01	BF310888.1	EST_HUMAN	501894933F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124244 5'
1622	11526	21384	1.05	3.5E-01	U57776.1	NT	Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds
2593	12725	22327	1.85	3.5E-01	AA223252.1	EST_HUMAN	5708490.s1 Striatogen NT2 neuronal precursor 987230 Homo sapiens cDNA clone IMAGE:959872 3'
2672	12837		0.86	3.5E-01	U05897.1	NT	Escherichia coli K-12 MG1655 section 225 of 400 of the complete genome
4166	14065	22639	1.92	3.5E-01	AF071233.1	NT	Drosophila melanogaster protein (Kc-98B) gene, complete cds
4379	14275	24056	1.29	3.5E-01	BE146863.1	EST_HUMAN	RC5170218-181089-011-g2.H 10218 Homo sapiens cDNA
4790	14675	24462	0.84	3.5E-01	N81203.1	EST_HUMAN	788E1 fetal brain DNA Homo sapiens cDNA clone 788E-1K similar to R07879, Z04098
4549	14730	24513	3.84	3.5E-01	M18349.1	NT	Rat taurocyte common antigen (L-CAT) gene, exons 1 through 5
6199	15959		3.47	3.5E-01	X08505.1	NT	S. aureus mRNA for GCSF protein (PECAM-1) -
6704	16594		1.88	3.5E-01	11448042	NT	Homo sapiens tumor protein p53-binding protein, 2 (TP53BP2), mRNA
7171	17048	27238	3.21	3.5E-01	4607670	NT	Homo sapiens tyrosine kinase non-receptor 1 (TNK1), mRNA
7612	17463	27860	1.51	3.5E-01	Q00294	SWISSPROT	VOLTAGE-DEPENDENT N-TYPE CALCIUM CHANNEL ALPHA-1B SUBUNIT (CALCIUM CHANNEL, L TYPE, ALPHA-1 POLYPEPTIDE ISOMER 9) (BRAIN CALCIUM CHANNEL II) (BII)
7988	17598	27764	2.66	3.5E-01	Z26825.1	NT	Xkernin gene for albumin including HPI enhancer
8116	18005	28251	2.99	3.5E-01	X051084.1	NT	C-glycine modulator gene for opsin protein
8360	18263	28513	2.34	3.5E-01	AA243178.1	NT	Gallus gallus SPARC gene for osteonectin, promoter and exon 1
8366	18263	28514	2.34	3.5E-01	AA243178.1	NT	Gallus gallus SPARC gene for osteonectin, promoter and exon 1

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Databases Source	Top Hit Descriptor
8851	18798	28652	3.34	3.4E-01	AL161501.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 13
9206	18837		2.12	3.4E-01	X64955.1	NT	B.aurus sap1 gene for (T)OT1 ATP synthase alpha-subunit
9941	19576	24699	2.26	3.4E-01	H08014.1	EST_HUMAN	yeastH1T1 Scores ratia N204HR Homo sapiens cDNA clone IMAGE:216697 6
9941	19516	25000	2.26	3.4E-01	H08014.1	EST_HUMAN	yeastH1T1 Scores ratia N204HR Homo sapiens cDNA clone IMAGE:216697 5
6891	10024		1.19	3.4E-01	AJ242956.1	NT	Homo sapiens paraf 11-type (exon 3), HPV45 L2, HPV45 E6, HPV45 E7 and HPV45 E1 genes isolated from ICA cervical carcinoma cell line
990	10893	20731	4.53	3.4E-01	Y00738.2	NT	Pseudomonas fluorescens cdtR, cdtS genes, orf222 and partial lnaA gene
1304	11211	21068	1.73	3.4E-01	Y00564.1	NT	Azotobacter vinelandii nifA gene for NifA protein (positive regulatory element)
2352	12320	22245	2.81	3.4E-01	D90909.1	NT	Synedrobacter sp. POC5803 complete genome, 11227, 1311235-130419
2842	12203	22400	1.48	3.4E-01	AL161516.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 28
2971	12688	22697	0.91	3.4E-01	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
2971	12688	22698	0.91	3.4E-01	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3124	13049	22849	5.41	3.4E-01	U63905.1	NT	Centis familiaris rod photoreceptor GMP-gated channel (alpha-subunit) (ONGOT1) mRNA, complete cds
3488	13404	23209	3.48	3.4E-01	AF106835.1	NT	Methylothermus sp. strain SS1 putative GpE (ppeE), DnaK (dnaK), and putative DnaJ (dnaJ) genes, complete cds
3722	13834		2.03	3.4E-01	BE140010.1	EST_HUMAN	TR34001.v1 NCI_GGAP_Ov18 Homo sapiens cDNA clone IMAGE:3672283 3' similar to TR3401U15
3855	13972		1.18	3.4E-01	JA5854158.1	EST_HUMAN	CT1010.v1 NCI_GGAP_Ph1 Homo sapiens cDNA clone IMAGE:1100347 3'
4394	14290	24074	0.78	3.4E-01	AF108341.1	NT	Homo sapiens integrin alpha 6 (ITGA6) gene, exons 12 through 23
4544		24221	1.82	3.4E-01	BC069972.1	EST_HUMAN	IK43151405-20020-22650-21 BT0403 Homo sapiens cDNA
4828	14710	24464	0.83	3.4E-01	BE1483761.1	EST_HUMAN	hp71609.v1 NCI_GGAP_G04 Homo sapiens cDNA clone IMAGE:3197656 3' similar to contains L1.9.1 repetitive element
4870	14700		3.57	3.4E-01	AI240973.1	EST_HUMAN	g6505.v1 NCI_GGAP_K08 Homo sapiens cDNA clone IMAGE:1897280 3' similar to contains A1u repetitive element
4970	14846	24814	1.12	3.4E-01	X116544.1	NT	Sac urctin hsp70 gene II for heat shock protein 70
5487	15006	25169	2.86	3.4E-01	AL161564.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 30
5951	15467		4.71	3.4E-01	AA080313.1	EST_HUMAN	znt2411.v1 Studeisera (NT neuron) (#637233) Homo sapiens cDNA clone IMAGE:547221 3'
6654	15654		2.06	3.4E-01	U02971.1	NT	Enthrus-25 1AB, 1C, 1D, 2A, 2B, 3A, 3B, 3D proteins cDNA, complete mature peptides and cds
5716	15523	25724	2.57	3.4E-01	AJ204905.1	EST_HUMAN	UHH8H-wae-12-Ou1 NCI_GGAP_Sub3 Homo sapiens cDNA clone IMAGE:2716862 3'
5780	15697	25795	1.47	3.4E-01	AL161544.1	EST_HUMAN	DKF267B12A26.t1 791 (synonym: hamy2) Homo sapiens cDNA clone IMAGE:307349 5
6046	16248		1.92	3.4E-01	N95226.1	EST_HUMAN	hsp5a12.v1 hamy1 complete lung, NHLH19W Homo sapiens cDNA clone IMAGE:307349 3

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6148	16021	26161	1.41	3.4E-01	A480682.1	EST_HUMAN	Im59g5x1 NCI CGAP_Bm35 Homo sapiens cDNA clone IMAGE:2102840 3 similar to gb:37431
6943	16821		1.77	3.4E-01	AA337053.1	EST_HUMAN	LAMININ RECEPTOR (HUMAN);
7139	17016	27200	1.62	3.4E-01	9633624	NT	EST14765 Endometrial tumor Homo sapiens cDNA 5 and
7313	17189	27300	3.88	3.4E-01	P29013	SWISSPROT	Bovine enterotroic strain K2577, complete genome
7313	17189	27301	3.88	3.4E-01	P29013	SWISSPROT	INTEGRIN BETA-3 PRECURSOR
7433	16446	26635	4.17	3.4E-01	U10492.1	NT	Saccharomyces cerevisiae Maf1p (MAF1) gene, complete cds
7433	16446	26636	4.17	3.4E-01	U10492.1	NT	Saccharomyces cerevisiae Maf1p (MAF1) gene, complete cds
7600	17540	27766	2.22	3.4E-01	AJ226084.1	NT	Homo sapiens FAA gene, exon 16, 17 and 18
8390	18257		4.09	3.4E-01	AE000881.1	NT	Methanobacterium thermoautotrophicum from bases 1018444 to 1029212 (section 87 of 148) of the complete genome
8407	18283	28536	2.2	3.4E-01	P06025	SWISSPROT	PROBABLE E4 PROTEIN
8440	18314	28572	2.26	3.4E-01	AF045891.1	NT	Rutilla atsal cytochrome b (cyb) gene, mitochondrial gene encoding mitochondrial protein, partial cds
8904	18471	28743	1.77	3.4E-01	N23506.1	NT	Human von Willebrand factor gene, exons 35 and 37
8904	18471	28743	1.77	3.4E-01	N23506.1	NT	Human von Willebrand factor gene, exons 35 and 37
8700	18605	28665	1.8	3.4E-01	AB035697.1	NT	Rattus norvegicus mRNA for s-glycylMUC18, complete cds
8914	18627	28516	4.03	3.4E-01	AI 01515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
9203	18814		2.01	3.4E-01	U63904.1	NT	Oribas trifoliation virus putative replicase gene, partial cds
9130	18837		1.3	3.4E-01	J22482.1	NT	S cerevisiae RIB3 gene encoding Ribosomal synthase
9229	19508		1.82	3.4E-01	AF254351.1	NT	Schistosoma japonica porins Cyf6 (cyf6) gene, complete cds
9347	19524		4.9	3.4E-01	J20336.1	NT	Human intercalating RNA, complete cds
9278	19538		2.48	3.4E-01	BE218302.1	EST_HUMAN	YAC3638x1 NCI CGAP_1421 Homo sapiens cDNA clone IMAGE:376127 3 similar to contains PTRY3.3
9432	19539		2.13	3.4E-01	9833601	NT	PTSD repetitive element;
9537	19140	26294	1.70	3.4E-01	AJ297131.1	NT	Sten vulgaris mitochondrion, complete genome
9537	19140	26294	1.70	3.4E-01	AJ297131.1	NT	Mus musculus S1L, MAF-17, CTP-3, SCL-3, CTP-3 genes
9829	19330		1.70	3.4E-01	AF016413.1	NT	Homo sapiens HLA class II region containing tetranucleotide (tetranucleotide) gene, partial cds; cytochrome P450 21-
14	10000	16791	7.01	3.3E-01	X07960.1	NT	hydroxylase (CYP21B), complement component C4 (C4B) G11, heliase (GR2W), RD, complement factor B
100	10000	16791	3.92	3.3E-01	X07960.1	NT	(B), and complement component C2 (C2) genes>
440	10384	20208	1.16	3.3E-01	AI 01515.2	NT	Rhizobium leguminosarum syn plasmid pRL301 nodX gene
617	10554	20366	1.41	3.3E-01	7662495	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 45
1182	11093	20840	3.05	3.3E-01	Q12448	SWISSPROT	Homo sapiens KIAA1100 protein (KIAA1100), mRNA
							PROLINE-RICH PROTEIN LAS17

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Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) Blast E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1295	11193	21046	4.62	3.3E-01	BF68880.1	EST_HUMAN	602184016T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:430251 3'
1598	11492	21342	1.11	3.3E-01	6753685	NT	Mus musculus diantegrin 5' (Digno), mRNA
1704	11605		1.05	3.3E-01	AA332734.1	EST_HUMAN	EST36722 Embryo, 3 week/1 Homo sapiens cDNA 5' end
2355	12235		4.74	3.3E-01	4507834	NT	Homo sapiens uridine monophosphate synthetase (uridine phosphorylase) transferase and oridine-5'-decarboxylase (UMPS) mRNA
2819	12848	22948	2	3.3E-01	AL251805.1	NT	Bacteriophage phi-YO2-12 complete genome
2982	12910		1.12	3.3E-01	002743	SWISSPROT	INTERLEUKIN-12 ALPHA CHAIN PRECURSOR (IL-12A) (CYTOTOXIC LYMPHOCYTE MATURATION
3016	12944	22797	1.01	3.3E-01	AL007832.2	NT	FACTOR 35 KD SUBUNIT (CLMF P85)
3490	13367	26170	1.14	3.3E-01	AB012922.1	NT	Streptomyces arifaciens methylammon biosynthetic genes
3768	13660	24433	2.17	3.3E-01	084045	SWISSPROT	Homo sapiens MTA1-L1 gene, complete cds
3824	13765	23962	1.69	3.3E-01	AL101688.2	NT	EXODEOXYRIBONUCLEASE V BETA CHAIN
3920	13929	23006	1.93	3.3E-01	AF200445.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10
4271	14170		2.74	3.3E-01	D31662.1	NT	Hypoxylon tridactylum chitin synthase gene, partial cds
4580	14477		1.48	3.3E-01	AJ509114.1	EST_HUMAN	Rattus norvegicus DNA for reusculin, partial cds
5083	15185	24630	2.68	3.3E-01	269818.1	NT	PEPTIDE TRANSPORTER 1 (HUMAN);
5083	15185	24631	2.68	3.3E-01	269818.1	NT	R. norvegicus mRNA for 3UTR of ubiquitin-like protein
5623	15337	25623	2.71	3.3E-01	BE19550.1	EST_HUMAN	R. norvegicus mRNA for 3UTR of ubiquitin-like protein
5623	15337	25624	2.71	3.3E-01	BE19550.1	EST_HUMAN	80142726T1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3875763 3'
6117	16011	26148	3.64	3.3E-01	NC28191.1	EST_HUMAN	80142726T1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3875763 3'
6117	16011	26149	3.64	3.3E-01	NC28191.1	EST_HUMAN	1564001.X1 NCI_GCAP_1081 Homo sapiens cDNA clone IMAGE:2265809 3' similar to contains Alu
6875	16433	26616	1.5	3.3E-01	NC8146.1	EST_HUMAN	1564001.X1 NCI_GCAP_1081 Homo sapiens cDNA clone IMAGE:2265809 3' similar to contains Alu
6981	16839	27053	19.46	3.3E-01	BF033564.1	EST_HUMAN	J2608F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2608 5' similar to TEGT
7477	17337	27842	3.26	3.3E-01	BF08666.1	EST_HUMAN	602140372F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301600 5'
7507	17256	27904	2.81	3.3E-01	BF376745.1	EST_HUMAN	2467H01.s1 Soares field line NHRL19W Homo sapiens cDNA clone IMAGE:297649 3'
7739	17599		2.07	3.3E-01	L11044.1	NT	RC4-TN0077.230030.001 gila TN0077 Homo sapiens cDNA
8104	17924	28242	2.71	3.3E-01	X68953.1	NT	Homo sapiens high-mobility group phosphoprotein (HMGP-C) gene, exons 1-3, complete cds
8104	17924	28243	2.71	3.3E-01	X68953.1	NT	D.mauritiana Adh gene
8389	18265		1.82	3.3E-01	BF23466.1	EST_HUMAN	602079020F1 NCI_GCAP_Bm64 Homo sapiens cDNA clone IMAGE:4219565 5'
8561	18431	28700	12.76	3.3E-01	BE216951.1	EST_HUMAN	hm51g02.x1 NCI_GCAP_Lu24 Homo sapiens cDNA clone IMAGE:3176978 3'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8652	15541	28925	3.94	3.5E-01	P47953	SWISSPROT	GALACTIN-3 (GALACTOSE SPECIFIC LECTIN 3) (M2C-2 ANTIGEN) (GE-BINDING PROTEIN) (S8-2O LECTIN) (CARBOHYDRATE BINDING PROTEIN 19) (CBP 36) (LAMININ-BINDING PROTEIN) (LECTIN L-20) (CBP36)
8655	19733		4.79	3.5E-01	AJ500352.1	EST_HUMAN	Ribulose biphosphate synthetase (EC 1.1.1.30)
8672	10000	19791	1.38	3.5E-01	X07950.1	NT	Human sapiens diacylglycerol 1 (DAG1)
9119	10831	28749	1.33	3.5E-01	0683919	NT	Human sapiens diacylglycerol 1 (DAG1)
9517	10323		5.05	3.5E-01	AF000002.1	NT	Human sapiens diacylglycerol 1 (DAG1)
448	10393		1.98	3.5E-01	AF000299.1	NT	Human sapiens diacylglycerol 1 (DAG1)
701	10394		2.05	3.5E-01	AF107061.2	NT	Human sapiens diacylglycerol 1 (DAG1)
1148	11059	26932	13.69	3.5E-01	AF107061.2	NT	Human sapiens diacylglycerol 1 (DAG1)
1281	11161	21019	1.04	3.5E-01	258032.1	NT	Human sapiens diacylglycerol 1 (DAG1)
1388	11274	21130	8.25	3.5E-01	Q40624	SWISSPROT	Human sapiens diacylglycerol 1 (DAG1)
1737	11693	21606	1.22	3.5E-01	Z38004.1	EST_HUMAN	Human sapiens diacylglycerol 1 (DAG1)
1744	11645	21513	5.5	3.5E-01	AF000179.1	EST_HUMAN	Human sapiens diacylglycerol 1 (DAG1)
1744	11645	21514	5.5	3.5E-01	AF000179.1	EST_HUMAN	Human sapiens diacylglycerol 1 (DAG1)
1800	11648	21574	1.76	3.5E-01	AF111655.1	NT	Human sapiens diacylglycerol 1 (DAG1)
2141	12023	21901	2.59	3.5E-01	BF203817.1	EST_HUMAN	Human sapiens diacylglycerol 1 (DAG1)
2484	12383	21901	2.9	3.5E-01	7710079	NT	Human sapiens diacylglycerol 1 (DAG1)
2677	12542	22433	1.55	3.5E-01	AF000598.1	EST_HUMAN	Human sapiens diacylglycerol 1 (DAG1)
3557	13470		0.95	3.5E-01	D10872.1	NT	Human sapiens diacylglycerol 1 (DAG1)
3938	13779		0.97	3.5E-01	AF107546.2	NT	Human sapiens diacylglycerol 1 (DAG1)
4295	14193	23977	1.35	3.5E-01	MF1818.1	NT	Human sapiens diacylglycerol 1 (DAG1)
4375	14291	24052	0.81	3.5E-01	AF111167.2	NT	Human sapiens diacylglycerol 1 (DAG1)
4397	14293	24077	1.33	3.5E-01	Q10239	SWISSPROT	Human sapiens diacylglycerol 1 (DAG1)
4532	14520		5.85	3.5E-01	BF069317.1	EST_HUMAN	Human sapiens diacylglycerol 1 (DAG1)
4907	15091		1.18	3.5E-01	M23852.1	NT	Human sapiens diacylglycerol 1 (DAG1)
5123	15000	24771	0.95	3.5E-01	AF100848.1	NT	Human sapiens diacylglycerol 1 (DAG1)
5133	15406		2.47	3.5E-01	BE173954.1	EST_HUMAN	Human sapiens diacylglycerol 1 (DAG1)
5223	15406	24613	2.32	3.5E-01	BE173954.1	EST_HUMAN	Human sapiens diacylglycerol 1 (DAG1)
6752	16531	26819	1.42	3.5E-01	M60293.1	NT	Human sapiens diacylglycerol 1 (DAG1)
6872	16751	23946	13.32	3.5E-01	X02088.1	NT	Human sapiens diacylglycerol 1 (DAG1)
6875	16754	23951	14.28	3.5E-01	BF131635.1	EST_HUMAN	Human sapiens diacylglycerol 1 (DAG1)
8751	17551		1.26	3.5E-01	AF107061.2	NT	Human sapiens diacylglycerol 1 (DAG1)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Max Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6929	1607		1.35	3.2E-01	AL161674.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment NC_70
6986	1693	27056	1.5	3.2E-01	AEO02015.1	NT	Dinococcus radiodurans R1 section 152 of 228 of the complete chromosome 1
7247	17124		2.19	3.2E-01	H68911.1	NT	Human monoclonal antigen CD14 (CD14) mRNA, complete cds
7741	17591	27812	3	3.2E-01	U44914.1	NT	Borrelia burgdorferi plasmid qp32.2, erpC and erpD genes, complete cds; and unknown genes
8098	17949	28199	3.25	3.2E-01	U48011396.1	NT	Human sapiens gene for AF-6, complete cds
9152	19652		2.7	3.2E-01	T06813.1	EST_HUMAN	EST104702 Fetal brain, Stratiogene (catalp32026) Homo sapiens cDNA clone HBD0221
9699	19228		3.28	3.2E-01	L07285.1	NT	Drosophila melanogaster lamA (Lam-A) mRNA, complete cds
9801	19313		2.97	3.2E-01	C83217	SWISSPROT	ELONGATION FACTOR TU (EF-TU)
9865	19995	24998	1.68	3.2E-01	C39474.1	NT	Homo sapiens deoxyribonucleic acid, complete cds
			1.87	3.2E-01	EE385776.1	EST_HUMAN	601275480F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3616748 5'
2036	12503	22997	3.73	3.1E-01	R18051.1	EST_HUMAN	g5000041 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:126051 5' similar to g5000041 OM PROTEIN (HUMAN);
2065	12653	22419	3.45	3.1E-01	7091971	NT	Homo sapiens KIAA0174 gene product (KIAA0174), mRNA
2065	12655	22420	3.45	3.1E-01	7091971	NT	Homo sapiens KIAA0174 gene product (KIAA0174), mRNA
2027	12765		1.01	3.1E-01	AV020036.1	EST_HUMAN	H68908.31 Soares, NFI, T, GBC, S1 Homo sapiens cDNA clone IMAGE:3975391 3'
3158	13061		2.78	3.1E-01	A5020369.1	NT	Human musculus gene for Scf/Trk kinase KIAARE, exon 6
3832	13743	23533	1.15	3.1E-01	AJ251586.1	NT	Drosophila melanogaster gene for transcription factor Ebf (Ebf gene)
5073	14543	24717	0.89	3.1E-01	A4576308.1	EST_HUMAN	hm51065.1 NCI_CGAP_B33 Homo sapiens cDNA clone IMAGE:1072761 3'
5395	15285	28719	8.65	3.1E-01	AF176111.1	NT	Homo sapiens Hepatocyte nuclear factor-3 alpha (NFY3A) gene, exon 1
5447	15398		45.03	3.1E-01	T13278.1	NT	Human musculus mRNA for polyribin
5527	15444	25510	1.94	3.1E-01	AF184122.1	NT	Homo sapiens fibroblast 2 (FLN2) gene, exons 10 through 22
5990	15795	25918	1.34	3.1E-01	AF086548.1	EST_HUMAN	RC3-HN0001-310300-011404 HN0001 Homo sapiens cDNA
6160	16438	24981	2.4	3.1E-01	EE73792.1	EST_HUMAN	U34061.21 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3940420 5'
7023	16900	27092	1.87	3.1E-01	R45318.1	EST_HUMAN	Y94801.1s1 Soares infant brain IN1B Homo sapiens cDNA clone IMAGE:35559 3'
7791	17641	27874	7.76	3.1E-01	BF096939.1	EST_HUMAN	602124743F1 NIH_MGC_36 Homo sapiens cDNA clone IMAGE:4261611 5'
7791	17641	27875	7.76	3.1E-01	BF096939.1	EST_HUMAN	602124743F1 NIH_MGC_36 Homo sapiens cDNA clone IMAGE:4261611 5'
7632	17682	27226	1.90	3.1E-01	AJ244001.1	EST_HUMAN	q91611.1x1 NCI_CGAP_K45 Homo sapiens cDNA clone IMAGE:189380 3' similar to g556700
8211	18095	28348	1.95	3.1E-01	BF176117.1	EST_HUMAN	HYDROXYMETHYLGLUTARYL-COA LYASE PRECURSOR (HUMAN);
8823	18639	28620	1.80	3.1E-01	BF176117.1	EST_HUMAN	601883302F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:406814 5'
					7682291	NT	Homo sapiens KIAA0764 gene product (KIAA0764), mRNA
9279	18982		1.83	3.1E-01	AF294308.1	NT	Anolis opalinus lissule Q5 NAOH dehydrogenase subunit 2 (ND2) gene, complete cds; mitochondrial gene for mitochondrial product
9315	19007		1.64	3.1E-01	AF304182.1	NT	Stizolobus viridum 40S ribosomal protein S11 mRNA, partial cds
9457	19089		2.45	3.1E-01	AF156933.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6006	19318		3.11	3.1E-01	AF196779.1	NT	Homo sapiens transcription factor (GCM) enhancer 3, JM11 protein, JM4 protein, JM6 protein, TE4 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synapophyllin genes, complete cds; and L-type calcium channel α
66	12335	18965	1.86	3.0E-01	6768063	NT	Homo sapiens protein kinase C, epsilon (Pkcε) mRNA
284	10220	20037	11.12	3.0E-01	AJ271735.1	NT	Homo sapiens Xq pseudocautosomal region, segment 1/2
1204	11114	20960	1.89	3.0E-01	AW300400.1	EST_HUMAN	hs633003.x1 NO_CGAP_Kd11 Homo sapiens cDNA clone IMAGE:2774339 3'
1491	11396	21256	6.26	3.0E-01	AJ006765.1	NT	Balanophora physalis gene encoding atrial natriuretic peptide
2089	11978	21673	0.86	3.0E-01	AF23778.1	NT	Rattus norvegicus Cas2/calmodulin-dependent protein kinase II, alpha subunit mRNA, 3' untranslated region
375	13100		0.89	3.0E-01	AF230481.1	NT	Corynebacterium sp. ALY-1 avpC gene for polyglutamate lysine, complete cds
3769	13701	23488	1.34	3.0E-01	AW81786.1	EST_HUMAN	PM1-S10262-26100-001-001 S10262 Homo sapiens cDNA
4412	14306	24050	1.91	3.0E-01	AJ006765.1	NT	Balanophora physalis gene encoding atrial natriuretic peptide
8293	15205	24891	5.34	3.0E-01	BE741629.1	EST_HUMAN	601594650F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3946734 5'
8378	15208	25147	3.18	3.0E-01	BE693575.1	EST_HUMAN	RC3-B10333-180700-11-403 B10333 Homo sapiens cDNA
8379	15209	25148	3.18	3.0E-01	BE693575.1	EST_HUMAN	RC3-B10333-180700-11-403 B10333 Homo sapiens cDNA
8401	15220	25368	3.61	3.0E-01	U01247.1	NT	Mus musculus 129/Ola cell 10 kd protein (mCG10) gene, complete cds
6098	16031	25717	2.61	3.0E-01	D16313.1	NT	Muscle actin, 16 gene, complete cds
6358	16109	26149	2.67	3.0E-01	U0647007	NT	Mus musculus myotubularin (Mtn) perlecan mRNA
6429	16200	26461	1.38	3.0E-01	AJ4071810.1	NT	Streptococcus pneumoniae strain D6L5 PsaA (psaA) gene, partial cds
9425	16965	26953	1.28	3.0E-01	AEO01785.1	NT	Thermoplasma volcanum protein 7 of 136 of the complete genome
6977	16756		4.67	3.0E-01	5910161	NT	Homo sapiens Cyp17 (cytochrome P450c17) gene, partial cds
6937	16515	27007	1.27	3.0E-01	BE666083.1	EST_HUMAN	AF133078F1 NIH_MGC_35 Homo sapiens cDNA clone IMAGE:3551664 5'
7844	17794	28034	1.89	3.0E-01	AJ5030231.1	NT	Argyrophilus oxyphaga genes for CR chaperone BP, complete cds
8980	18785	20074	2.89	3.0E-01	H51029.1	EST_HUMAN	y648101.1 Soares fetal liver spleen INL3 Homo sapiens cDNA clone IMAGE:164107 5'
8980	18785	20075	2.89	3.0E-01	H51029.1	EST_HUMAN	y648101.1 Soares fetal liver spleen INL3 Homo sapiens cDNA clone IMAGE:164107 5'
9594	19947		1.43	3.0E-01	AJ297931.1	NT	Rattus norvegicus mRNA for glyceraldehyde-3-phosphate dehydrogenase type 2 (gapdh-2 gene)
9636	19960		2.76	3.0E-01	6877768	NT	Mus musculus ribose 5-phosphate isomerase A (RpiA) mRNA
1978	11871	21762	1.8	2.9E-01	AEO00736.1	NT	Aquilex aedulis section 68 of 160 of the complete genome
2207	12089	21980	0.89	2.9E-01	AF2722718.1	NT	Chrysidomyces synuroideus mitochondrion, complete genome
3147	13072	22873	1.03	2.9E-01	AF078111.1	NT	Xenopus laevis transcription factor E2F mRNA, complete cds
3213	13137	22959	2.29	2.9E-01	AW767239.1	EST_HUMAN	PM1-CT0326-171299-001-412 CT0326 Homo sapiens cDNA
3213	13137	22940	2.29	2.9E-01	AW767239.1	EST_HUMAN	PM1-CT0326-171299-001-412 CT0326 Homo sapiens cDNA

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor	
3821	43733	23523	1.28	2.5E-01	AI610838.1	EST_HUMAN	h21a11.1 NCL CGAP_Gas4 Homo sapiens cDNA clone IMAGE:218412 3' similar to gp.D19550 N1L-2-4	
3824	13901		0.82	2.5E-01	AW020202.1	EST_HUMAN	ZINC FINGER PROTEIN (HUMAN) contains element L1, repetitive element; w02f10.1 NCL CGAP_G302 Homo sapiens cDNA clone IMAGE:2480368 3'	
4364	14290	24069	1.01	2.5E-01	AA264468.1	EST_HUMAN	z57412.1 NCL CGAP_G0381 Homo sapiens cDNA clone IMAGE:701591 5' similar to contains A1u repetitive element;	
4368	14284	24068	0.78	2.5E-01	AF134113.1	NT	Mus musculus SKO1 (Skf1) gene, complete cds	
4369	14284	24068	0.78	2.5E-01	AF134113.1	NT	Mus musculus SKO1 (Skf1) gene, complete cds	
4725	14515	24401	0.92	2.5E-01	AB916020.1	NT	Mus musculus gene, complete cds, similar to EXLH1	
5218	15141		1.48	2.5E-01	R07445.1	EST_HUMAN	h77412.1 Scores from brain N18 Homo sapiens cDNA clone IMAGE:36291 3'	
5522	15440	25804	4.45	2.5E-01	X66038.1	NT	6 acilites leucines-opsin (cod, lnc, lnc, lnc and lnc) genes for fructose 6-phosphatransferase system polyphosphate P10,16,23,30 and lnc	
5523	15448	25815	5.83	2.5E-01	X66038.1	NT	6 acilites leucines-opsin (cod, lnc, lnc, lnc and lnc) genes for fructose 6-phosphatransferase system polyphosphate P10,16,23,30 and lnc	
6171	15724	25938	2.24	2.5E-01	U03420.1	NT	Mus musculus Epi receptor A5 (EpiA5), mRNA	
6171	15724	25938	2.4477	1.81	2.5E-01	AF142353.1	NT	Bos taurus myosin IIRNA, complete cds
6218	16064	26534	2.52	2.5E-01	Q04369	SWISSPROT	Mus musculus PHL protein (P10) gene, complete cds; and Lghn protein (Lghn) gene, partial cds	
6249	16115	26587	1.74	2.5E-01	AF100666.1	NT	Mus musculus major histocompatibility locus class II region; Fas-binding protein Dxxx (Dxxx) gene, partial cds; Bnlg1 (Bnlg1), lipulin (lipulin), RafGOS-like factor (R/LP), KE2 (KE2), BNG4 (BNG4), beta1, 3- galactosyl (transferase) (beta1 3-galactosyl)	
6619	16456	26866	1.78	2.5E-01	BE540422.1	EST_HUMAN	90106830P1 NH1 JGCG, 10 Homo sapiens cDNA clone IMAGE:3462891 5'	
6619	16456	26867	1.78	2.5E-01	BE540422.1	EST_HUMAN	90106830P1 NH1 JGCG, 10 Homo sapiens cDNA clone IMAGE:3462891 5'	
8267	18147	28387	1.98	2.5E-01	AF128843.1	NT	Tropoecoma cod stige-specific surface glycoprotein gp82 (gp82) mRNA, partial cds	
8502	18376	28639	2.68	2.5E-01	V01194.1	NT	Chlamydomonas reinhardtii mRNA for nitrite reductase structural locus	
8502	18376	28640	2.68	2.5E-01	V01194.1	NT	Chlamydomonas reinhardtii mRNA for nitrite reductase structural locus	
8502	18376	28640	2.68	2.5E-01	V01194.1	NT	Chlamydomonas reinhardtii mRNA for nitrite reductase structural locus	
8884	18678	28966	1.77	2.5E-01	AA93573.1	EST_HUMAN	Torpedo californica mRNA, encoding acetylcholine receptor gamma subunit myS9H02.51 NCL CGAP_P112 Homo sapiens cDNA clone IMAGE:1273779 similar to contains LTR8.12 LTR8 repetitive element;	
8886	18687	28967	4.54	2.5E-01	AA139078.1	NT	Compendium plasmid NGTCT11188 complete genome; segment 8/8	
9514	19127	35260	1.83	2.5E-01	AW006871.1	EST_HUMAN	w288905.1 NCL CGAP_Bmg25 Homo sapiens cDNA clone IMAGE:2656621 3' similar to contains element MER239 repetitive element	
9502	19424	26248	2.74	2.5E-01	AF062483.1	EST_HUMAN	Homo sapiens TNP-e-inducible RNA binding protein (TRP) gene, complete cds	
9544	19512		1.33	2.5E-01	BE71881100.1	NT	90148203P1 NH1 JGCG, 68 Homo sapiens cDNA clone IMAGE:3384556 5'	
9563	19587	26188	4.86	2.5E-01	Y08537.1	NT	Chlamydomonas reinhardtii mRNA for nitrite reductase structural locus	
9563	19587	26188	4.86	2.5E-01	Y08537.1	NT	Chlamydomonas reinhardtii mRNA for nitrite reductase structural locus	
9563	19587	26188	4.86	2.5E-01	Y08537.1	NT	Chlamydomonas reinhardtii mRNA for nitrite reductase structural locus	

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
556	10497		1.84	2.E-01	U67193.1	NT	Rattus norvegicus A-kinase anchoring protein AKAP150 mRNA, complete cds
1057	10983	20328	2.47	2.E-01	AF168550.1	NT	Gaura guayanae malate dehydrogenase (mdh) gene, partial cds
1256	11193	21013	2.11	2.E-01	BE131442.1	EST_HUMAN	601148733.F1 NH_MGC_19 Homo sapiens cDNA clone IMAGE:316386 5'
1256	11193	21014	1.11	2.E-01	BE131442.1	EST_HUMAN	601148733.F1 NH_MGC_19 Homo sapiens cDNA clone IMAGE:316386 5'
1256	11176	21025	1.01	2.E-01	D68550.1	NT	Human mRNA for serine/threonine protein kinase, complete cds
1965	11598	21470	1.55	2.E-01	AF166020.1	EST_HUMAN	OV1-CT0394-12020-065-405 CT0394 Homo sapiens cDNA
1965	11598	21470	1.77	2.E-01	AF166020.1	EST_HUMAN	OV1-CT0394-12020-065-405 CT0394 Homo sapiens cDNA
2084	11974	21689	1.47	2.E-01	AF147620.1	EST_HUMAN	h47403.X1 Soares_NFL_X_686311 Homo sapiens cDNA clone DKF-Z65802321
2428	12300	22197	2.94	2.E-01	AF000494.1	NT	Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome
2428	12300	22198	2.94	2.E-01	AF000494.1	NT	Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome
2500	12375		2.47	2.E-01	AF15661.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
2830	12498	22388	1.37	2.E-01	AB020975.1	NT	Arabidopsis thaliana mRNA for lipoyltransferase, complete cds
2840	12657		1.45	2.E-01	AF170493.1	NT	Tetrahymena gracilis 900Da heat-shock protein (HSP90) mRNA, partial cds
2841	12658	22867	2.48	2.E-01	AF170493.1	NT	Tetrahymena gracilis 900Da heat-shock protein (HSP90) mRNA, partial cds
2841	12658	22868	2.48	2.E-01	AF170493.1	NT	Tetrahymena gracilis 900Da heat-shock protein (HSP90) mRNA, partial cds
3332	12332	22607	1.11	2.E-01	AF000404.1	NT	Pyrococcus horikoshii CT19 genome DNA, 777031-994000 nt, position 417
3915	13824	22604	1.75	2.E-01	AF001150.1	NT	Sonchella oleracea (section 08 of 70) of the complete genome
4103	14003		2.21	2.E-01	AB009883.1	EST_HUMAN	044910.X1 Soares_NFL_X_686311 Homo sapiens cDNA clone IMAGE:1640226 3' similar to contains AU repetitive element/contains element 1/ER22 repetitive element.1.
4352	14248	24034	0.98	2.E-01	AL021427.2	NT	Mus musculus chromosome X contig, putative Magasin gene, Cullin3, NAD(P) steroid dehydrogenase and Zinc finger protein 185
4357	14253	24038	2.2	2.E-01	P10915	SWISSPROT	RNA POLYMERASE BETA SUBUNIT (LARGE STRUCTURAL PROTEIN) (L. PROTEIN)
4573	14559	24352	1.03	2.E-01	D15550.1	NT	Human mRNA for transcription factor AREB5, complete cds
4573	14559	24353	1.03	2.E-01	D15550.1	NT	Human mRNA for transcription factor AREB5, complete cds
4722	14608	24394	2.8	2.E-01	AF000154.1	NT	Bovine albumin 3' complete genome
4755	14640	24427	1.54	2.E-01	BF026168.1	EST_HUMAN	92242307.F1 NCI_CGAP_Bim57 Homo sapiens cDNA clone IMAGE:418125 5'
4787	14672	24469	1.7	2.E-01	A072969.1	EST_HUMAN	q95111.X1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1876528 3' similar to contains AU repetitive element/contains element 1/LITS negative element.1.
5252	15440	24948	21.36	2.E-01	AA346997.1	EST_HUMAN	EST157072 Infant brain Homo sapiens cDNA 5' and
5443	15393	25419	2.33	2.E-01	AB019525.1	NT	Human sapiens OCTN2 gene, complete cds
5770	15677	25794	1.44	2.E-01	AF000124.1	NT	Mesembryanthemum crystallinum fructose-bisphosphate aldolase mRNA, complete cds
5770	15677	25795	1.44	2.E-01	AF000124.1	NT	Mesembryanthemum crystallinum fructose-bisphosphate aldolase mRNA, complete cds
5938	15941	26073	7.67	2.E-01	BF011215.1	EST_HUMAN	U1-H-BH-sei-10-0-0-1 X1 NCI_CGAP_Su88 Homo sapiens cDNA clone IMAGE:3085182 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6713	16693	26781	1.24	2.8E-01	A1346126.1	EST_HUMAN	qp48001.x1 NCL CGAP_C68 Homo sapiens cDNA clone IMAGE:1922386 3' similar to gbX08323_cds1
6713	16693	26782	1.24	2.8E-01	A1346126.1	EST_HUMAN	MITOCHONDRIAL 695 RIBOSOMAL PROTEIN L3 (HUMAN);
6778	16957	26947	2.39	2.8E-01	U51681.1	NT	qp48001.x1 NCL CGAP_C68 Homo sapiens cDNA clone IMAGE:1922386 3' similar to gbX08323_cds1
6804	16871		7.25	2.8E-01	BF347847.1	EST_HUMAN	MITOCHONDRIAL 695 RIBOSOMAL PROTEIN L3 (HUMAN);
7011	17187	27388	1.35	2.8E-01	AF090392.1	NT	Homo sapiens uncatalyzed 14-alpha demethylase cyclochrome P450 (CYP61) gene, exon 5
7000	17457		1.15	2.8E-01	L13854.1	NT	Mus musculus centrin (Centn2) gene, complete cds
7785	17539	27772	2.79	2.8E-01	7769163	NT	Lycopodium obscurum peroxidase (LPOX) mRNA, complete cds
8126	18014	28261	2.27	2.8E-01	BF241062.1	EST_HUMAN	Homo sapiens hypodermal protein (LOC31319), mRNA
8126	18014	28262	2.27	2.8E-01	BF241062.1	EST_HUMAN	601880794F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4103650 5'
8163	18041	28281	3.01	2.8E-01	BF65670.1	EST_HUMAN	601880794F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4103650 5'
8254	18134	28382	2.62	2.8E-01	AF051682.1	NT	601882148F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4075028 5'
8590	18468		3.49	2.8E-01	BF674023.1	EST_HUMAN	601882148F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4075028 5'
9452	19150		6.37	2.8E-01	C832326.1	NT	Desophylla heterocarpa trullipes (fru) gene, alternative splice products, 5' flanking region, exons 1 through 7 and complete cds
9457	19219	28526	3.11	2.8E-01	BE176999.1	EST_HUMAN	60213718F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4273853 5'
9526	19851		4.89	2.8E-01	11433629	NT	Mus musculus DNA for proteoglycan D2 synthase, complete cds
468	10411	20230	2.33	2.7E-01	Y17324.1	NT	PM4.H1 08968.030409.001.407 HT0805 Homo sapiens cDNA
597	10833	20341	3.14	2.7E-01	AA450061.1	EST_HUMAN	Homo sapiens CDCA2-binding protein kinase beta (DMPK18a) (CDCA2BP5), mRNA
1243	11147	20846	1.49	2.7E-01	A5004003.1	NT	269410 x1 Searns_doll [Mus_Nu2HFE_5w Homo sapiens cDNA clone IMAGE:788827 3' similar to
1604	11665		1.73	2.7E-01	X78915.1	NT	contains A14 repetitive element
1698	11600	21471	2.96	2.7E-01	W58057.1	EST_HUMAN	Genomic human transposable element Tsp100 gene for transposase, complete cds
1738	11939	21507	1.26	2.7E-01	P03541	SWISSPROT	GAG POLYPROTEIN [CONTAINS INNER COAT PROTEIN P12, CORE PROTEIN P16, CORE SHELL
2038	12712		2.38	2.7E-01	A0407676.1	NT	PROTEIN P30, NUCLEOPROTEIN P10]
2316	12197	22094	8.78	2.7E-01	Y13858.1	NT	Ratios non-specific vesicular monoamine transporter type 2, promoter region and exon 1
2408	12283	22180	3.51	2.7E-01	A1310888.1	EST_HUMAN	Feline immunodeficiency virus env gene, isolate ITT0808PU (M85), partial
2566	12883		1.25	2.7E-01	BF068284.1	EST_HUMAN	183831.12 NCL CGAP_Luz25 Homo sapiens cDNA clone IMAGE:2048539 3' similar to contains element L1
3029	13838	23018	1.89	2.7E-01	A1628015.1	EST_HUMAN	repetitive element, 1
3843	13851	23526	2.31	2.7E-01	L177699.1	NT	CH1 HT10875-06000-385-cds HT10875 Homo sapiens cDNA
4760	14681	24468	0.89	2.7E-01	L27519.1	NT	W052911.x1 NCL CGAP_KGRT1 Homo sapiens cDNA clone IMAGE:2402328 3'
							Homo sapiens Dicerase syndrome critical region, telomeric end
							Triticum aestivum (Wc68) gene, complete cds

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar Top Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4673	14848		3.5	2.7E-01	AW595131.1	EST_HUMAN	RC1-CT0280-23020-016-ct03-0286 Homo sapiens cDNA
5221	15144	24338	3.46	2.7E-01	P17277	SWISSPROT	HOMEOBOX PROTEIN HOXA4 (HOXA4)
6064	16047	26162	2.25	2.7E-01	Q61554	SWISSPROT	FIBRILLIN 1 PRECURSOR
6027	16386	26565	2.23	2.7E-01	AF248054.1	NT	Bos laurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
6527	16386	26566	2.23	2.7E-01	AF248054.1	NT	Bos laurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
7376	17247	27453	10.05	2.7E-01	Q63809	SWISSPROT	THREONYL-L-TRNA SYNTHETASE (THREONINE-TRNA LIGASE) (THRRS)
7378	17247	27464	10.06	2.7E-01	Q63809	SWISSPROT	THREONYL-L-TRNA SYNTHETASE (THREONINE-TRNA LIGASE) (THRRS)
7379	17248		2.24	2.7E-01	P37928	SWISSPROT	FIMBRIN 1 PROTEIN
7801	17651	27688	1.26	2.7E-01	AF091448.1	NT	Oryzobryopsis carolinensis calmodulin C mRNA, partial cds
7827	17673	27921	1.63	2.7E-01	AF091434.1	NT	Mus musculus transcription factor NF-ATc1 isoform a (NF-ATc1) mRNA, complete cds
8167	18073	28322	1.76	2.7E-01	AF070543.1	EST_HUMAN	AV705043 ADB Homo sapiens cDNA clone ADB05043.5'
8167	18073	28323	1.76	2.7E-01	AF070543.1	EST_HUMAN	AV705043 ADB Homo sapiens cDNA clone ADB05043.5'
8167	18082	28333	4.05	2.7E-01	AJ133269.1	NT	Homo sapiens caveolin-1/2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2),
9369	19304		1.27	2.7E-01	X63267.1	NT	G. gallus mRNA for nanodisc receptor type 3
9810	19320		2.15	2.7E-01	AF27409.1	NT	Homo sapiens fragile 160 cDNA reduplicates (FGR) gene, exon 6
462	12657	20224	1.54	2.6E-01	P78411	SWISSPROT	RCQ1053 CLASS HOMEODOMAIN PROTEIN RX-2
472	10416		1.38	2.6E-01	P76456.1	NT	Bos laurus mRNA for mb1, complete cds
1371	11277	21133	2.23	2.6E-01	EE68087.1	EST_HUMAN	601510535F1 NH1_MGC_2 Homo sapiens cDNA clone IMAGE:36712345 5'
1418	11324	21168	0.97	2.6E-01	AJ013300.1	NT	Cypine max pseudogene for B3 30K
1654	11750	21624	8.50	2.6E-01	AL161472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
1854	11750	21625	8.50	2.6E-01	AL161472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
							RCQ1053 CLASS HOMEODOMAIN PROTEIN RX-2 (HUMAN); gb:M14695_cds1 Mouse surfeit locus surfeit 3 protein gene (MOUSE);
2046	11837		9.9	2.6E-01	AW73162.1	EST_HUMAN	Human prealbumin gene, complete cds
2106	11956	21696	1.2	2.6E-01	M11644.1	NT	B. maritimus ribL gene
2424	12301		2.68	2.6E-01	V12506.1	NT	60112601BET1 NH1_MGC_2 Homo sapiens cDNA clone IMAGE:2660043 5'
2490	12374		9.66	2.6E-01	BE27440.1	EST_HUMAN	EST368053 IMAGE reassessments, MAGM Homo sapiens cDNA
3093	12980		1.03	2.6E-01	AW074531.1	EST_HUMAN	h300402.x1 NC1_OGAP_Lu24 Homo sapiens cDNA clone IMAGE:3174914 3' similar to contains L1:18 L1
3485	13401		0.84	2.6E-01	BE274916.1	EST_HUMAN	h300402.x1 NC1_OGAP_Lu24 Homo sapiens cDNA clone IMAGE:3174914 3' similar to contains L1:18 L1
3532	13448	23245	1.12	2.6E-01	M22942.1	NT	Bacteriophage T2 DNA (phosphatase-N6 methyltransferase (dam) gene, complete cds

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Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Meat Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3591	13505	23256	1.7	2.6E-01	AF229718.1	NT	Homo sapiens acylcholinesterase-like tail subunit (COLQ) gene, exons 1A, 2, 3, 4, and 5
3651	13565	23361	0.9	2.6E-01	AB017446.1	NT	Rattus norvegicus mRNA for organic anion transporter 3, complete cds
4010	13916	23891	1	2.6E-01	AF0956510.1	EST_HUMAN	ES171690 IMAGE resources, MAGF Homo sapiens cDNA
4082	13964	23742	13.13	2.6E-01	BC000595.1	EST_HUMAN	Q17167030 IMAGE resources, MAGF Homo sapiens cDNA
4259	14160	23935	0.95	2.6E-01	AF175293.1	NT	Enterococcus faecium strain N67-330 w/o D glycopeptide resistance gene cluster, complete cds; and unknown gene
4393	14289	24072	0.84	2.6E-01	AB021180.1	NT	Gallus gallus mRNA for skeletal myosin heavy chain, complete cds
4393	14289	24073	0.84	2.6E-01	AB021180.1	NT	Gallus gallus mRNA for skeletal myosin heavy chain, complete cds
4448	14342	24134	1.17	2.6E-01	AA457817.1	EST_HUMAN	aa08407.1 Striatogen fetal retina 037202 Homo sapiens cDNA clone IMAGE383477 5'
4548	14441	24224	1.63	2.6E-01	U01103.1	NT	Arabidopsis thaliana PSI type II chlorophyll a/b-binding protein (Lhca3*) mRNA, complete cds
4610	14504	24292	1.20	2.6E-01	AF142703.1	NT	Ochropleura radialis malarase-like protein (malK) gene, complete cds; chloroplast gene for chloroplast product
4898	14778	24554	3.66	2.6E-01	U04558.1	EST_HUMAN	AF1605.1 Scarsa desantis N2-P Homo sapiens cDNA clone IMAGE15288 5'
5051	14923	24960	0.86	2.6E-01	P08603	SWISSPROT	ADY-COA DEHYDROGENASE, MEDIAN-CHAIN SPECIFIC, MITOCHONDRIAL PRECURSOR (MGAD)
5700	16784		2.03	2.6E-01	AE001811.1	NT	Thermoplasma maritima section 123 of 185 of the complete genome
5783	15870	25777	1.83	2.6E-01	A1552557.1	EST_HUMAN	1502412.1 NC1 CGAP_Pari1 Homo sapiens cDNA clone IMAGE-2227438 3' similar to SW-NDP1, RAT Q94289 NEUROGENIC DIFFERENTIATION FACTOR 1, combines element LTR1 repetitive element;
5783	15870	25778	1.83	2.6E-01	A1552557.1	EST_HUMAN	1502412.1 NC1 CGAP_Pari1 Homo sapiens cDNA clone IMAGE-2227438 3' similar to SW-NDP1, RAT Q94289 NEUROGENIC DIFFERENTIATION FACTOR 1, combines element LTR1 repetitive element;
6582	16410	26586	1.62	2.6E-01	R10365.1	EST_HUMAN	9747323.1 NC1 CGAP_Pari1 Homo sapiens cDNA clone IMAGE-2227438 3' similar to SW-NDP1, RAT Q94289 NEUROGENIC DIFFERENTIATION FACTOR 1, combines element LTR1 repetitive element;
6585	16465	26586	1.27	2.6E-01	R02441.1	EST_HUMAN	9747323.1 NC1 CGAP_Pari1 Homo sapiens cDNA clone IMAGE-2227438 3' similar to SW-NDP1, RAT Q94289 NEUROGENIC DIFFERENTIATION FACTOR 1, combines element LTR1 repetitive element;
6582	16731	26925	3.01	2.6E-01	BF343388.1	EST_HUMAN	9747323.1 NC1 CGAP_Pari1 Homo sapiens cDNA clone IMAGE-2227438 3' similar to SW-NDP1, RAT Q94289 NEUROGENIC DIFFERENTIATION FACTOR 1, combines element LTR1 repetitive element;
6900	16779	26973	2.04	2.6E-01	U010199	SWISSPROT	1502407.1 Scarsa fetal liver subunit INFL5 Homo sapiens cDNA clone IMAGE15096 5'
7040	16823	27112	4.34	2.6E-01	BE080339.1	EST_HUMAN	HYPOHECTED 78.2 NO PROTEIN CT101.02 IN CHROMOSOME II
7046	16823	27113	4.34	2.6E-01	BE080339.1	EST_HUMAN	R05-E10082-310500-021-F10 E10082 Homo sapiens cDNA
7854	17704		1.16	2.6E-01	Q28295	SWISSPROT	VON WILLEBRAND FACTOR PRECURSOR (VWF)
6812	16825		83.65	2.6E-01	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
9136	16892		1.80	2.6E-01	10190655	NT	Mus musculus jerky (JH), mRNA
9328	16955		1.92	2.6E-01	BE083491.1	EST_HUMAN	601511052F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE3912012 5'
9395	19053	25309	2.6	2.6E-01	AF316864.1	NT	Homo sapiens Naik-ATPase gamma subunit (FYD2) gene, complete cds, alternatively spliced

Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Even SEQ ID NO.	ORF SEQ ID NO.	Expression Signal Value	Most Similar (Top) Ht BLAST E Signal	Top Ht Accession No.	Top Ht Database Source	Top Ht Descriptor
9833	10333		8.03	2.5E-01	AF141325.2	NT	Homo sapiens localized polyphosphatase 1-phosphatase (NPP1L) gene, complete cds
9899	18376		1.15	2.5E-01	Q01631	SWISSPROT	ADENYLATE CYCLASE (ATP-PI-PROPHOSPHATELYASE) (ADENYLATE CYCLASE)
241	10299	20025	2.12	2.5E-01	4502366	NT	Homo sapiens ATP synthase, H ⁺ transporting, mitochondrial F1 complex, delta subunit (ATP6D), nuclear gene encoding mitochondrial protein, mRNA
242	10269	20025	1.98	2.5E-01	4502366	NT	Homo sapiens ATP synthase, H ⁺ transporting, mitochondrial F1 complex, delta subunit (ATP6D), nuclear gene encoding mitochondrial protein, mRNA
255	10221		3.24	2.5E-01	M26981.1	NT	Starfish (P. schinosus) cytoplasmic actin gene, complete cds
815	10743	20589	1.32	2.5E-01	U09994.1	NT	Mus musculus (CR)Swiss glyceraledehyde 3-phosphate dehydrogenase (Gapo-S) gene, complete cds
1044	10692		1.98	2.5E-01	AE0002166.1	NT	Ureaplasma urealyticum, accession 57 of 59 of the complete genome
1108	11021	20964	9.8	2.5E-01	U78637.1	EST_HUMAN	ye1707/r11 Stragelange strain (M527210) Homo sapiens cDNA clone IMAGE:177488.5
1593	11407	21268	0.85	2.5E-01	AL119524.1	NT	Bovine chinea strain T4 cDNA library under conditions of nitrogen deprivation
1697	11696		6.43	2.5E-01	4895408	NT	Homo sapiens hyperpolarization activated cyclic nucleotide-gated potassium channel 4 (HCN4) mRNA
1840	12706	21612	0.88	2.5E-01	BC089604.1	EST_HUMAN	PMA-C10400-310700-005-006 C10400 Homo sapiens cDNA
1840	12706	21612	0.88	2.5E-01	BC089604.1	EST_HUMAN	PMA-C10400-310700-005-006 C10400 Homo sapiens cDNA
2347	12237		8.29	2.5E-01	AE000076.1	NT	Aquifex aerophilus section 7 of 109 of the complete genome
2348	12233		1.35	2.5E-01	AA24816897.1	EST_HUMAN	25a112/r1 NCL GGNP GC31 Homo sapiens cDNA clone IMAGE:684862.5
2597	12460	22359	0.97	2.5E-01	X06510.1	NT	B. murina mRNA for D-separate oxidase
3396	13286		2.97	2.5E-01	AF0197477.1	EST_HUMAN	EST389454 IMAGE resequence, MAGM Homo sapiens cDNA
3490	13409	23211	0.86	2.5E-01	AF233877.1	NT	Danio rerio papilio YY precursor gene, complete cds
3502	13419	23220	7.93	2.5E-01	AF101577.2	NT	Aquatic reticulated YY precursor gene, complete cds
3714	13686	23468	1.15	2.5E-01	AF1741483.1	EST_HUMAN	Wnt1067.x1 Soares_NSF_F9_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2364780.3
3774	13690	23469	1.15	2.5E-01	AF1741483.1	EST_HUMAN	Wnt11067.x1 Soares_NSF_F9_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2364780.3
3977	13824		0.83	2.5E-01	P33223	SWISSPROT	AAGLUTININ ATTACHMENT SUBUNITPRECURSOR
4227	14120		1.2	2.5E-01	Q03314	SWISSPROT	RHB PROTEIN
4614	14407		0.96	2.5E-01	AF242431.1	NT	Mus musculus neuronal apoptosis inhibitory protein 6 (Nap6) gene, complete cds; and Nap63 gene, exons 2-9 and 11-16
4643	14531		1.14	2.5E-01	Q27225	SWISSPROT	MOLT-INHIBITING HORMONE PRECURSOR (MH)
4646	14535	24324	3.78	2.5E-01	AF0071788.1	SWISSPROT	Chlorisrupea fumifera disease associated protein 2 (DAP2) mRNA, complete cds
4672	14559	24351	2.19	2.5E-01	AE004416.1	NT	Vario chlosterne chromosome II, section 73 of 83 of the complete chromosome
4698	14584		3.16	2.5E-01	AE239113.1	NT	Mus musculus annexin V gene, intron 4 segment containing 5' 1TR and gag portion of MUEVNL (murine endogenous retrovirus) element
4726	14612	24359	0.79	2.5E-01	BC089695.1	EST_HUMAN	901474681.1 NH_M3C_72 Homo sapiens cDNA clone IMAGE:392200.9

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Table 4
Single Exon Probes Expressed in Heart

Probe Seq ID NO:	Exon Seq ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4750	14636	24421		0.89	2.5E-01 AB011070.1	NT	Mus musculus gene for uncoupling protein 3, 5'-flanking region and partial 5'UTR
5169	15035	24902	0.86	2.5E-01 AW663183.1	EST_HUMAN	NT	h17606.y1 NC01CGAP_G01 Homo sapiens cDNA clone IMAGE:2988949 5' similar to contains TARI.12
5169	15035	24903	0.86	2.5E-01 AW663183.1	EST_HUMAN	NT	h17606.y1 NC01CGAP_G01 Homo sapiens cDNA clone IMAGE:2988949 5' similar to contains TARI.12
5264	15180	24902	11.02	2.5E-01 S33390.1	NT	NT	TAR1 repetitive element;
6360	16229		1.32	2.5E-01 AF193419.1	NT	NT	h17606.y1 NC01CGAP_G01 Homo sapiens cDNA clone IMAGE:2988949 5' similar to contains TARI.12
6500	16359	26032	3.73	2.5E-01 AF193419.1	NT	NT	TAR1 repetitive element;
6583	16463	26955	2.99	2.5E-01 BF109040.1	EST_HUMAN	NT	Mus musculus SKOT1 (Skd1) gene, complete cds
6788	16697	26956	2.25	2.5E-01 BF038955.1	EST_HUMAN	NT	Homo sapiens chromosome 21 segment H931C082
7020	16897	27087	3.05	2.5E-01 H53236.1	EST_HUMAN	NT	8014492238.F1 NH MGCG 06 Homo sapiens cDNA clone IMAGE:3982809 5'
7481	17351	27554	16.11	2.5E-01 U89651.2	NT	NT	8014492238.F1 NH MGCG 06 Homo sapiens cDNA clone IMAGE:3982809 5'
7481	17351	27555	16.11	2.5E-01 U89651.2	NT	NT	8014492238.F1 NH MGCG 06 Homo sapiens cDNA clone IMAGE:3982809 5'
7522	17341	27547	2.04	2.5E-01 AF095164.1	NT	NT	Homo sapiens matrix metalloproteinase MMP Reas-1 gene, promoter region
7522	17341	27548	2.04	2.5E-01 AF095164.1	NT	NT	Homo sapiens matrix metalloproteinase MMP Reas-1 gene, promoter region
7614	17664	27904	1.5	2.5E-01 AW181607.1	EST_HUMAN	NT	Homo sapiens matrix metalloproteinase MMP Reas-1 gene, promoter region
8010	17860	28105	1.62	2.5E-01 AW152246.1	EST_HUMAN	NT	Homo sapiens matrix metalloproteinase MMP Reas-1 gene, promoter region
8011	17861	28106	1.68	2.5E-01 X58499.1	EST_HUMAN	NT	Homo sapiens matrix metalloproteinase MMP Reas-1 gene, promoter region
8436	18300	28566	2.32	2.5E-01 D59514.1	NT	NT	Homo sapiens matrix metalloproteinase MMP Reas-1 gene, promoter region
8074	18651	29117	2.45	2.5E-01 AF203524.1	NT	NT	Homo sapiens matrix metalloproteinase MMP Reas-1 gene, promoter region
9599	19681	25072	1.28	2.5E-01 AF170721.1	NT	NT	Homo sapiens matrix metalloproteinase MMP Reas-1 gene, promoter region
9599	19681	25073	1.28	2.5E-01 AF170721.1	NT	NT	Homo sapiens matrix metalloproteinase MMP Reas-1 gene, promoter region
1000	19720		4.2	2.5E-01 AF170721.1	NT	NT	Homo sapiens matrix metalloproteinase MMP Reas-1 gene, promoter region
1030	19797	20008	1.53	2.5E-01 AF06716.1	EST_HUMAN	NT	Homo sapiens matrix metalloproteinase MMP Reas-1 gene, promoter region
1282	11150	21041	17.41	2.4E-01 BF576124.1	EST_HUMAN	NT	Homo sapiens matrix metalloproteinase MMP Reas-1 gene, promoter region
1282	11150	21042	17.41	2.4E-01 AF209890.1	NT	NT	Homo sapiens matrix metalloproteinase MMP Reas-1 gene, promoter region
1362	11268	21123	1.04	2.4E-01 Y17263.1	NT	NT	Homo sapiens matrix metalloproteinase MMP Reas-1 gene, promoter region
1808	11705		24.08	2.4E-01 AF267183.1	NT	NT	Homo sapiens FLI-1 gene, partial
1859	11754	21026	1.41	2.4E-01 AF267183.1	NT	NT	Homo sapiens FLI-1 gene, partial
2091	11980	21975	0.86	2.4E-01 AF267183.1	NT	NT	Monoclonal antibody to human platelet-derived growth factor receptor (PDGFR) cDNA, complete cds
2122	12010		1.16	2.4E-01 AF111083.2	NT	NT	Zinc finger domain protein 100 (ZFP100) cDNA, complete cds
2215	12101	22005	2.01	2.4E-01 AF4594.1	SWISSPROT	NT	Homo sapiens cDNA for proteinase 3, complete cds
							IMMUNOGLOBULIN A1 PROTEASE PRECURSOR (IGAP1 PROTEASE)
							Aquilex sedulicus section 12 of 108 of the complete genome

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2332	12213	22111	0.85	2.4E-01	BF002171.1	EST_HUMAN	7b2340Lx1 NCL CGAP C-16 Homo sapiens cDNA clone IMAGE:3310807.3 similar to SW:PR88_XENLA
2481	12366	22260	1.63	2.4E-01	Z36534.1	NT	O42880 28S PROTEASE REGULATORY SUBUNIT 6A;
2734	12366	22491	2.14	2.4E-01	AF1783.1	NT	D. discoidium (AUS-C) pmkA gene;
2765	12618	22810	6.69	2.4E-01	AF030184.1	NT	S. pombe swf6 gene
3093	13020		2.82	2.4E-01	U7728.1	NT	Bovine adonovirus 3 complete genome
3108	13035	22831	1.85	2.4E-01	X74206.1	NT	Oryza longistaminella receptor kinase-like protein, family member D, and retrof (gag/pol) genes, complete cds
4817	14700	24466	0.88	2.4E-01	BE6090.1	EST_HUMAN	H. sapiens AGT gene, Pcd fragment of fcton 4
4881	14855	24622	50.15	2.4E-01	D00844.1	NT	Q1V1-H10412-020400-195410 HT0412 Homo sapiens cDNA
5468	15359	25481	7.53	2.4E-01	AF097216.1	NT	Hepatitis C virus genomic RNA for polyprotein, complete cds
5468	15359	25482	7.53	2.4E-01	AF097216.1	NT	Mus musculus Wrm protein (Wrm) gene, complete cds
5468	15359	25482	7.53	2.4E-01	AF097216.1	NT	Mus musculus Wrm protein (Wrm) gene, complete cds
5593	15506	25593	2.13	2.4E-01	BF592336.1	EST_HUMAN	754404.x1 NCL CGAP B-16 Homo sapiens cDNA clone IMAGE:3338503.3 similar to SW:SFR4_HUMAN
5642	15553	25543	2.86	2.4E-01	AF035546.1	NT	O08170 SPLICING FACTOR, ARGININE/SERINE-RICH 4; contains element TARI 1 repetitive element
5705	15613	25714	2.16	2.4E-01	765180.1	NT	Drosophila melanogaster p38a MAP kinase gene, complete cds
5907	15842	25869	1.79	2.4E-01	A093699.1	EST_HUMAN	Homo sapiens HSPC112 protein (HSPC112), mRNA
6345	16203	25371	8.97	2.4E-01	L33001.1	NT	W35211.x1 NCL CGAP P-act1 Homo sapiens cDNA clone IMAGE:2323220.3 similar to gb:U03464
6560	16730	26831	1.62	2.4E-01	AJ072385.1	NT	PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR (HUMAN);
7617	17308	27811	572	2.4E-01	A083545.1	EST_HUMAN	Bos taurus guanylyl cyclase activating protein 2 (gucc2) mRNA, complete cds
7665	17615	26956	1.93	2.4E-01	C03692	SWISSPROT	Tetrahymena thermophila microcystin gene encoding ribosomal protein L3, exons 1,2
8149	18037	26265	3.63	2.4E-01	AL161494.2	NT	W40422.x1 Scarec, NTL, T_GBO, S1 Homo sapiens cDNA clone IMAGE:2330006.3 similar to contains
8209	18063	26347	1.99	2.4E-01	AF030189.1	NT	MER22B1 TARI repetitive element
8534	18406		2.42	2.4E-01	Z21647.1	NT	COLLAGEN ALPHA 1(X) CHAIN PRECURSOR
9080	18821	29108	1.65	2.4E-01	AF217491.1	NT	Arabisopsis thaliana DNA chromosome 4, contig fragment No. 6
9162	18926		2.39	2.4E-01	AF004243.1	NT	Mus musculus type 1 sigma receptor gene, complete cds
9222	18945		2.54	2.4E-01	AJ278191.1	NT	P. estivalis mosaic virus genomic RNA
9439	19609		1.89	2.4E-01	V01507.1	NT	Homo sapiens fragile 16D sodium reductase (FDR) gene, exon 6
9650	19716		1.29	2.4E-01	BF225979.1	EST_HUMAN	Arabisopsis thaliana ethylene-inactivating-1-like1 (EL1) mRNA, complete cds
9655	19855		3.35	2.4E-01	AF163281.2	NT	Mus musculus mRNA for putative mcf protein (mcf gene)
383	10330	20153	0.9	2.3E-01	S75968.1	NT	Gallus gallus gene coding for c-actin
						NT	RC3-CTD13-100800-023-506 CTD13 Homo sapiens cDNA
						NT	Homo sapiens chromosome 21 segment HS21C081
						NT	aromatase [P. opisthala guilarte-zabala finches, ovary, mRNA, 3186 nt]

Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Even SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
621	10358		4.42	2.3E-01	U09713.1	NT	Myxidia genitulum section 35 of 51 of the complete genome
631	10361	20403	18.94	2.3E-01	U09786.1	NT	Myxococcus xanthus cell section 133 of 150 of the complete genome
916	10367	20367	10.67	2.3E-01	E031163.1	EST_HUMAN	11HMO3273F1 NH_MGC_11 Homo sapiens cDNA clone IMAGE:3050818 5'
1494	10382	21258	3.35	2.3E-01	6077660	NT	Mus musculus vacuolar protein coding 4b (vacu4b) (Vp44b), mRNA
1546	11451		0.88	2.3E-01	U02837.2	NT	Yersinia pestis HmsH (HmsH), HmsH (HmsH), and HmsS (HmsS) genes, complete cds
1598	11470	21351	1.38	2.3E-01	A024460.1	NT	Brevibacterium agave gene for S400s glycoprotein, cluster 12
1614	11478	21378	2.75	2.3E-01	U10887.2	NT	Mus musculus calyx gene, exon 1, partial
1699	11692		1.3	2.3E-01	A024593.1	NT	Mus musculus calyx gene, exon 1, partial
2398	12274	22169	1.86	2.3E-01	E0297583.1	EST_HUMAN	Homo sapiens partial intron 3 of the wild type AF-4/PEL gene
2674	12483	22372	1.02	2.3E-01	E0297583.1	EST_HUMAN	Homo sapiens partial intron 3 of the wild type AF-4/PEL gene
2815	12483	22372	1.02	2.3E-01	M111316.1	NT	Human erythropoietin gene, complete cds
2914	12483	22372	0.88	2.3E-01	A001803.1	NT	Human erythropoietin gene, complete cds
2984	12691	22601	1.29	2.3E-01	A001376.1	EST_HUMAN	not605 of 101, CGAP_P161 Homo sapiens cDNA clone IMAGE:1100843 3' similar to contains Alu repetitive elements; contains element THIR (topoisomerase II)
3045	12872		5.73	2.3E-01	R21373.1	EST_HUMAN	YF7107.11 Scores placenta NB2HP Homo sapiens cDNA clone IMAGE:213328 5'
3324	13244	22051	1.09	2.3E-01	H06935.1	EST_HUMAN	YF7107.11 Scores fetal liver spleen NF1LS Homo sapiens cDNA clone IMAGE:213328 5'
3769	13979	23461	1.11	2.3E-01	S83821.1	NT	GSTA9-gliothione S-transferase Yc2 subunit 9 (region, intron 1) [rat, Morris hepatoma cell line, Genomic, 2212 nt, segment 1 of 3]
3856	13767		3.72	2.3E-01	7982133	NT	Homo sapiens KIAA0450 gene product (KIAA0450), mRNA
4253	14152	23926	0.95	2.3E-01	R62262.1	EST_HUMAN	Y17601.11 Scores placenta NB2HP Homo sapiens cDNA clone IMAGE:146017 5'
4300	14188		3.35	2.3E-01	L78788.1	NT	Mus musculus retn (Retn-10) gene, promoter region
4349	14245	24031	1.02	2.3E-01	D06903.1	EST_HUMAN	Synecchococcus sp. PC06903 complete genome, 1/27, 1-33849
4380	14282	24091	2.08	2.3E-01	AF092635.1	NT	Homo sapiens nucleolar-activated protein kinase p30beta (PRKNA13) mRNA, complete cds
4454	14348	24140	5.1	2.3E-01	A001803.1	NT	Homo sapiens nuclear transport factor 2 (placental) (NP2) mRNA
4956	14689	24456	0.82	2.3E-01	J03280.1	EST_HUMAN	Human phenylethylamine N-methyltransferase gene, complete cds
5002	14877	24941	0.95	2.3E-01	F016135.1	EST_HUMAN	601895103F1 NH_MGC_19 Homo sapiens cDNA clone IMAGE:212358 5'
5101	14989		0.98	2.3E-01	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Rickett gene, and sodium phosphates transporter (NP73) gene, complete cds
5146	15013	24783	28.95	2.3E-01	A0500240.1	NT	Escherichia coli K-12 MG1655 section 130 of 400 of the complete genome
5246	15099	24942	2.6	2.3E-01	A0004945.1	NT	Mus musculus retn (Retn-10) gene, promoter region
5332	15552	25074	1.71	2.3E-01	BF008381.1	EST_HUMAN	7430005.1 NCI_G018 Homo sapiens cDNA clone IMAGE:3478899 3' similar to SW_GAG SMSAV/PG3330 GAL POLYPROTEIN (CONT'AINS: CORE PROTEIN P16, INNER COAT' PROTEIN P12, CORE SHELL' PROTEIN P30, NUCLEOPROTEIN P10) :

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit (BLAST E-Value)	Top Hit Accession No.	Top Hit Disease Source	Top Hit Description
5395	15314	23561	4.83	2.3E-01	X95697.1	NT	C.familialis contig gene
5618	15533	25617	1.87	2.3E-01	AJ098400.1	EST_HUMAN	cytochrome C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN)
5618	15533	25618	1.87	2.3E-01	AJ098400.1	EST_HUMAN	cytochrome C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN)
6111	16035	26142	3.33	2.3E-01	AJ101848.1	EST_HUMAN	cytochrome C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN)
6334	16246	26408	2.02	2.3E-01	AF173388.1	NT	cytochrome C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN)
6487	16349	26519	3.16	2.3E-01	U79479.1	EST_HUMAN	cytochrome C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN)
6491	16349	26519	1.39	2.3E-01	BE688071.1	EST_HUMAN	cytochrome C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN)
6590	16478		2.19	2.3E-01	N069883.1	EST_HUMAN	cytochrome C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN)
6664	16544	26741	2.26	2.3E-01	M06983.1	NT	cytochrome C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN)
7657	17502	27732	1.37	2.3E-01	X82124.1	NT	cytochrome C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN)
7712	17502	27737	2.14	2.3E-01	BE170060.1	EST_HUMAN	cytochrome C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN)
7740	17509	27611	2.26	2.3E-01	AJ333261.1	NT	cytochrome C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN)
7741	17524		4.95	2.3E-01	BF133577.1	EST_HUMAN	cytochrome C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN)
8329	18263	28663	2.54	2.3E-01	AJ201489.1	NT	cytochrome C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN)
8329	18397	28663	2.54	2.3E-01	AJ201489.1	NT	cytochrome C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN)
8658	18547	28830	2.39	2.3E-01	AJ502167.2	NT	cytochrome C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN)
9144	18586		2.33	2.3E-01	AJ50426.1	NT	cytochrome C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN)
9232	18917		20.46	2.3E-01	TJ72331.1	EST_HUMAN	cytochrome C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN)
9258	19477		1.65	2.3E-01	AJ089819.1	EST_HUMAN	cytochrome C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN)
9266	18670		2.07	2.3E-01	AJ0853940.1	EST_HUMAN	cytochrome C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN)
9324	19665	24990	2.05	2.3E-01	AJ030023.1	EST_HUMAN	cytochrome C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN)
9350	19700	24905	4.88	2.3E-01	BE883464.1	EST_HUMAN	cytochrome C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN)
9407	19308		1.93	2.3E-01	BF60318.1	EST_HUMAN	cytochrome C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN)
9456	19085		2.09	2.3E-01	AJ000519.1	NT	cytochrome C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN)
9459	19085		4.54	2.3E-01	AJ000519.1	NT	cytochrome C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN)
9793	19510		2.67	2.3E-01	BF175611.1	EST_HUMAN	cytochrome C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
84	10068	18985	0.96	2.2E-01/A052190.1	EST_HUMAN		cc14c10.x1 Sources: fetal liver, spleen, TNLS S1 Homo sapiens cDNA clone IMAGE:1675290 3' similar to TRC13040 Q13040 ATP-BINDING CASSETTE PROTEIN;
1545	11450	21311	3.13	2.2E-01/AF187800.1	NT		Homo sapiens PPAR delta gene, promoter region
1972	11993		0.91	2.2E-01/AF171901.1	NT		Timecourse malabaricus cyto gene, partial cds; mitochondr al gene for mitochondrial product
2042	11939	21029	2.76	2.2E-01/M3/640.1	NT		Fresh-water sponge Emri1 alpha collagen (COL1F) gene
2364	12234	22131	6.24	2.2E-01/BF077838.1	EST_HUMAN		602055038F1 NIH_MGC_33 Homo sapiens cDNA clone IMAGE:4246899 5'
2543	12417	22207	2.41	2.2E-01/BE181265.1	EST_HUMAN		601462329F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3886190 5'
2543	12417	22208	2.41	2.2E-01/BE181265.1	EST_HUMAN		601462329F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3886190 5'
2653	12761	22570	4.04	2.2E-01/BE156263.1	EST_HUMAN		FM2-HT10353-281/299-003-412 HT10353 Homo sapiens cDNA
2663	12761	22571	4.04	2.2E-01/BE156263.1	EST_HUMAN		FM2-HT10353-281/299-003-412 HT10353 Homo sapiens cDNA
2690	12817		1.60	2.2E-01/AF020503.1	NT		Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
3348	13266		2.67	2.2E-01/AL161962.2	NT		Ana10p61a thalassaemia DNA chromosome 4, contig fragment No. 82
3743	13956		1.05	2.2E-01/AF165728.1	NT		Xiphophorus maculatus truncated Rict retrotransposon reverse transcriptase (RT) pseudogene
4007	13913	23688	0.81	2.2E-01/AF133901.1	NT		Mus musculus ATP-binding cassette protein (Abcb8) mRNA, partial cds
4118	14018		1.19	2.2E-01/AF119102.1	NT		Drosophila melanogaster UNC-119 (unc-119) gene, complete cds
4125	14025	23900	5.07	2.2E-01/AF165142.1	NT		Mus musculus mixed lineage kinase 3 (MLK3) and two pore domain K ⁺ channel subunit (Kcnk16) genes, complete cds
4166	14056	23840	1.97	2.2E-01/AF117340.1	NT		Mus musculus MAP kinase kinase kinase 1 (Meek1) mRNA, complete cds
4166	14056	23841	1.97	2.2E-01/AF117340.1	NT		Mus musculus MAP kinase kinase kinase 1 (Meek1) mRNA, complete cds
4268	14157	23933	1.16	2.2E-01/U01307.1	NT		Human scRNA (BC200 beta) pseudogene
4268	14157	23934	1.16	2.2E-01/U01307.1	NT		Human scRNA (BC200 beta) pseudogene
4396	14294	24078	1.06	2.2E-01/254148.1	NT		B. acutis 1926 gene
4719	14905		1.22	2.2E-01/D50904.1	NT		Human beta-cyanoaseic acid (ACTBP9) pseudogene
4724	14910	24396	2.47	2.2E-01/A4211218.1	EST_HUMAN		24875005.1 Stradiene INT neuron (6837233) homo sapiens cDNA clone IMAGE:548968 5'
4891	14771	24549	1.19	2.2E-01/M08924.1	NT		Human cytochrome gene
4975	14950		1.21	2.2E-01/L13290.1	NT		Mus musculus virlulin gene, exon 3
5513	15436	25486	3.99	2.2E-01/D54002.1	NT		Mus musculus virlulin gene, exon 3
5518	15436	25486	3.99	2.2E-01/D54002.1	NT		Mus musculus virlulin gene, exon 3
6180	16074	26223	10.59	2.2E-01/AF176238.1	EST_HUMAN		Human diaphanous (Drosophila, homolog) 2 (DIP42-H2), transcript variant 156, mRNA
6319	16182	26342	2.01	2.2E-01/M24138.1	NT		Synchrocytic sp. POC5803 complete genome, 19/27, 238272-238399
6319	16182	26343	2.01	2.2E-01/M24138.1	NT		Synchrocytic sp. POC5803 complete genome, 19/27, 238272-238399
6976	16566		2.19	2.2E-01/AF165143.1	NT		Human glycoprotein B gene, exon 4
7157	17034	27227	4.27	2.2E-01/AE007113.1	NT		Mus musculus mnc2-M1 gene, promoter region
							Thermodoga maritima section 25 of 136 of the complete genome

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Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7217	17064		2.26	2.2E-01	AW50309.1	EST_HUMAN	PM3-CT02083-3247-209-009-007 CT02083 Homo sapiens cDNA
7270	17147	27341	1.66	2.2E-01	8393247	EST_HUMAN	Mus muscularis dermal epidermal autoregulatory factor 1 (Drosophila) (Deaf1), mRNA
7904	17180	27382	1.36	2.2E-01	BF76354.1	EST_HUMAN	MR1-TN0046-11080-006-002 TN0046 Homo sapiens cDNA
7363	17221	27421	1.41	2.2E-01	U02088.1	EST_HUMAN	MA0408-1.1 Sorens melanocyte ZNF4M Homo sapiens cDNA clone IMAGE:201591.5
7366	17344	27850	13.13	2.2E-01	U46834	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-BASSOCIATED TRANSCRIPT 2)
7397	17315	27622	3.98	2.2E-01	U89643.1	NT	Bradykinin receptor 1, human beta and gamma chains (Epo) gene, complete cds
7648	17408	27720	3.57	2.2E-01	AF107941.1	NT	Fusaria hyomastri chloroplast-localized small heat shock protein (GFP-Sp21) mRNA, complete cds; nuclear gene for chloroplast product
7718	17569	27764	2.2	2.2E-01	BF206907.1	EST_HUMAN	6011850724F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4100189.5
8723	18540	28624	4.94	2.2E-01	X01618.1	NT	Drosophila 680 glue gene cluster
8766	17905	28149	2.91	2.2E-01	7706215	NT	Homo sapiens H-2K binding factor-2 (LOC351890), mRNA
9077	18854		2.2	2.2E-01	BE070950.1	EST_HUMAN	601146957F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3856070.5
9183	19720		3.72	2.2E-01	U83671.2	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A3b (MAGEA3B), melanoma antigen family A3 (MAGEA3), salivadin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and L2
9290	18973		2.34	2.2E-01	AF188943.1	NT	Vicia villosa cultivar Pinot Noir plasma membrane aquaporin (PIPF1a) mRNA, complete cds
9570	15053	24887	2.66	2.2E-01	AW361008.1	EST_HUMAN	RCH-CT02498-141199-021-024 CT02498 Homo sapiens cDNA
9676	19713		3.76	2.2E-01	AV69490.1	EST_HUMAN	AV694901 GKG Homo sapiens cDNA clone GKG4H1802.5
985	10879	20727	1.74	2.1E-01	U4566286.1	EST_HUMAN	nc31e1.1 at NC1 CGAP L2d Homo sapiens cDNA clone IMAGE:1061804
986	10881	20729	0.9	2.1E-01	U416180.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 16
1108	11023		2.68	2.1E-01	U5022914.2	NT	Glycylalanyl nucleoside, section 45 of 85 of the complete genome
1180	11001	20936	1.24	2.1E-01	0754298	NT	Mus musculus interferon (alpha and beta) receptor 2 (Ifnar2), mRNA
1180	11091	20937	1.24	2.1E-01	0754298	NT	Mus musculus interferon (alpha and beta) receptor 2 (Ifnar2), mRNA
1871	11767	21642	1.84	2.1E-01	AA060824.1	EST_HUMAN	672602.61 NC1 CGAP C4d Homo sapiens cDNA clone IMAGE:1916610.5 similar to gb:K02766
2111	12000	21990	3.08	2.1E-01	BF06075.1	EST_HUMAN	602051724F1 NIH_MGC_51 Homo sapiens cDNA clone IMAGE:4247893.5
2894	12821	22613	1.66	2.1E-01	0914445	NT	Homo sapiens potassium voltage-gated channel, subfamily H (seg-related), member 4 (KCNH4), mRNA
3736	13648		5.05	2.1E-01	9838361	NT	Beta vulgaris mitochondrion, complete genome
3867	13874	23651	1.01	2.1E-01	P11676	SWISSPROT	IMMEDIATE-EARLY PROTEIN IE180
3867	13874	23652	1.01	2.1E-01	P11676	SWISSPROT	IMMEDIATE-EARLY PROTEIN IE180
4279	14178		1.28	2.1E-01	AB033041.1	NT	Homo sapiens mRNA for KIAA1215 protein, partial cds
4474	14368	24157	1.21	2.1E-01	AB010273.1	NT	Homo sapiens pitp47 gene, complete cds
4766	14651	24439	1.28	2.1E-01	AA009784.1	NT	Homo sapiens hox11 proto-oncogene, exons 1 to 3 and hox-1 gene

Table 4

Table 4

Probe SEQ ID NO.	Exon SEQ ID NO.	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
5134	15091	24772	0.99	21E-01 M82491.1	NT	Sox10 myocyte cell-line fusion 138 (TF3C) gene, complete cds
5243	15167	24036	5.89	21E-01 BE972696.1	EST_HUMAN	82915203 (FT1) MGC_81 Homo sapiens cDNA clone IMAGE:4293001 5'
6123	16370	28106	1.88	21E-01 AF00442.1	NT	Human diacylglycerol receptor (OR172) gene, partial cds
6380	16247	28781	1.97	21E-01 AC009472.1	NT	Archaeoglobus fulgidus section 135 of 172 of the complete genome
6535	16393	28572	1.74	21E-01 AF000946.1	NT	Caris familiaris keratin (KRT19) gene, complete cds
6569	16417	26596	1.35	21E-01 AF068687.1	NT	Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds
6589	16477	26597	1.35	21E-01 AF068687.1	NT	Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds
6705	16595		1.21	21E-01 7930350	NT	Mus musculus erythrocyte protein Band 4.1-like 3 (EPB413), mRNA
6981	16629	27292	4.78	21E-01 U68599.1	NT	Haemophilus influenzae hmdC, putative haemocin processing protein (hmdC), putative ABC transporter (hmdB), putative haemodrin structural protein (hmdA), and haemochin immunity protein (hmdI) genes, complete cds
7224	17101	27389	5.88	21E-01 X973786.1	NT	S. cerevisiae chromosome II reading frame ORF YEL025hw
7479	17349	27563	2.38	21E-01 X97378.1	NT	A. thaliana mRNA for AtRAN1P1b protein
7547	17598	27611	1.19	21E-01 AC004659.1	NT	Human sapiens p53R2 gene for ribonucleotide reductase, exon 8
7917	17787	28006	2.49	21E-01 Z57097.1	NT	Dactylis glomerata mRNA for elongation factor 1-beta
7929	17791	28018	1.49	21E-01 P63824	SWISSPROT	Diacylglycerol kinase, delta (diGLYCERIDE KINASE) (DGK-DELTA) (DAG KINASE DELTA) (80 KD DIA-CYL-GLYCEROL KINASE)
8849	18891		2.31	21E-01 11038947	NT	Human sapiens pancreatic polypeptide 2 (PP2Y), mRNA
8892	18947	28964	1.16	21E-01 BE180422.1	EST_HUMAN	RC3-H10622-040500-013-5111 H10622 Homo sapiens cDNA
9522	19132		2.16	21E-01 AF217490.1	NT	Human sapiens fragile 18D oxidoreductase (FOR) gene, exons 8, 9, and partial cds
9730	19634		1.4	21E-01 L32588.1	NT	Human gadinin 1
9805	19382	25174	1.29	21E-01 BE572330.1	EST_HUMAN	Taf6b-02.1 NCI_GADP_G08 Homo sapiens cDNA clone IMAGE:3223034 3'
8979	19436		1.29	21E-01 6635904	NT	Salivellus alpinus mitochondrion, complete genome
103	10165	19983	1.72	21E-01 A3017437.1	NT	Gallus gallus mRNA for avensin, complete cds
623	10465		2.39	21E-01 7709801	NT	Human sapiens CGI-18 protein (LOC51008), mRNA
684	10917	20440	1.19	21E-01 M77085.1	NT	O. carniculus germline light heavy chain V-H pseudogene, allele type VHA2
793	10722	20563	1.81	21E-01 AF027895.1	NT	Mus musculus Major Histocompatibility Locus class II region
9095	107169	20769	1.03	21E-01 D00065.1	NT	Synedrobryalis sp. POC59903 complete genome, 7127, 781146-202915
1109	11024	20866	2.97	21E-01 AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
1234	11141	20953	1.42	21E-01 A4132695.5	NT	Homo sapiens tae1 gene
1288	11136	21047	1.29	21E-01 AV384037.1	EST_HUMAN	PMH-H10422-2917200-002-05 H10422 Homo sapiens cDNA
1471	11876	21241	13.51	21E-01 4593468	NT	Homo sapiens dydrobryon, alpha (DTNA), mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
1554	11438	21295	2.51	2.0E-01	AB007974.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIA0093
1558	11440	21300	1.59	2.0E-01	AF200700.1	NT	Homo sapiens scd4c600c1c symplectic mRNA, partial cds
1563	11450		1.82	2.0E-01	AF111170.3	NT	Homo sapiens 14q32.3 Jagged2 gene, complete cds and unknown gene
1725	11725		1.84	2.0E-01	U74758.1	NT	Melanoblastoma jaggedsh1 section 87 of 150 of the complete genome
184	11743	21618	1.33	2.0E-01	BE5371330.1	EST_HUMAN	60114844(F) NH_KJC, 65 Homo sapiens cDNA, clone IMAGE:355330.8
1847	11741	21619	1.33	2.0E-01	BE5371330.1	EST_HUMAN	60114844(F) NH_KJC, 65 Homo sapiens cDNA, clone IMAGE:355330.8
2289	12181		1.07	2.0E-01	X62977.1	NT	H. sapiens Nucleo-1 gene
2661	12180		0.95	2.0E-01	AF071490.1	NT	Homo sapiens 10p11.23 long heart cDNA YH5641.1
3442	13359	23166	0.8	2.0E-01	P46687	SWISSPROT	MEIOGALIN-PROTEIN GLOBULIN (HOMIOGLOBULIN) ZIPPER PROTEIN A1HB-10 (ND-ZIP PROTEIN A1HB-10)
3520	13436		0.89	2.0E-01	AW236005.1	EST_HUMAN	sp13002X1 NCI_QOMP_NH8 Homo sapiens cDNA, clone IMAGE:2740395.3 similar to contains element
3546	13560	23346	0.81	2.0E-01	P34641	SWISSPROT	Cys411 PROTEIN
3545	13553	23528	0.8	2.0E-01	P53597.1	NT	Cys411 PROTEIN
4454	14356		8.47	2.0E-01	BE528195.1	EST_HUMAN	Homo sapiens gamma-glutamyl hydrolase gene, exons 8 and 9 and complete cds
4859	14739		1.07	2.0E-01	AF147083.1	NT	Homo sapiens hypothetical protein ASH1 (ASH1), mRNA
4972	14873	24816	8.01	2.0E-01	P4622080	NT	Homo sapiens putative p46HSD pseudogene for hair keratin, exons 1 to 9
5041	14971	24887	1.1	2.0E-01	U19216.1	NT	Rat SOD-2 gene for manganese-containing superoxide dismutase
5342	15263	25069	2.85	2.0E-01	X99600.1	NT	Homo sapiens putative p46HSD pseudogene for hair keratin, exons 1 to 9
5510	15428	25461	2.13	2.0E-01	U115300.1	NT	Rat SOD-2 gene for manganese-containing superoxide dismutase
5994	16053	25705	5.29	2.0E-01	X110303.1	NT	Homo sapiens putative p46HSD pseudogene for hair keratin, exons 1 to 9
6917	15790	25900	4.31	2.0E-01	X110303.1	NT	Scotcharomys cerevisiae Hsf5p (HAL5) mRNA, complete cds
5954	16539	25962	3.54	2.0E-01	AF060665.1	EST_HUMAN	M. auratus mu class glutathione transferase gene
6657	16517		6.95	2.0E-01	AF029026.1	EST_HUMAN	PMH-CT0247-1 01095-007-g05 CT0247 Homo sapiens cDNA
6712	16657	26858	4.18	2.0E-01	X61151.1	NT	Anti-CD247-1 01095-007-g05 CT0247 G1 and G2 precursor, gene, partial cds
7511	17299		4.39	2.0E-01	X61151.1	NT	M. musculus sp2 gene exon 14
7692	17564		2.07	2.0E-01	AF149992.1	NT	Chlamydia trachomatis section 5 of 87 of the complete genome
7774	17602	27957	1.95	2.0E-01	AF149992.1	NT	Homo sapiens filamin 2 (FLN2) mRNA, complete cds
7774	17602	27956	1.95	2.0E-01	AF059097.1	NT	Autophagy inhibitor root granitropin coritid protein (P1N2) gene, complete cds
8214	18098	28354	2.7	2.0E-01	AF049007.1	NT	Autophagy inhibitor root granitropin coritid protein (P1N2) gene, complete cds
8214	18098	28351	2.7	2.0E-01	D96038.1	NT	Salvelinus plusium mRNA for transferrin, complete cds
8214	18098		2.7	2.0E-01	D96038.1	NT	Salvelinus plusium mRNA for transferrin, complete cds
9503	19118		1.37	2.0E-01	AF026657.2	NT	Phenylphos promotes liver glucose-6-phosphate-1-dehydrogenase mRNA, partial cds
9747	19208	25202	3.22	2.0E-01	AF023492.1	EST_HUMAN	omega101.5 Soares, testis, NHT Homo sapiens cDNA, clone IMAGE:1743610.3
9747	19208		3.22	2.0E-01	AF023492.1	EST_HUMAN	Homo sapiens Kufs-binding protein (KUBS) mRNA, partial cds
9749	19349		6.61	2.0E-01	AF078164.2	NT	Homo sapiens Kufs-binding protein (KUBS) mRNA, partial cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Max Similar Protein BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
9997	19374	25193	1.6	1.0E-01	11529465	NT	Mus musculus fructosamine 3 kinase (Fn3K), mRNA
105	10096		10.36	1.0E-01	7549743	NT	Rattus norvegicus Aryl hydrocarbon receptor nuclear translocator 1 (Ahrnt), mRNA
349	10308	20126	6	1.0E-01	AF004953.1	NT	Mus musculus pale ear (per) gene, wild type allele, 3' region, partial cds
640	10577	20392	1.31	1.0E-01	U32561.2	NT	Mus musculus lamella reticula protein kinase C-interacting protein mRNA, complete cds
640	10577	20393	1.31	1.0E-01	U32561.2	NT	Mus musculus lamella reticula protein kinase C-interacting protein mRNA, complete cds
647	10594	20400	5.37	1.0E-01	BC070801.1	EST_HUMAN	RC3-BT0502-261199-011-401 BT0502 Homo sapiens cDNA
648	10594	20400	7.32	1.0E-01	BC070801.1	EST_HUMAN	RC3-BT0502-261199-011-401 BT0502 Homo sapiens cDNA
970	10893		1.61	1.0E-01	7305160	NT	Mus musculus interleukin 2 receptor, gamma chain (IL2g), mRNA
1096	11004	20846	9.3	1.0E-01	AA359813.1	EST_HUMAN	EST187784 Fetal lung II Homo sapiens cDNA, 5' end
1348	11254	21110	2.3	1.0E-01	AF081262.1	NT	Sorghum bicolor 22 kDa kafirin cluster
1416	11322	22109	3.91	1.0E-01	AF14623.1	NT	Plasmodium vivax reticulocyte binding protein-2 (pbp-2) gene, complete cds
2330	12211	22109	3.31	1.0E-01	AF14623.1	NT	Homo sapiens hypothetical protein FLJ10593 (FLJ10395), mRNA
2862	12819	22611	3.91	1.0E-01	8622633	NT	Stenodermis hirsuta 253 gene, partial cds
2906	12834		5.56	1.0E-01	U69068.1	NT	Gallus gallus ovalbumin (V) gene, complete cds
3349	13299	23072	3.4	1.0E-01	D19197.1	NT	Mouse gene for immunoglobulin diversity region D1
3434	13351	23166	4.83	1.0E-01	R13497.1	EST_HUMAN	X12710.11 Sarcosine fetal liver spleen 1 INFLS Homo sapiens cDNA clone IMAGE:126447.5
3726	13947	24332	0.63	1.0E-01	AF294017.1	NT	Rattus norvegicus arylsulfatase disaccharidase gene, complete cds
3752	13975	24457	0.66	1.0E-01	U627938	SWISSPROT	PLA2-RLU PROTEIN, QID:PA6ED
3910	13820	23900	3.02	1.0E-01	AF006754.1	NT	Schistosoma japonicum protease DNA for glycoprotein dypsin heavy chain, complete cds
3962	13869	23976	1.88	1.0E-01	AF1754106.1	NT	Schistosoma japonicum protease DNA for glycoprotein dypsin heavy chain, complete cds
4138	14038	23813	1.06	1.0E-01	BC036445.1	EST_HUMAN	Q182C10316-271199-045-1 OT0316 Homo sapiens cDNA
4368	14256	25049	0.68	1.0E-01	AF101465.2	NT	MRI-FN001-0-287000-007-401 FN0010 Homo sapiens cDNA
4662	14548	24338	0.84	1.0E-01	U62780.1	NT	Arabidopsis thaliana DNA dehydrogenase 4, coding fragment No. 5
4672	14791	21066	0.86	1.0E-01	AF194620.1	EST_HUMAN	Pgxr rathepes genes encoding carboxyl phosphate synthetase II, myosin light chain, MAP2
4945	14821		1.04	1.0E-01	AF223942.1	NT	IL3-C10215-160200-367-D02 C10215 Homo sapiens cDNA
4952	14837	24605	1.11	1.0E-01	U656239	SWISSPROT	Rattus norvegicus chemokine receptor CXCR3 mRNA, complete cds
5031	14903	24675	1.03	1.0E-01	AF231176.1	NT	KINESIN-LIKE PROTEIN KIF4
5113	14681	24756	0.96	1.0E-01	U70298.1	NT	Phoca vitulina partial ac26 gene for alpha adrenergic receptor 2B
						NT	S. musonin chloride HPI gene
5123	14691		1.16	1.0E-01	AF081196.1	EST_HUMAN	ts83912.x1 NC1 CGAP_G08 Homo sapiens cDNA clone IMAGE:223886.3 similar to gb:M21574 ALPHA
5153	15020	24789	0.66	1.0E-01	8670005	NT	PLATELET DERIVED GROWTH FACTOR RECEPTOR PRECURSOR (HUMAN);
						NT	Mus musculus Nod1 gene homolog 3, (Drosophila) (Nod1), mRNA
5441	15391		4.26	1.0E-01	AF130146.1	EST_HUMAN	X23407.x1 NC1 CGAP_UH Homo sapiens cDNA, clone IMAGE:267944.3 similar to gb:M73779 RETINOIC
5466	15396	25446	7.67	1.0E-01	U71837.1	NT	ACID RECEPTOR ALPHA-1 (HUMAN);
						NT	Homo sapiens DNA polymerase epsilon catalytic subunit protein (POLE1) gene, exon 1a

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Probe SEQ ID NO:	Exon NO:	ORF SEQ ID NO:	Expression Signal	Mean Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
5888	15503		2.28	1.0E-01	AF133116.1	EST_HUMAN	AF133116.1 Homo sapiens cDNA clone NT2RP4001328 6'
6162	18119	24963	1.7	1.0E-01	AF43212.1	EST_HUMAN	Y00612.1 Soares infant brain 1NB Homo sapiens cDNA clone IMAGE:31663 3' similar to contains MER13 repetitive element
6425	16254	25446	1.43	1.0E-01	U60922.1	NT	Arabidopsis thaliana serine/threonine protein phosphatase type one (TOPPB) gene, complete cds
9449	18310	25476	3.06	1.0E-01	AF077274.1	NT	Zea mays starch branching enzyme 1 (dsb1) gene, complete cds
6958	16538	26735	1.62	1.0E-01	AF181657.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 57
7041	16918	27109	12.89	1.0E-01	AB033024.1	NT	Homo sapiens mRNA for MAA1169 protein, partial cds
5035	17930	28176	2.16	1.0E-01	AF181603.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 15
6039	17930	28177	2.16	1.0E-01	AF181603.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 15
6137	18025	28271	1.75	1.0E-01	AF233931.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
5961	18768	28050	2.61	1.0E-01	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
8548	18146		1.67	1.0E-01	AF055903.1	NT	Drosophila melanogaster daf1191 light onlin mRNA, complete cds
8890	18548		1.28	1.0E-01	AF001168.1	NT	Arabidopsis thaliana receptor-like kinase LECRK1 (LECRK1) gene, complete cds
26	10016	18811	2.26	1.0E-01	U73200.1	NT	Mus musculus p11950 mRNA, complete cds
260	13863	20041	1.22	1.0E-01	AB022080.1	NT	Mus musculus Cdbp gene for chaperone containing TOP-1 gamma subunit, partial cds
966	10322	20145	2.41	1.0E-01	4502532	NT	Homo sapiens calcium channel, voltage-dependent, beta 2 subunit (CACNB2) mRNA, and translated products
729	10551	20493	2.15	1.0E-01	AB021480.2	NT	Oryza latipes gene for membrane guanylyl cyclase OGC-1, complete cds
698	10886	20735	0.85	1.0E-01	AF192121.1	EST_HUMAN	cd7102.31 NC1 CGAP Luc24 Homo sapiens cDNA clone IMAGE:2337051 3'
1078	10990	20832	1.21	1.0E-01	AF000580.1	NT	Oxyechidnum diabolicum plasmid Dap3, complete genome
1267	11174	21024	0.28	1.0E-01	AF117183.1	NT	Yersinia pestis plasmid pCD1
1487	11352	21252	1.28	1.0E-01	6753547	NT	Mus musculus glycylate nucleotide binding protein 1 (Gbp1), mRNA
1487	11352	21252	1.28	1.0E-01	6753547	NT	Mus musculus glycylate nucleotide binding protein 1 (Gbp1), mRNA
1903	11700		0.92	1.0E-01	4509098	NT	Homo sapiens lamin transforming growth factor binding protein 4 (LTBP4) mRNA
1925	11720		1.93	1.0E-01	AF73706.1	EST_HUMAN	gq220103 NC1 CGAP X483 Homo sapiens cDNA clone IMAGE:1761811 3' similar to TR-O76898 O76898 GAMMA BUTYROBETAINE HYDROXYLASE
1073	11769	21644	1.6	1.0E-01	AB051897.1	NT	Mus musculus Scyb6l, Scyb6l, Scyb6l-ps, Scyb6l genes for small inducible cyclin A6 precursor, small inducible cyclin A6 precursor, Scyb6l pseudogene, small inducible cyclin A6 precursor, complete cds
2660	12527		2.99	1.0E-01	AF095726.1	EST_HUMAN	Q13-D710018-081259-036-gd4 D710018 Homo sapiens cDNA
2898	12798		1.67	1.0E-01	AF184569.1	NT	Juniperus aculeata LEAF1 protein (LEAF1) gene, partial cds
2873	12900	22695	1.00	1.0E-01	AF162300.1	EST_HUMAN	Y14103.31 Soares, NFL_1, GBC, ST Homo sapiens cDNA clone IMAGE:2689785 3'
3095	13012	22803	1.28	1.0E-01	AF095178.1	EST_HUMAN	Q10-BN0041-070300-147-gd4 BN0041 Homo sapiens cDNA

Table 4

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3570	13464	23275	1.07	1.3E-01	H033369.1	EST_HUMAN	Y45601 at 1 Soares placenta INo2P Homo sapiens cDNA clone IMAGE:161704.3 similar to contains AU repetitive element.
3570	13464	23276	1.07	1.3E-01	H033369.1	EST_HUMAN	Y45601 at 1 Soares placenta INo2P Homo sapiens cDNA clone IMAGE:161704.3 similar to contains AU repetitive element.
4154	14054	23328	0.8	1.3E-01	AJ271735.1	EST_HUMAN	Homo sapiens Xq pseudautosomal region; segment 12
4298	14371	23351	1.13	1.3E-01	DJ7594.1	NT	Bovine N233 mRNA for MHC class I (B2A-JDOB), complete cds
4465	14350	24141	5.12	1.3E-01	AL161566.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 58
4683	14849	24339	2.36	1.3E-01	AB011887.1	NT	Mus musculus Soy6i, Soy6i, Soy6i-4-pa, Soy6i-5 genes for small inducible cytosolic A9 precursor, small inducible cytosolic A9 precursor, Soy6i-6 pseudogene, small inducible cytosolic A5 precursor, complete cds
4700	14598	24377	0.93	1.3E-01	X021776.1	EST_HUMAN	S. tuberosum mRNA for alcohol dehydrogenase
4977	14482	24618	1.77	1.3E-01	AJ1814270.1	EST_HUMAN	MF3-370320-161395-112-p05 S10203 Homo sapiens cDNA
5027	14600	24670	4.17	1.3E-01	AF181288.1	EST_HUMAN	Mus musculus auratus Na-taurichordate cotranscripting polypeptide mRNA, partial cds
5093	14825	24867	1.38	1.3E-01	AJ438981.1	EST_HUMAN	3576dA1 NCI G6211 Lym12 Homo sapiens cDNA clone IMAGE:2154680.3
5117	14846	25035	1.03	1.3E-01	AJ400942.1	NT	Homo Sapiens h1h1 gene, 5' UTR
5549	15485	25535	1.41	1.3E-01	AF161694.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 50
5922	16287	25562	1.29	1.3E-01	Q00194	SWISSPROT	FORK-EAD BOX PROTEIN E3
5948	16093	26043	2.5	1.3E-01	N04853.1	EST_HUMAN	Y5292A12 Soares, multiple, acetosis, 2'NHMS3P Homo sapiens cDNA clone IMAGE:276163.5
6179	16065	26214	1.38	1.3E-01	AB010591.1	NT	Citullus lanatus mRNA for wusa, complete cds
6179	16065	26215	1.38	1.3E-01	AB010591.1	NT	Citullus lanatus mRNA for wusa, complete cds
7392	17251	27450	1.72	1.3E-01	MT3248.1	NT	Human cellular DNA/Human papillomavirus proviral DNA
7396	17314	27521	1.22	1.3E-01	9602323	NT	Bacteriophage Iva, complete genome
7953	17793	28022	1.19	1.3E-01	X63440.1	NT	Mus musculus mRNA for P19-protein tyrosine phosphatase
8033	17925	28125	3.19	1.3E-01	X707336.1	NT	A. thaliana mRNA for ribonucleotide reductase R2
8085	17656	28205	6.85	1.3E-01	U93806.1	NT	Bacteriophage T1 integrase, repressor protein (trp), dUTPase, holin and lyso genes, complete cds
8118	16065	28214	2.9	1.3E-01	AB010591.1	NT	Citullus lanatus mRNA for wusa, complete cds
8118	16065	28215	2.9	1.3E-01	AB010591.1	NT	Citullus lanatus mRNA for wusa, complete cds
8119	18007	28254	3.88	1.3E-01	AF19107.1	NT	Dicyostelium discoideum unknown (DG1041) genes, complete cds
8391	18259	29507	2.84	1.3E-01	M65257.1	NT	Human carcinoembryonic antigen (CEA) genes, exon 4
8756	17907	29152	3.98	1.3E-01	X70733.1	NT	B. laurus mRNA for potassium channel
9076	18781	29773	2.33	1.3E-01	8394421	NT	Rattus norvegicus Thrombospondin receptor (Tbox27), mRNA
9169	18202	29344	1.95	1.3E-01	BF348623.1	EST_HUMAN	9020199287 NCI, OCAP, Bmr67 Homo sapiens cDNA clone IMAGE:415518.5
9625	19000	30662	2.05	1.3E-01	Q06692	SWISSPROT	DNA TERMINAL PHOSPHATE (PTP) PROTEIN

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BlastE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9738	19272		7.94	1.8E-01	R2464.1	EST_HUMAN	yf48n10r1 Scores placenta N2b2p Homo sapiens cDNA clone IMAGE:13027 5'
9779	19284		1.63	1.8E-01	Y11114.1	NT	E. dispar mRNA for hecliculase (hec1)
593	10593	20069	1.9	1.7E-01	BE395164.1	EST_HUMAN	601274504F1 NIT1_MGC_20 Homo sapiens cDNA clone IMAGE:3615788 5'
786	10717	20556	2.04	1.7E-01	X53330.1	NT	P. dumerilii histone gene cluster for core histones H2A, H2B, H3 and H4
846	10670		1.69	1.7E-01	P35616	SWISSPROT	NEUROFLAMMENT TRIPLET L PROTEIN (NEUROFLAMMENT LIGHT POLYPEPTIDE) (NFL-L)
1042	10660	20002	1.6	1.7E-01	AF081910.1	NT	Lymantria dispar nucleopod/mesoderm, complete genome
1042	10660	20003	1.6	1.7E-01	AF081910.1	NT	Lymantria dispar nucleopod/mesoderm, complete genome
1838	11833		3.6	1.7E-01	AF255051.1	NT	Homo sapiens BNIP3H (BNIP3H) gene, complete cds; nuclear gene for mitochondrial product
2626	12756	22546	1.63	1.7E-01	AF000716.1	NT	Vibrio cholerae hypoxanthine phosphotransferase (hpt) gene, partial cds; hemagglutinin/protease regulatory protein (htrp) gene, complete cds, and YRAL_VIBCO gene, partial cds
2626	12756	22546	1.63	1.7E-01	AF000716.1	NT	Vibrio cholerae hypoxanthine phosphotransferase (hpt) gene, partial cds; hemagglutinin/protease regulatory protein (htrp) gene, complete cds, and YRAL_VIBCO gene, partial cds
2698	12823	23016	1.74	1.7E-01	A333699.1	EST_HUMAN	EST14651 Endometrial tumor Homo sapiens cDNA 5' and
2697	12884	22983	1.35	1.7E-01	AJ238761.1	NT	Naja naja atra oca1 gene, exon 1-3
2697	12884	22984	1.35	1.7E-01	AJ238761.1	NT	Naja naja atra oca1 gene, exon 1-3
3067	12964	22765	1.66	1.7E-01	AF081914.1	NT	T. axoni carboxamide gamma/gamma2 dihydroxyphosphate synthase mRNA, complete cds
3401	13316	23119	1.80	1.7E-01	AJ238065.1	NT	Anabaena sp. ORF4 (partial), ORF3, ORF2, ORF1, adpA gene, adpA gene, adpC gene, adpD gene, adpE gene and adpF gene
3557	13471	23382	1	1.7E-01	AJ224977.1	NT	Homo sapiens hsp70 gene, complete CDS
3659	13770	23562	4.41	1.7E-01	AJ293577.1	NT	Homo sapiens derivative 11 breakpoint fragment; partial hitron 10 of the ALL-1/MLL/HRX gene fused to hitron 9 of the AF-4/TEL gene
4450	14553		1.88	1.7E-01	X52556.1	NT	Schistosoma gregatti alpha repetitive DNA
4732	14617	24403	1.4	1.7E-01	AJ247695.1	EST_HUMAN	qf07946r1 Scores, fetal liver, pituitary, INFL5, S1 Homo sapiens cDNA clone IMAGE:1646608 3' similar to contains ORF1 ORF2 repetitive element;
4966	14851		1.16	1.7E-01	U28376.1	NT	Zea mays calcium-dependent protein kinase (ZCDPK2) mRNA, complete cds
5067	14637		1.18	1.7E-01	AF072725.1	NT	Zea mays starch branching enzyme 1b (ae) gene, complete cds
5321	15241	25046	1.76	1.7E-01	AA470686.1	EST_HUMAN	nt13402.s1 NCI CGAP_C03 Homo sapiens cDNA clone IMAGE:881068 3' similar to gbM17685 50S
5321	15241	25047	1.76	1.7E-01	AA470686.1	EST_HUMAN	nt13402.s1 NCI CGAP_C03 Homo sapiens cDNA clone IMAGE:881068 3' similar to gbM17685 50S
5820	15726	25339	12.31	1.7E-01	HT12118.1	EST_HUMAN	ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);
6112	16005		2.15	1.7E-01	AF026562.3	NT	ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);
							502096.s1 Scores fetal liver spleen INFL5 Homo sapiens cDNA clone IMAGE:213656 3'
							Mesocricetus auratus outculet precursor (OVI) gene, complete cds

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6320	16183	28344	7.96	1.7E-01	BT34179.1	EST HUMAN
6558	16466	26558	1.2	1.7E-01	AF000573.1	NT
6814	16903	26882	7.03	1.7E-01	7706426	NT
6814	16903	26883	7.03	1.7E-01	7706426	NT
7056	16949	27135	2.46	1.7E-01	U00394.1	NT
7331	17382	27593	7.38	1.7E-01	AF001503.1	NT
7601	17452	27666	2.06	1.7E-01	U16283.1	NT
7875	17725		2.42	1.7E-01	AL163284.2	NT
7942	17792	28032	1.48	1.7E-01	11427203	NT
7849	17793	28033	1.57	1.7E-01	AA82797.1	EST HUMAN
8007	17938	28208	9.13	1.7E-01	BC89083.1	EST HUMAN
8182	18058	28317	2.47	1.7E-01	BA814617.1	EST HUMAN
8456	18329	28589	7.88	1.7E-01	1069300	NT
8456	18329	28590	7.88	1.7E-01	1069300	NT
8940	18757		1.92	1.7E-01	U16272	SWISSPROT
9012	18811	29107	4.38	1.7E-01	11448157	NT
9139	18953		1.5	1.7E-01	AL163278.2	NT
9420	19513		1.28	1.7E-01	AB34404.1	EST HUMAN
9708	19233	25218	5.78	1.7E-01	U01317.1	NT
120	10037	18917	1.86	1.6E-01	AF217532.1	NT
654	12841	20416	1.53	1.6E-01	U031497.1	EST HUMAN
1505	11409	21268	4.05	1.6E-01	AF286177.1	NT
1882	11778	21653	2.4	1.6E-01	U22263	SWISSPROT
1941	11838		1	1.6E-01	U10334.1	NT
2335	12719	22115	0.96	1.6E-01	X09232.1	NT
2443	13230	22218	2.19	1.6E-01	AB037729.1	NT
2883	12791	22593	8.9	1.6E-01	AF185950.1	NT
2883	12791	22594	8.9	1.6E-01	AF185950.1	NT
3351	13495	23285	1.31	1.6E-01	UJ003105.1	NT
3351	13495	23286	1.31	1.6E-01	UJ003105.1	NT
3919	13828		2.61	1.6E-01	AE004413.1	NT
9420	19513		1.28	1.7E-01	AB34404.1	EST HUMAN
9708	19233	25218	5.78	1.7E-01	U01317.1	NT
120	10037	18917	1.86	1.6E-01	AF217532.1	NT
654	12841	20416	1.53	1.6E-01	U031497.1	EST HUMAN
1505	11409	21268	4.05	1.6E-01	AF286177.1	NT
1882	11778	21653	2.4	1.6E-01	U22263	SWISSPROT
1941	11838		1	1.6E-01	U10334.1	NT
2335	12719	22115	0.96	1.6E-01	X09232.1	NT
2443	13230	22218	2.19	1.6E-01	AB037729.1	NT
2883	12791	22593	8.9	1.6E-01	AF185950.1	NT
2883	12791	22594	8.9	1.6E-01	AF185950.1	NT
3351	13495	23285	1.31	1.6E-01	UJ003105.1	NT
3351	13495	23286	1.31	1.6E-01	UJ003105.1	NT
3919	13828		2.61	1.6E-01	AE004413.1	NT
601560022F1 NIH_MGC_21						Homo sapiens cDNA clone IMAGE:3513084 5'
						Homo sapiens homogentate 1,2-dioxygenase gene, complete cds
						Homo sapiens clonogen and polyacrylamide specificity factor 3, 73kD subunit (CPSF3), mRNA
						Homo sapiens clonogen and polyacrylamide specificity factor 3, 73kD subunit (CPSF3), mRNA
						Rat (SHR strain) SKI gene
						Bacillus halodurans genomic DNA, section 2/14
						Human class IV alcohol dehydrogenase (ADH7) gene, exon 3
						Homo sapiens chromosome 21 segment H821084
						Homo sapiens solute carrier family 7 (calcium amino acid transporter, y ⁺ system), member 2 (SLC7A2), mRNA
						h960407.at1 NC1 CGAP_C98 Homo sapiens cDNA clone IMAGE:1148292 3' similar to gbL25091
						TRANSFORMING PROTEIN RHOC (HUMAN);
						60126547F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3613358 5'
						d434033.1 NC1 CGAP_CNS1 Homo sapiens cDNA clone IMAGE:1435924 3'
						Mus musculus adenomatous polyposis cell binding protein Ebt1 (Ebt1), mRNA
						Mus musculus adenomatous polyposis cell binding protein Ebt1 (Ebt1), mRNA
						AMP NUCLEOSIDASE
						Homo sapiens calcium channel, voltage-dependent, alpha 1 subunit (CACNA1), mRNA
						Homo sapiens chromosome 21 segment H821076
						h960405.1 NC1 CGAP_UH Homo sapiens cDNA clone IMAGE:2274872 3' similar to gb:U73779 RETNOC
						ACID RECEPTOR ALPHA-1 (HUMAN);
						Human beta globin region on chromosome 11
						Homo sapiens merodionin thesis gene, exon 5 and 7
						X751121.1 Genes placental Nucleo-Homo sapiens cDNA clone IMAGE:135560 5'
						Homo sapiens homeobox protein O122 gene, complete cds
						ACONIN-1 PRECURSOR (ACONAL) GLYCOPROTEIN TAG-1
						Crausolites glabra RNA polymerase II largest subunit mRNA, partial cds
						H. sapiens mRNA for novel T-cell activation protein
						Homo sapiens mRNA for KIAA1308 protein, partial cds
						Homo sapiens cyclin-like P450 3A4 (CYP3A4) gene, promoter region
						Homo sapiens cyclin-like P450 3A4 (CYP3A4) gene, promoter region
						Populus trichocarpa cv. Trichobol AB33 gene
						Populus trichocarpa cv. Trichobol AB33 gene
						Vibrio cholerae chromosome II, section 70 of 86 of the complete chromosome

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Max Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4234	14132	23808	7.92	1.5E-01	AF199801.1	NT	Homo sapiens apelin gene, complete cds
4353	12429		2.44	1.5E-01	AW598901.1	EST_HUMAN	EST1380577 MAGI Homo sapiens cDNA
4361	14267		4.01	1.5E-01	6753315	NT	Mus musculus chaperonin subunit 3 (gamma) (Cct3), mRNA
4781	14965	24451	0.86	1.5E-01	U23330.1	NT	S. cerevisiae chromosome XI reading frame ORF YKR105c
4781	14965	24432	0.86	1.5E-01	U23330.1	NT	S. cerevisiae chromosome XI reading frame ORF YKR105c
4865	14745	24524	1.14	1.5E-01	AA088343.1	EST_HUMAN	284409.11 Straligenes codon (6927204) Homo sapiens cDNA clone IMAGE:511361 similar to TR.E22185
4889	14769	24546	1.92	1.5E-01	AJ005365.1	NT	EST11958 38 855 bp SEGMENT OF CHROMOSOME XIV.1
4889	14769	24547	1.92	1.5E-01	AJ005365.1	NT	Lyopercion eculetum Rad fragment 2, satellite region
4956	14833	24901	1.09	1.5E-01	SEC18707.1	EST_HUMAN	h683905.Y1 NIH, MSC, 10 Homo sapiens cDNA clone IMAGE:394923 similar to gb.M81715
5390	15309	25162	3.12	1.5E-01	AW197498.1	EST_HUMAN	TRYPTOPHAN-TRNA SYNTHETASE (HUMAN); gp-X99457 M. musculus (MOUSE); HYPOTHETICAL 127 kD PROTEIN ;
5390	15309	25162	3.12	1.5E-01	AW197498.1	EST_HUMAN	h43801.X1 NGL, CGAP, G93 Homo sapiens cDNA clone IMAGE:396969 similar to TR.O75984 O75984
5396	15317	25364	2.07	1.5E-01	AF034761.1	NT	h43801.X1 NGL, CGAP, G93 Homo sapiens cDNA clone IMAGE:396969 similar to TR.O75984 O75984
5396	15317	25364	2.07	1.5E-01	AF034761.1	NT	Rattus norvegicus CCNA1 centromere binding protein actin (cabin) gene, complete cds
5973	15779	25899	2.24	1.5E-01	AL161962.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
5973	15779	25899	2.24	1.5E-01	AL161962.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
6157	15115	24686	3.7	1.5E-01	AW291215.1	EST_HUMAN	U14813.aph-b4545.01 J1 NGL, CGAP, S104 Homo sapiens cDNA, clone IMAGE:2724418 3
6371	16426	25912	1.84	1.5E-01	AW245559.1	EST_HUMAN	2622245.5p106.01 NIH, MSC, 7 Homo sapiens cDNA, clone IMAGE:2822248 5
6392	16472	25932	1.42	1.5E-01	U0349.1	NT	S. cerevisiae chromosome XII reading frame ORF YLR031w
7187	17034	27254	1.89	1.5E-01	U4501.1	NT	S. cerevisiae chromosome XII reading frame ORF YLR031w
7554	17416		1.77	1.5E-01	BF375171.1	EST_HUMAN	SC3-S10230.01119-01T461 S10230 Homo sapiens cDNA
7555	17416		1.97	1.5E-01	U4501.1	NT	S. cerevisiae chromosome XII reading frame ORF YLR031w
8049	17940	25190	2.71	1.5E-01	AW85983.1	EST_HUMAN	IL3-C10220-11195-025-001 C10220 Homo sapiens cDNA
8394	16241	25490	1.78	1.5E-01	014647	SWISSPROT	CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 2 (CHD-2)
8394	16241	25491	1.78	1.5E-01	014647	SWISSPROT	CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 2 (CHD-2)
8459	15332		7.6	1.5E-01	AF106064.1	NT	Pleurodon mactranum calcium-dependent protein kinase-3 (cdpk3) gene, complete cds
8713	18330	28814	10.07	1.5E-01	6971652	NT	Mus musculus adaptor-related protein complex 4P-1, beta 1 subunit (A0151), mRNA
9001	18804	29037	2.09	1.5E-01	AW87127.1	EST_HUMAN	QV2 PT0001-160400-133-408 PT0010 Homo sapiens cDNA
9025	19578		2.17	1.5E-01	AF19665.1	NT	Mus musculus protein kinase, cAMP-dependent, type II (Prkg2), mRNA
9141	18658	28795	2.33	1.5E-01	AF19665.1	EST_HUMAN	AV179985 GLC Homo sapiens cDNA, clone GCEMPF 5
9566	19493		6.33	1.5E-01	AB04510.1	NT	Cuembia salinus KS mRNA for est-luciferase synthase, complete cds
9727	19286		2.84	1.5E-01	AK024468.1	NT	Homo sapiens mRNA for FLJ00104 protein, partial cds

Probes Expressed in Heart

Probes Expressed in Heart

Probe SEQ ID NO.	Exon SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description	
6807	18319	2.47	1.5E-01	AF267244.1	NT	Fuslike hybrid cellular Qm 91208 ribosomal protein S10 gene, partial cds; nuclear gene for mitochondrial product	
6827	18328	26208	1.37	9606822	EST_HUMAN	Rattus norvegicus chondroitin sulfate proteoglycan 5 (perlecan) cDNA (Ctag65) mRNA	
248	10214	20020	1.87	1.5E-01	BE1710387.1	EST_HUMAN	L3-11T0819-040700-197-E03 HT0510 Homo sapiens cDNA
248	10214	20021	1.87	1.5E-01	BE1710387.1	EST_HUMAN	L3-11T0819-040700-197-E03 HT0510 Homo sapiens cDNA
572	12540	20524	2.28	1.5E-01	AF1711036.1	EST_HUMAN	AY171689 DCA Homo sapiens cDNA, clone DCA43868.5
766	10587	20524	1.84	1.5E-01	AL153284.2	NT	Homo sapiens chromosome 21 segment HS210384
1076	10582	20524	0.88	1.5E-01	AJ009735.1	NT	Oryzopsis carpio mrip1 for EGGS12 myosin heavy chain, 3'UTR
1087	10587	20528	1.87	1.5E-01	AF151865.1	NT	Homo sapiens partial SL22242 gene for organic cation transporter (OCT2), exon 1
1087	11013	20983	1.82	1.5E-01	U136725.1	NT	Rattus norvegicus insulin-responsive glucose transporter (GLUT4) gene, 5' end
1159	11108	21093	1.36	1.5E-01	AW159516.1	EST_HUMAN	nonbeta1-11 NCI CGAP Kc111 Homo sapiens cDNA, clone IMAGE:286068.3
1254	11161	21070	2.81	1.5E-01	D26693.1	NT	Human gene for aldehyde-binding succinyltransferase, complete cds (exon 1-15)
1254	11161	21071	2.81	1.5E-01	D26693.1	NT	Human gene for aldehyde-binding succinyltransferase, complete cds (exon 1-15)
1466	11371	21238	1.49	1.5E-01	AF17340.1	NT	Mus musculus MAP kinase kinase kinase 1 (Msk1) mRNA, complete cds
1666	11782	21658	1.72	1.5E-01	AW444451.1	EST_HUMAN	U048183-abb-049-01-11 NCI CGAP S308 Homo sapiens cDNA, clone IMAGE:2753641.3
2676	12344	22455	1.14	1.5E-01	BF696393.1	EST_HUMAN	RR385329P N1-MGC_871 Homo sapiens cDNA, clone IMAGE:4247537.5
2669	12827	22716	0.86	1.5E-01	M61141.1	NT	Bos taurus fetus V variant 2 (coat V) mRNA, complete cds
3328	13226	23024	4.22	1.5E-01	AA82049.1	EST_HUMAN	0068405.51 NCI CGAP G041 Homo sapiens cDNA, clone IMAGE:1571337.3 similar to gbM11433
3332	13242	23048	0.87	1.5E-01	Z23104.1	NT	RETINOL-BINDING PROTEIN I, CELLULAR (HUMAN); L-alanine mRNA for G protein-coupled receptor
3322	13242	23049	0.87	1.5E-01	Z23104.1	NT	L-alanine mRNA for G protein-coupled receptor
3350	13296	23057	0.96	1.5E-01	AW612237.1	EST_HUMAN	HS2602.1 NCI CGAP L124 Homo sapiens cDNA, clone IMAGE:256559.9 similar to containe element
3350	13296	23057	0.96	1.5E-01	AW612237.1	EST_HUMAN	HS2602.1 NCI CGAP L124 Homo sapiens cDNA, clone IMAGE:256559.9 similar to containe element
3656	13610	23364	1.34	1.5E-01	U00964.1	NT	Mus musculus pyruvate glyceraldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds
3706	13610	23403	185.26	1.5E-01	71085368	EST_HUMAN	Homo sapiens purine-specific pyridoxaldehyde kinase, isoenzyme 1 (PCK1), nuclear gene encoding mitochondrial protein, mRNA
3761	13763	23450	2.35	1.5E-01	AF656833.1	EST_HUMAN	HT0065.01 Soere, NFL_T_GBC S11 Homo sapiens cDNA, clone IMAGE:2681411.3
3806	13718	23505	0.8	1.5E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichobal ABIS gene
3905	13718	23507	0.8	1.5E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichobal ABIS gene
3964	13871	23549	0.96	1.5E-01	AF356959.1	EST_HUMAN	RC2-1T1046-191059-012-c09 HT0146 Homo sapiens cDNA
4006	13912	23587	0.97	1.5E-01	Z17823.1	NT	B. napus microclonated DNA for ORF168
4091	13881	23768	8.36	1.5E-01	AL162264.2	NT	Homo sapiens chromosome 21 segment HS210384
4521	14561	24301	1.34	1.5E-01	BE687225.1	EST_HUMAN	302067129P N1-MGC_571 Homo sapiens cDNA, clone IMAGE:4066223.1

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Htt BLAST E Value	Top Htt Accession No.	Top Htt Database Source
4845	12544	22435	2.18	1.5E-01	BF903381.1	EST_HUMAN
4846	14561	24361	1.08	1.5E-01	BE177996.1	EST_HUMAN
4850	14569	24362	1.09	1.5E-01	BE177996.1	EST_HUMAN
4929	14608	24576	1.3	1.5E-01	AL161590.2	NT
5072	14842	24716	0.94	1.5E-01	AF003106.1	NT
5218	15139	24833	2.02	1.5E-01	P07668	SWISSPROT
5299	15188		5.67	1.5E-01	P16196	SWISSPROT
5400	18319	25307	4.05	1.5E-01	AW850754.1	EST_HUMAN
5424	18345	25348	8.77	1.5E-01	U65016.1	NT
5424	18345	25356	8.77	1.5E-01	U65016.1	NT
5632	15594	25560	1.9	1.5E-01	6733959	NT
5632	15594	25561	1.9	1.5E-01	6733959	NT
5694	15593	25564	1.87	1.5E-01	AL275053.1	NT
5780	16638	26774	2.44	1.5E-01	BE727058.1	EST_HUMAN
5785	16691		1.86	1.5E-01	4563626	NT
5828	15724	25945	1.78	1.5E-01	AF134007.1	NT
5917	19485	25548	1.98	1.5E-01	AEO1039.1	NT
5935	15540	25963	5.3	1.5E-01	11417236	NT
5942	1847	26971	1.81	1.5E-01	R48538	SWISSPROT
5972	18379	25900	2.09	1.5E-01	Q28402	SWISSPROT
6031	15635	25037	1.4	1.5E-01	P30743	SWISSPROT
6155	15723	24996	5.53	1.5E-01	AF207026.1	EST_HUMAN
6294	19148	25396	1.77	1.5E-01	AF210842.1	NT
6374	19288	25396	1.88	1.5E-01	AF210842.1	EST_HUMAN
6481	15340	25517	1.88	1.5E-01	AF252611.1	EST_HUMAN
6481	15340	25518	1.88	1.5E-01	AF252611.1	EST_HUMAN
6786	19695	26956	1.22	1.5E-01	AA607037.1	EST_HUMAN
6925	15774		11.77	1.5E-01	U27636.1	EST_HUMAN
6912	15780	25953	1.86	1.5E-01	U27636.1	NT
6936	19873	27064	1.44	1.5E-01	D64476.1	NT

Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7190	17007	27200	1.71	1.5E-01	4301972	NT	Homo sapiens adictor-related protein complex 1, beta 1 subunit (AD1B1), mRNA
7205	17142	27353	2.48	1.5E-01	NF4226.1	EST_HUMAN	zsf606.s1 Scores field liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:260886 3 similar to PIR-S44443 S44443 RAO23 protein homolog-2_human; 1
7308	17162		2.98	1.5E-01	AY74819.1	EST_HUMAN	AV754819 TP Homo sapiens cDNA clone TPA4812 5'
7438	16451	26641	6.6	1.5E-01	U00455.1	NT	Adiponectin transmembrane (Villobonin) mRNA, partial cds
7638	17656	27781	7.02	1.5E-01	AF007570.1	NT	Apjapla californica carboxypeptidase D mRNA, complete cds
7706	17586	27782	7.02	1.5E-01	AF007570.1	NT	Apjapla californica carboxypeptidase D mRNA, complete cds
7860	17710	27955	2.86	1.5E-01	X96852.1	NT	P. leuciscus mRNA for inlay in beta subunit
7900	17786	27996	2.45	1.5E-01	A81406.1	EST_HUMAN	WAL3312.x1 NQI_CGAP_P122 Homo sapiens cDNA clone IMAGE:2416175 3 similar to gbM27508 BETA
7906	17756	27999	2.45	1.5E-01	A81406.1	EST_HUMAN	WAL3312.x1 NQI_CGAP_P122 Homo sapiens cDNA clone IMAGE:2416175 3 similar to gbM27508 BETA
7959	17769	28031	1.54	1.5E-01	U43932.1	NT	Danio rerio transcription factor Pac6b (Pac6) mRNA, complete cds
8008	17859	28103	1.35	1.5E-01	AJ011884.1	NT	Clovisia purpurina p61 gene
8009	17859	28104	1.35	1.5E-01	AJ011884.1	NT	Clovisia purpurina p61 gene
8189	18084	28334	8.15	1.5E-01	AL163380.2	NT	Homo sapiens chromosome 21, segment HS21C080
8342	18219		5.16	1.5E-01	AL163380.2	NT	Homo sapiens chromosome 21, segment HS21C080
8425	18259	28655	1.73	1.5E-01	AJ262976.1	EST_HUMAN	Human sapiens chromosome 21, segment HS21C080
8500	18236	29390	2.17	1.5E-01	AF673167.1	EST_HUMAN	Human sapiens chromosome 21, segment HS21C080
9090	19347		20.02	1.5E-01	AF700682.1	EST_HUMAN	HS-OMC24303030-025-043 OM204 Homo sapiens cDNA
9091	19348		20.02	1.5E-01	AF700682.1	EST_HUMAN	HS-OMC24303030-025-043 OM204 Homo sapiens cDNA
9321	19586		4.14	1.5E-01	R63077.1	EST_HUMAN	6051283731 NQI_CGAP_LRT Homo sapiens cDNA clone IMAGE:24613131
9691	19586		2.14	1.5E-01	AF741272.1	EST_HUMAN	6051283731 NQI_CGAP_LRT Homo sapiens cDNA clone IMAGE:24613131
9726	19407	25133	3.99	1.5E-01	AL1139074.1	EST_HUMAN	AY747424.1 Scores field liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:194430 5'
9932	19407	25179	3.01	1.5E-01	AL1139074.1	EST_HUMAN	AY747424.1 Scores field liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:194430 5'
9972	19432		1.58	1.5E-01	AF702346.1	NT	Camphidolipid fatty acid NQCTC11188 complete genome, segment 1/8
206	10260		1.96	1.4E-01	AF700363.1	NT	Rattus norvegicus pyridoxal kinase mRNA, complete cds
862	10818		1.97	1.4E-01	D76538.1	NT	Homo sapiens 1 cell receptor, beta locus, TORB2/VSPT to TORB2/VS242 region
1298	11145		2.62	1.4E-01	T01884.1	EST_HUMAN	Xenopus laevis mRNA for DNA (guanine-5'-methyltransferase, complete cds
1711	16115		1.43	1.4E-01	A15201170.1	NT	Human sapiens cDNA clone IMAGE:2416175 3 similar to gbM27508 BETA
1653	11759		0.94	1.4E-01	AW135741.1	EST_HUMAN	UHHB01 human skin section 22 of 136 of the complete genome
1283	11603		10.35	1.4E-01	AW126915.1	EST_HUMAN	UHHB01 human skin section 22 of 136 of the complete genome
2426	12303	22199	0.97	1.4E-01	P30706	SWISSPROT	GLYCERALDEHYDE-3-PHOSPHATE ACYLTRANSFERASE PRECURSOR (GPA1)

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar Unigene E-VALUE	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8764	17913	28158	2.23	1.4E-01	U29780.1	NT	Serratia burgdorferi glyceroldehyde-3-phosphate dehydrogenase (GAPDH), phosphoglycerate kinase (PGK), triosephosphate isomerase (TPI) genes, complete cds
8813	18526		3.02	1.4E-01	X52102.1	NT	Mus musculus p18k gene for 18 kDa protein
9365	19617	28139	1.48	1.4E-01	AE000800.1	NT	Epithelial flavinella mcrA for aldolase, partial cds
9413	19065	28277	2.32	1.4E-01	X74778.1	NT	P. salina plastid gene seq
9427	19073		1.89	1.4E-01	11928117	NT	Rattus norvegicus desmin (Des), mRNA
9470	18734		1.82	1.4E-01	BE613802.1	EST_HUMAN	36131638F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3934329 5'
9560	19156		3.01	1.4E-01	AF083021.1	NT	Fugu rctspies putative reeler of anion channel receptor, YDR140w homolog, and glycylamide ribonucleotide transferase (GART) genes, complete cds
9573	19183		2.29	1.4E-01	D64004.1	NT	Syngochrysis sp. POC8803 complete genome, 23/27_2883767-3003265
9646	19754		3.28	1.4E-01	D14047.1	SWISSPROT	TYROSINE-PROTEIN KINASE TRANSFORMING PROTEIN ABL
9762	18282		1.41	1.4E-01	BE78738.1	EST_HUMAN	36146557F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:3948796 5'
9831	19332		1.42	1.4E-01	11422031	NT	Homo sapiens ephrin-B3 (EFNB3), mRNA
9850	19366		3.41	1.4E-01	D32963.1	NT	Mus musculus mRNA for prolactin, complete cds
9858	19368		1.77	1.4E-01	AW377698.1	EST_HUMAN	MR0H10208-221289-201-c08 H10208 Homo sapiens cDNA
319	19381	20098	2.69	1.3E-01	U789487	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
319	19381	20099	2.68	1.3E-01	U789487	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
818	19460	20271	1.90	1.3E-01	AB013138.1	NT	Homo sapiens gene for NES1, complete cds
620	10557	20369	0.89	1.3E-01	AJ277806.1	NT	Hirax calcarivus HUNLV/GChinglan930UK RNA for caspase protein (ORF2), strain HUNLV/GChinglan930UK
620	10557	20370	0.89	1.3E-01	AJ277806.1	NT	Hirax calcarivus HUNLV/GChinglan930UK RNA for caspase protein (ORF2), strain HUNLV/GChinglan930UK
826	10753	20603	1.09	1.3E-01	X55330.1	NT	R. Jurellii histone gene cluster for core histones H2A, H2B, H3 and H4
876	10952	20652	1.83	1.3E-01	AFL19518.1	NT	Rattus norvegicus A-kinase anchor protein mRNA, complete cds
1010	10928	20771	1.65	1.3E-01	AL111078.1	NT	Sophia chinea strain 14 cDNA library under conditions of nitrogen deprivation
1111	11036		2.23	1.3E-01	AL118268.1	NT	Sophia chinea strain 14 cDNA library under conditions of nitrogen deprivation
1197	11107	20852	1.07	1.3E-01	AFV12467.1	EST_HUMAN	AY172467 DCA Homo sapiens cDNA clone DCAAT-005 5'
1426	11331		1.96	1.3E-01	AFL46277.1	NT	Homo sapiens adapter protein GMS mRNA, complete cds
1916	11811	21689	2.56	1.3E-01	AL111078.1	NT	Sophia chinea strain 14 cDNA library under conditions of nitrogen deprivation
2124	12012		1.29	1.3E-01	AJ243978.1	NT	Rhodospirillum rubrum additolin pucB8, pucA5, pucB9, pucA6, pucA7, pucA8 and pucC genes and ORF161
2245	12129		1.17	1.3E-01	AW812104.1	EST_HUMAN	RC4-ST0173-1791080-032-471 ST0173 Homo sapiens cDNA
2329	12210		2.99	1.3E-01	AE001016.1	NT	Archaeoglobus fulgidus section 91 of 172 of the complete genome
2512	12416	22006	3.49	1.3E-01	M89918.1	NT	Carassius auratus keratin type I mRNA, complete cds

Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3404	13321	23122	0.05	1.3E-01	M21972.1	NT	Scine branched chain alpha-keto acid dehydrogenase mRNA, complete cds
3561	13370	23362	1.18	1.3E-01	AF000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1,287,000 nt, position (1/7)
3561	13370	23363	1.18	1.3E-01	AF000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1,287,000 nt, position (1/7)
3561	13370	23364	0.78	1.3E-01	A0302168.1	NT	Hom sapiens DGL gene for dihydrolipoamide gamma-5 [AKR] (cd), exon 2
3561	13370	23365	0.88	1.3E-01	AF000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1,287,000 nt, position (1/7)
3744	13375	23365	0.88	1.3E-01	AF000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1,287,000 nt, position (1/7)
3744	13375	23365	0.88	1.3E-01	AF000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1,287,000 nt, position (1/7)
3744	13346	23431	0.85	1.3E-01	6878940	NT	Rattus norvegicus Parvogen, gamma polyprotein (Fg) mRNA
3900	13515	24041	1.77	1.3E-01	AL161581.2	NT	Anopheles gambiae chromosome 4, coding fragment (Fg) mRNA
4046	13548	24041	1.15	1.3E-01	AF020713.1	NT	Bacteroides sp262 complete genome
4046	13548	24041	1.15	1.3E-01	AF020713.1	NT	Bacteroides sp262 complete genome
4056	13568	23750	3.44	1.3E-01	AF034841.1	EST_HUMAN	Q10370101-057593-035-003 D10018 Homo sapiens cDNA
4075	13577	23750	1.89	1.3E-01	AF020905.1	EST_HUMAN	Schistosoma mansoni nucleoside triphosphate adenosine mRNA, complete cds
4083	13593	23770	1.99	1.3E-01	AF020905.1	EST_HUMAN	sch3010.74 Soesies, NTC, GBC, S1 Homo sapiens cDNA clone IMAGE:2813895.3
4192	14020	23870	0.65	1.3E-01	AF073741.1	EST_HUMAN	AV752729 NP0 Homo sapiens cDNA clone NP042602.5
4192	14020	23871	0.85	1.3E-01	AF073279.1	EST_HUMAN	AV752729 NP0 Homo sapiens cDNA clone NP042602.5
4218	14115	24041	1.65	1.3E-01	AL163320.1	NT	Homo sapiens chromosome 21 segment HS21C0380
4218	14115	24041	1.65	1.3E-01	BE527359.1	EST_HUMAN	80112600801 NH1, LMC6, 9 Homo sapiens cDNA clone IMAGE:2960008.5
4252	14418	24202	2.16	1.3E-01	BE527359.1	EST_HUMAN	80112600801 NH1, LMC6, 9 Homo sapiens cDNA clone IMAGE:2960008.5
4252	14418	24202	0.81	1.3E-01	BF076554.1	EST_HUMAN	80112600801 NH1, LMC6, 9 Homo sapiens cDNA clone IMAGE:2960008.5
4252	14418	24202	0.81	1.3E-01	BE564017.1	EST_HUMAN	80112600801 NH1, LMC6, 9 Homo sapiens cDNA clone IMAGE:2960008.5
4403	14783	24716	0.86	1.3E-01	AF013671.1	EST_HUMAN	80112600801 NH1, LMC6, 9 Homo sapiens cDNA clone IMAGE:2960008.5
4403	14783	24716	1.21	1.3E-01	AL163324.2	NT	AV138916 PLACET Homo sapiens cDNA clone PLACE1004698.5
6074	14844	24716	1.21	1.3E-01	AL163324.2	NT	Homo sapiens chromosome 21 segment HS21C0384
6074	14844	24716	1.21	1.3E-01	AL163324.2	NT	Homo sapiens chromosome 21 segment HS21C0384
6074	14844	24716	1.21	1.3E-01	AL163324.2	NT	Homo sapiens chromosome 21 segment HS21C0384
5173	15039	24809	0.09	1.3E-01	BF078919.1	EST_HUMAN	80216140101 NH1, LMC6, 83 Homo sapiens cDNA clone IMAGE:4263544.3
5173	15039	24809	0.09	1.3E-01	BF078919.1	EST_HUMAN	80216140101 NH1, LMC6, 83 Homo sapiens cDNA clone IMAGE:4263544.3
5173	15039	24809	0.09	1.3E-01	BF078919.1	EST_HUMAN	80216140101 NH1, LMC6, 83 Homo sapiens cDNA clone IMAGE:4263544.3
5292	16231	25013	2.51	1.3E-01	AF0904417.1	EST_HUMAN	Q10400693-100400-189-405 UM0093 Homo sapiens cDNA
5292	16231	25013	2.51	1.3E-01	AF0904417.1	EST_HUMAN	Q10400693-100400-189-405 UM0093 Homo sapiens cDNA
5428	16348	25063	1.79	1.3E-01	AF0904417.1	EST_HUMAN	Q10400693-100400-189-405 UM0093 Homo sapiens cDNA
5428	16348	25063	1.79	1.3E-01	AF0904417.1	EST_HUMAN	Q10400693-100400-189-405 UM0093 Homo sapiens cDNA
5904	16510	25063	13.21	1.3E-01	AB031326.1	NT	Helicobacter C virus C6, CL-10 genome polyprotein gene, partial cds
5996	16589	25063	2.04	1.3E-01	AF088891.1	NT	Schizosaccharomyces pombe gene for Alp-1, complete cds
5996	16589	25063	2.04	1.3E-01	AF088891.1	NT	Schizosaccharomyces pombe gene for Alp-1, complete cds
6305	16160	25724	2	1.3E-01	HA4984.1	EST_HUMAN	Cj04002.1 Soesies field liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:207076.5
6529	16529	25724	1.34	1.3E-01	11623294	EST_HUMAN	Homo sapiens PRO06911 protein (PRO06911), mRNA
6529	16529	25724	1.34	1.3E-01	11623294	EST_HUMAN	Homo sapiens PRO06911 protein (PRO06911), mRNA
6529	16529	25724	1.34	1.3E-01	11623294	EST_HUMAN	Homo sapiens PRO06911 protein (PRO06911), mRNA
6588	16737	26043	1.28	1.3E-01	BF060522.1	EST_HUMAN	8021870151 NH1, LMC6, 49 Homo sapiens cDNA clone IMAGE:4260074.3
6588	16737	26043	4.54	1.3E-01	Z714102.1	NT	S. cerevisiae chromosome IV resulting frame ORF YOL046
6588	16737	26043	4.54	1.3E-01	Z714102.1	NT	S. cerevisiae chromosome IV resulting frame ORF YOL046
6588	16737	26043	4.54	1.3E-01	Z714102.1	NT	S. cerevisiae chromosome IV resulting frame ORF YOL046
6900	16838	27031	1.27	1.3E-01	BF060522.1	EST_HUMAN	8021870151 NH1, LMC6, 49 Homo sapiens cDNA clone IMAGE:4260074.3
6900	16838	27031	1.27	1.3E-01	BF060522.1	EST_HUMAN	8021870151 NH1, LMC6, 49 Homo sapiens cDNA clone IMAGE:4260074.3
7462	17261	27467	4.45	1.3E-01	AF09023126.1	NT	Oxytelodonta cuniculus Hc-K-A-1TP sea alpha 2c subunit mRNA, complete

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Probe SEQ ID	Exon SEQ ID	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
8029	17021		2.88	1.3E-01	BC330999.1	EST_HUMAN	MFAR1 10352-130/100-010-008 B1 03358 Homo sapiens cDNA
8456	18444	28677	1.83	1.3E-01	AF118171.1	NT	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds
8576	18444		5.13	1.3E-01	6671745	NT	Mini musciculae cyclin 3, muscicla (C12), mRNA
8873	18465	28076	3.72	1.3E-01	B5279449.1	EST_HUMAN	h01159052F1 NH1_KGC_67 Homo sapiens cDNA clone IMAGE:3504804.5*
9261	18966	23520	1.07	1.3E-01	BS518346.1	EST_HUMAN	h01402741F1 NH1_KGC_67 Homo sapiens cDNA clone IMAGE:3566004.5*
9399	18064		3.18	1.3E-01	AJ242780.1	EST_HUMAN	Calyx callus 3047, genes for transplastoma, clones 1-3
9737	12297		1.36	1.3E-01	A5002628.1	NT	Human cDNA 3047, genes for transplastoma, clones 1-3
9764	12297		1.32	1.3E-01	AW091114.1	EST_HUMAN	TRC000267 Sarcosin Dehydratase cDNA, hK10D Homo sapiens cDNA clone IMAGE:2820977.3 similar to
9945	18474		1.26	1.3E-01	BF371764.1	EST_HUMAN	h000324F01 NH1_KGC_63 Homo sapiens cDNA clone IMAGE:3539403.5*
378	10382	20185	7.21	1.2E-01	AJ21744.1	EST_HUMAN	h000324 F1 NCI-GCAP_5203 Homo sapiens cDNA clone IMAGE:2965589.5 similar to pU08760_nst1
418	8855		1.53	1.2E-01	U08572.1	NT	ANNEKIN V (HUMAN);
885	10476		2.63	1.2E-01	A036542.1	NT	Human cDNA 3047, genes for transplastoma, clones 1-3
1385	12621	21117	2.78	1.2E-01	AU18146.1	EST_HUMAN	h000324 F1 NCI-GCAP_5203 Homo sapiens cDNA clone IMAGE:2965589.5 similar to pU08760_nst1
1395	12621	21118	2.78	1.2E-01	AU18146.1	EST_HUMAN	h000324 F1 NCI-GCAP_5203 Homo sapiens cDNA clone IMAGE:2965589.5 similar to pU08760_nst1
1397	11267		3.94	1.2E-01	AF793249.1	EST_HUMAN	h000324 F1 NCI-GCAP_5203 Homo sapiens cDNA clone IMAGE:2965589.5 similar to pU08760_nst1
1400	11395		1.13	1.2E-01	AJ489747.1	EST_HUMAN	h000324 F1 NCI-GCAP_5203 Homo sapiens cDNA clone IMAGE:2965589.5 similar to pU08760_nst1
1613	11517	21377	1.17	1.2E-01	Q14694	SWISSPROT	NUCLEAR FACTOR OF ACTIVATED T-CELLS, CYTOLYSIN 4 (T CELL TRANSCRIPTION FACTOR
1651	11535	21396	2.02	1.2E-01	A365402.1	EST_HUMAN	h000324 F1 NCI-GCAP_5203 Homo sapiens cDNA clone IMAGE:2965589.5 similar to pU08760_nst1
1730	11631		29.48	1.2E-01	X06211.1	NT	h000324 F1 NCI-GCAP_5203 Homo sapiens cDNA clone IMAGE:2965589.5 similar to pU08760_nst1
1770	11773		1.43	1.2E-01	AW144958.1	EST_HUMAN	h000324 F1 NCI-GCAP_5203 Homo sapiens cDNA clone IMAGE:2965589.5 similar to pU08760_nst1
2184	12022	21619	2.1	1.2E-01	BF24640.1	EST_HUMAN	h000324 F1 NCI-GCAP_5203 Homo sapiens cDNA clone IMAGE:2965589.5 similar to pU08760_nst1
2240	12124	22025	1.01	1.2E-01	AF163313.2	NT	h000324 F1 NCI-GCAP_5203 Homo sapiens cDNA clone IMAGE:2965589.5 similar to pU08760_nst1
2546	14220	22310	2.02	1.2E-01	AW86556.1	EST_HUMAN	h000324 F1 NCI-GCAP_5203 Homo sapiens cDNA clone IMAGE:2965589.5 similar to pU08760_nst1
2607	12561	22451	0.86	1.2E-01	A623388.1	EST_HUMAN	h000324 F1 NCI-GCAP_5203 Homo sapiens cDNA clone IMAGE:2965589.5 similar to pU08760_nst1
2812	12741	22637	1.5	1.2E-01	U18018.1	NT	h000324 F1 NCI-GCAP_5203 Homo sapiens cDNA clone IMAGE:2965589.5 similar to pU08760_nst1
2872	12664	22564	1.98	1.2E-01	AT720470.1	EST_HUMAN	h000324 F1 NCI-GCAP_5203 Homo sapiens cDNA clone IMAGE:2965589.5 similar to pU08760_nst1
2904	12831	22628	2.89	1.2E-01	MT0364.1	NT	h000324 F1 NCI-GCAP_5203 Homo sapiens cDNA clone IMAGE:2965589.5 similar to pU08760_nst1

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2974	12901	22700	0.96	1.2E-01	AF5892.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3192	13143	22623	2	1.2E-01	AW370698.1	EST_HUMAN	QY1-870259-201069-021-403 BT02359 Homo sapiens cDNA
3219	13149		0.97	1.2E-01	J67060.1	NT	Methanococcus jannaschii section 142 of 150 of the complete genome
3433	13350		0.79	1.2E-01	250118.1	NT	Bacillus subtilis complete genome (section 15 of 21); from 2765131 to 3013540
3477	13393	23198	1.14	1.2E-01	AF5892.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3477	13393	23189	1.14	1.2E-01	AF5892.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3554	13350		1.2	1.2E-01	250118.1	NT	Bacillus subtilis complete genome (section 15 of 21); from 2765131 to 3013540
3704	13617		0.86	1.2E-01	BF12655.1	EST_HUMAN	601810766R1 NIH MGSC 46 Homo sapiens cDNA clone IMAGE:4053585.3
4090	13990	23765	2.3	1.2E-01	254255.1	NT	P. cinctus mRNA; repeat region (ID 2NRTV)
4090	13990	23767	2.3	1.2E-01	254255.1	NT	P. cinctus mRNA; repeat region (ID 2NRTV)
5012	14898		1.04	1.2E-01	PI0496	SWISSPROT	HEXADYLIN PRECURSOR
5174	15040	24807	1.47	1.2E-01	Q10441	SWISSPROT	HYPOTHETICAL_52.4 KO PROTEIN G12810.05C IN CHROMOSOME I
5174	15040	24808	1.47	1.2E-01	Q10441	SWISSPROT	HYPOTHETICAL_52.4 KO PROTEIN G12810.05C IN CHROMOSOME I
5186	15052	24847	2.63	1.2E-01	N13003.1	EST_HUMAN	ULH6-8V0-348-1-01-01-11 NH MGSC 39 Homo sapiens cDNA clone IMAGE:2053617.5
5297	15174	25021	1.19	1.2E-01	246256.1	NT	2503602.1T Soanae_pseudofurcator_Lum27_NHCPA Homo sapiens cDNA clone IMAGE:327689.5
5762	15959	25776	1.89	1.2E-01	BE02045.1	EST_HUMAN	Homo sapiens gene encoding patkapsulin (locus 1-13)
5805	15711	25824	2.19	1.2E-01	AW84575.1	EST_HUMAN	001460161F1 NIH MGSC 70 Homo sapiens cDNA clone IMAGE:3856513.5
5939	15745	25858	1.90	1.2E-01	M26925.1	NT	IL04-01031-221095-115-04 C10031 Homo sapiens cDNA
6007	15487		1.21	1.2E-01	BE07072.1	EST_HUMAN	Mouse galactoseyltransferase mRNA, complete cds
6042	16522	26715	2.46	1.2E-01	AF91375.1	EST_HUMAN	PI03-BN0137-260300-002-70 BN0137 Homo sapiens cDNA
6893	16772		9.72	1.2E-01	AW063692.1	EST_HUMAN	W05903.xt NCI CGAP_C03 Homo sapiens cDNA clone IMAGE 232804.3 similar to SW-GST2_HUMAN
							Q99735 MICROSOMAL GLUTATHIONE S-TRANSFERASE II:
							xc-49007.xt NCI CGAP_E502 Homo sapiens cDNA clone IMAGE 2367597.3 similar to gb.M13462 LAMIN A (HUMAN);
6904	16782		3.86	1.2E-01	AF033772.1	NT	Staphylococcus aureus plasmid pSK23 putative isochromatase Sin (sin) gene, partial cds, and transcriptional regulator Dack (dack) and multidrug efflux protein DackB (dackB) genes, complete cds
7043	16920		2.27	1.2E-01	J32714.1	NT	Hemophilus influenzae Rd section 28 of 163 of the complete genome
7521	17340	27546	1.6	1.2E-01	K77891.1	NT	S.cerevisiae HXT5 gene
7747	17597	27819	1.51	1.2E-01	AV710887.1	EST_HUMAN	AV710887 Cu Homo sapiens cDNA clone CUARE08.5
8260	18140		2.96	1.2E-01	Q20184.1	NT	Yeast MPT15 gene for suppressor protein, complete cds
8417	18291		3.36	1.2E-01	BE002324.2	EST_HUMAN	601650787R1 NIH MGSC 65 Homo sapiens cDNA clone IMAGE:3546283.3
8467	18360		1.93	1.2E-01	BF11481.1	EST_HUMAN	601500763F1 NIH MGSC 19 Homo sapiens cDNA clone IMAGE:4110103.5
8579	18447	28715	2.6	1.2E-01	AF190493.1	NT	Homo sapiens dynein intermediate chain DNAI1 (DNAI1) gene, exon 17

Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
6768	16712		2.02	1.2E-01	M85106.1	NT	Rabbit glycogen-associated protein phosphatase regulatory subunit (RG1) mRNA, complete cds
9032	16823		2.22	1.2E-01	AF056033.1	EST_HUMAN	UV665032 GLC Homo sapiens cDNA clone GLCFB12.3
9383	16743		2.18	1.2E-01	AJ271736.1	NT	Human papilloma virus type 16, segment 22
9458	16693		2.4977	1.2E-01	QJ4912	SWISSPROT	MACROPHAGE-STIMULATING PROTEIN RECEPTOR PRECURSOR (MSP RECEPTOR) (P16-R6)
9597	16716		7.08	1.2E-01	AF039442.1	NT	Human papilloma virus type 16, segment 22
9671	16720		1.31	1.2E-01	U03391.1	NT	Human papilloma virus type 16, segment 22
9730	16726	24903	2.48	1.2E-01	U03391.1	EST_HUMAN	Human papilloma virus type 16, segment 22
9761	16281	25231	3.08	1.2E-01	U03391.1	EST_HUMAN	Human papilloma virus type 16, segment 22
9782	16281		2.07	1.2E-01	U01697.1	NT	Human papilloma virus type 16, segment 22
9786	16636		4.72	1.2E-01	U06443	SWISSPROT	Human papilloma virus type 16, segment 22
9860	16424		2.18	1.2E-01	BF314481.1	EST_HUMAN	Human papilloma virus type 16, segment 22
552	70463	20301	0.95	1.1E-01	AJ051003.1	EST_HUMAN	Human papilloma virus type 16, segment 22
599	10535	20344	3.38	1.1E-01	AF059008.1	EST_HUMAN	Human papilloma virus type 16, segment 22
1018	10956	20760	1.53	1.1E-01	AA667008.1	EST_HUMAN	Human papilloma virus type 16, segment 22
1069	10885		1.29	1.1E-01	AF101590.2	NT	Human papilloma virus type 16, segment 22
1143	12688	20859	4.09	1.1E-01	AF101590.2	EST_HUMAN	Human papilloma virus type 16, segment 22
1229	11137	20900	1.72	1.1E-01	D81001.1	NT	Human papilloma virus type 16, segment 22
1504	11408	21287	2.47	1.1E-01	AJ140933.1	EST_HUMAN	Human papilloma virus type 16, segment 22
2299	12160		2.26	1.1E-01	AF152119	NT	Human papilloma virus type 16, segment 22
2462	12683		1.17	1.1E-01	AF152119	EST_HUMAN	Human papilloma virus type 16, segment 22
2520	12364	22146	1.17	1.1E-01	AF152119	EST_HUMAN	Human papilloma virus type 16, segment 22
2825	12784		1.84	1.1E-01	U03418.1	NT	Human papilloma virus type 16, segment 22
2997	12625	22717	0.8	1.1E-01	F03205.1	EST_HUMAN	Human papilloma virus type 16, segment 22
3296	12625		1.39	1.1E-01	BE303186.1	EST_HUMAN	Human papilloma virus type 16, segment 22
3374	13293	23052	1.34	1.1E-01	BE303186.1	EST_HUMAN	Human papilloma virus type 16, segment 22
3406	13322		1.94	1.1E-01	U03418.1	NT	Human papilloma virus type 16, segment 22
3534	13450	23246	0.84	1.1E-01	U070695.1	NT	Human papilloma virus type 16, segment 22
3948	13592	23246	1.23	1.1E-01	U032708.1	NT	Human papilloma virus type 16, segment 22
4021	13625	23696	1.31	1.1E-01	AF161942.1	EST_HUMAN	Human papilloma virus type 16, segment 22
4021	13625	23696	1.31	1.1E-01	AF161942.1	EST_HUMAN	Human papilloma virus type 16, segment 22

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar Query Hit E-Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4027	13930		0.87	1.1E-01	AF030001.1	NT	Mus musculus major histocompatibility locus class III region/butyrylcholinesterase protein gene, partial cds;
4159	14059		7.93	1.1E-01	AF157069.1	NT	Nolch4, PB2, RAGE, Yeohaido acid acyl transferase-alpha, palmitoyl-protein biosynthesis 2 (PPT2), CREB-RP, and tenascin X (TNX) genes, complete cds
4189	14099	23867	0.8	1.1E-01	AW80209.1	EST_HUMAN	Drosophila melanogaster kareschi protein (kars) mRNA, complete cds
4466	14390	24150	0.81	1.1E-01	AF064564.2	NT	IL5-UM0070-020600-008-008 UN0070 Homo sapiens cDNA
4539	14432	24214	2.02	1.1E-01	S44957.1	NT	Fugu rubripes neurofilament type 1 (NF1), A-kinase anchor protein (AKAP84) BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds
4725	14611	24397	1.26	1.1E-01	Y07965.1	NT	Tupa-1 integral membrane protein TAPA-1 [Tupa, B cell lymphoma line 38C13, Genomic, 1973 nt, segment 1 of 7]
4819	14702	24487	1.26	1.1E-01	D90908.1	NT	A. immsutus gene for transposase
5470	15390		1.49	1.1E-01	AA747216.1	EST_HUMAN	S. yersiniae sp. PCO9803 complete genome, 1027, 1188898-1311234
5562	15478	25551	1.54	1.1E-01	X68851.1	NT	ncv6a03 at NCL CGAP_Ewt Homo sapiens cDNA clone IMAGE:1268140 similar to contains Auv repetitive element/contains element MER33 repetitive element;
5576	15494	25570	4.79	1.1E-01	N68583.1	NT	S. pombe sta8 gene encoding protein kinase
5672	15681	25681	1.46	1.1E-01	A007973.1	NT	Providencia religiosa penicillin G acitase gene
5687	15696	25697	1.70	1.1E-01	BE769152.1	EST_HUMAN	Homo sapiens LGMD2B gene
5697	15698	25709	7.01	1.1E-01	AW805696.1	EST_HUMAN	PM3-F10024-130609-004-12 FT0024 Homo sapiens cDNA
5676	15762	25703	1.30	1.1E-01	AF053746.1	EST_HUMAN	RC3-C10254-260999-011-001 CT0254 Homo sapiens cDNA
5836	15806	26012	3.48	1.1E-01	D69635	SWISSPROT	AF055746 Homo sapiens cDNA clone HSG Homo sapiens cDNA
6027	15931	26198	2.29	1.1E-01	AF032022.1	NT	ACETYLCOENZYME A SYNTHETASE (ACETATE-COALYLASE) (ACYL ACTIVATING ENZYME)
6068	16002	26198	2.21	1.1E-01	AF032022.1	NT	Homo sapiens acetyl A binding protein UNC-182 (UNC-182) mRNA, complete cds
6448	16309	26474	7.05	1.1E-01	BF084623.1	EST_HUMAN	Homo sapiens phosphatidylserine synthase 1 (PS1) mRNA, complete cds
6448	16309	26474	7.05	1.1E-01	BF084623.1	EST_HUMAN	6621409795F1 NM_150246 Homo sapiens cDNA clone IMAGE:4302019 5'
6513	16372	26500	1.74	1.1E-01	F41067	SWISSPROT	6621409795F1 NM_150246 Homo sapiens cDNA clone IMAGE:4302019 5'
6531	16390	26570	3.07	1.1E-01	AW78784.1	EST_HUMAN	TRAB PROTEIN
6777	16658	26845	1.57	1.1E-01	AF049574.1	EST_HUMAN	af049574.1 Scabies parathyroid, human, NHP4, Homo sapiens cDNA clone 1240403 3' similar to gb:U03493
6777	16658	26846	1.57	1.1E-01	AF049574.1	EST_HUMAN	CHROMOGANIN A PRECURSOR (HUMAN);
6803	16682	26872	1.22	1.1E-01	AF07293.1	NT	af049574.1 NCL CGAP_Ewt Homo sapiens cDNA clone IMAGE:943562
6826	16705	26934	1.24	1.1E-01	AW817918.1	EST_HUMAN	af049574.1 NCL CGAP_Ewt Homo sapiens cDNA clone IMAGE:943562
6802	16741	26934	1.78	1.1E-01	AL13446.1	EST_HUMAN	H. sapiens L11 gene
7119	16995	27186	2.19	1.1E-01	U02482.1	NT	PM1-S10270-05020-001-006 S10270 Homo sapiens cDNA
							DNK2p67P194 1' 947 (synonym: ltrtr) Homo sapiens cDNA clone DNK2p67P194 5'
							Pedicularis acedifolia H pedicel pSM674 pedicel ACh production (gap) gene cluster papA, papB, papC and papD genes, complete cds

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Next Similar EST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7228	17105	27204	2.24	1.1E-01	AA192153.1	EST_HUMAN	4P0812.1T Stratiogene muscle 607200 Homo sapiens cDNA clone IMAGE:627743 5'
7228	17105	27205	2.24	1.1E-01	AA192153.1	EST_HUMAN	4P0812.1T Stratiogene muscle 607200 Homo sapiens cDNA clone IMAGE:627743 5'
7287	17163	27352	2.48	1.1E-01	BF080148.1	EST_HUMAN	4P19003.1T Scores test liver sapiens INFLS Homo sapiens cDNA clone IMAGE:108725 3' similar to gk.M8181 SODIUMPOTASSIUM-TRANSPORTING ATPASE BETA-2 (HUMAN);
7467	17327	27362	2.08	1.1E-01	BF080148.1	EST_HUMAN	4P19003.1T Scores test liver sapiens INFLS Homo sapiens cDNA clone IMAGE:108725 3' similar to gk.M8181 SODIUMPOTASSIUM-TRANSPORTING ATPASE BETA-2 (HUMAN);
7851	17711	27361	1.23	1.1E-01	BF080500.1	EST_HUMAN	4P08003.1T Scores placenta N23-HP Homo sapiens cDNA clone IMAGE:147064 3'
8181	13205	22717	1.64	1.1E-01	AF02365.1	EST_HUMAN	HSCHR022 normalized infant brain cDNA Homo sapiens cDNA clone c-1702 3'
8294	18173		3.68	1.1E-01	AF16032.1	NT	Cereulata auratus activin beta A precursor, mRNA, complete cds
8402	18278	28530	2.63	1.1E-01	BC2708.1	EST_HUMAN	4P3812.1T Scores placenta N23-HP Homo sapiens cDNA clone IMAGE:131789 5' similar to contains Alu repetitive elementcontaining TAR1 repetitive element ;
8519	18391	28565	1.66	1.1E-01	X70058.1	NT	M.musculus cyclin gene
8539	18411	28676	3.21	1.1E-01	Y11910.1	NT	Z. mobilis ttd and lg genes encoding RNA guanine transylase and DNA ligase
8539	18411	28677	3.21	1.1E-01	Y11910.1	NT	Z. mobilis ttd and lg genes encoding RNA guanine transylase and DNA ligase
8626	18491	28763	2.79	1.1E-01	P17437	SWISSPROT	SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN)
9241	18958		3.19	1.1E-01	BF07023.1	EST_HUMAN	RG2.NT012:12650.014-03 NT0112 Homo sapiens cDNA
9495	19407		2.06	1.1E-01	BC074566.1	EST_HUMAN	6P19005.01R2 NIH_MGC_33 Homo sapiens cDNA clone IMAGE:345094 3'
9803	19372	25192	2.14	1.1E-01	BF020753.1	EST_HUMAN	6P19005.01R2 NIH_MGC_33 Homo sapiens cDNA clone IMAGE:415488 3'
1183	11094		4.08	1.0E-01	CC0365	SWISSPROT	DEOXYRIBONUCLEASE I (PRECURSOR) (ACID DIASE) (LYSOSOMAL DIASE II)
1251	11158	21007	1.89	1.0E-01	A098469.1	EST_HUMAN	MEER7 repetitive element ;
1370	11278	21132	2.86	1.0E-01	AL161804.2	NT	MEER7 repetitive element ;
2439	12316	22213	1	1.0E-01	AW451035.1	EST_HUMAN	AB244938.1 Human DNA, chromosome 4, coding fragment No. 18
3465	13384	23169	0.98	1.0E-01	BF033981.1	EST_HUMAN	UHHB24.07.01.U151 NC1_CGAP_S185 Homo sapiens cDNA clone IMAGE:2736420 3'
3656	13572	23369	1.01	1.0E-01	BF036911.1	EST_HUMAN	6P16500.01F1 NIH_MGC_361 Homo sapiens cDNA clone IMAGE:385649 5'
3871	13782	23574	2.44	1.0E-01	BF036703.1	EST_HUMAN	6P16500.01F1 NIH_MGC_34 Homo sapiens cDNA clone IMAGE:4154071 5'
4307	14204	23887	1.5	1.0E-01	AL002266.2	NT	Chlamydomonas reinhardtii AR38, section 91 of 94 of the complete genome
4435	14348		1.17	1.0E-01	AT02548.1	EST_HUMAN	6P16500.01F1 NIH_MGC_34 Homo sapiens cDNA clone IMAGE:170038 5'
4613	14501	24289	1.26	1.0E-01	U05490.1	NT	Arceuthobium perfoliatum AR38, section 91 of 94 of the complete genome
4838	14719	24502	2.06	1.0E-01	AW062344.1	EST_HUMAN	EST1364H414 MAC2:resiquinone, Homo sapiens cDNA
5166	15025	24792	0.87	1.0E-01	U040683.1	NT	Mouse F12.1.1 gene
5188	15051	24816	1.44	1.0E-01	BF116933.1	EST_HUMAN	UHHB24.07.01.U151 NC1_CGAP_S185 Homo sapiens cDNA clone IMAGE:3084023 3'
5280	15182		9.16	1.0E-01	U08490.1	EST_HUMAN	2P82904.1 Scores field liver, spleen, INFLS_S1 Homo sapiens cDNA clone IMAGE:410695 3'
5670	15590	25880	11.21	1.0E-01	AF274875.1	NT	Homo sapiens growth factor receptor-bound protein 7 (GRB7) gene, complete cds

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Table 4
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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Mean Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6187	16072			1.8E-01	R23821.1	EST_HUMAN	YF3406.1 Scores placenta NE2:ip Homo sapiens cDNA clone IMAGE:131676 5' similar to canine Au reproductive element
6549	16407		2.45	1.0E-01	Y12488.1	NT	Musculus: wtn gene
7239	17176	27376		1.0E-01	AF102652.2	NT	Rattus norvegicus synaptic SNAP-interacting protein Synonym mRNA, complete cds
7473	17333		1.8	1.0E-01	MF6729.1	NT	Human proelpha-1 (V) coding mRNA, complete cds
7505	17293		2.73	1.0E-01	AE001501.1	NT	Helicobacter pylori, strain J99, section 62 of 132 of fine complete genome
7651	17501	27724	1.84	1.0E-01	BF240154.1	EST_HUMAN	601905861F1 NIH_MGC 84 Homo sapiens cDNA clone IMAGE:4133487 5'
7713	17553	27788	0.08	1.0E-01	AB046799.1	NT	Homo sapiens mRNA for KIAA1879 protein, partial cds
7713	17553	27789	0.08	1.0E-01	AB046799.1	NT	Homo sapiens mRNA for KIAA1879 protein, partial cds
7918	17798	28007	1.28	1.0E-01	BE792750.1	EST_HUMAN	601884604F1 NIH_MGC 7 Homo sapiens cDNA clone IMAGE:3933006 5'
8059	17941		2.02	1.0E-01	AI169122.1	EST_HUMAN	AU159127 THYROT Homo sapiens cDNA clone THYROT00086 3'
8393	18399	28520	2.9	1.0E-01	BF242948.1	EST_HUMAN	601877703F1 NIH_MGC 55 Homo sapiens cDNA clone IMAGE:4106039 5'
8393	18399	28621	2.9	1.0E-01	BF242948.1	EST_HUMAN	601877703F1 NIH_MGC 55 Homo sapiens cDNA clone IMAGE:4106039 5'
8703	18621	28803	4.43	1.0E-01	BE790543.1	EST_HUMAN	601905556F1 NIH_MGC 7 Homo sapiens cDNA clone IMAGE:3934734 5'
9026	19235		2.6	1.0E-01	BE337719.1	EST_HUMAN	601905556F1 NIH_MGC 7 Homo sapiens cDNA clone IMAGE:3461933 5'
9463	19305		1.34	1.0E-01	7652185	NT	Homo sapiens KIAA0514 gene product (KIA00514), mRNA
9498	19309		2.03	1.0E-01	7652185	NT	Drosophila melanogaster fz gene
9738	19388		2.57	1.0E-01	U52891.1	NT	Gonadotropin-releasing hormone type-1 receptor (GR1) mRNA, complete cds
9815	19534		2.46	1.0E-01	U69534.1	EST_HUMAN	601905556F1 NIH_MGC 10 Homo sapiens cDNA clone IMAGE:3461933 5'
9871	19560	25187	3.69	1.0E-01	U69534.1	NT	Shachnon1005a, an immediate suppressor of IAP1 (SAGE) gene, complete cds
9877	19563		1.28	1.0E-01	AJ271049.1	NT	Zea mays mRNA for TACO2-2 protein (TACO2) gene, complete cds
			4.16	1.0E-01	AJ001507.1	NT	Banana habuans genome DNA, section 1714
						NT	Drosophila melanogaster cAMP-dependent protein kinase type II regulatory subunit (pla-R1) mRNA, complete cds
2762	12814	22505	1.09	9.8E-02	AF274088.1	NT	601907021F1 NIH_MGC 12 Homo sapiens cDNA clone IMAGE:3465905 5'
2767	12819	22811	1.44	9.8E-02	BE548564.1	EST_HUMAN	601907021F1 NIH_MGC 12 Homo sapiens cDNA clone IMAGE:3465905 5'
2767	12819	22812	1.44	9.8E-02	BE548564.1	EST_HUMAN	601907021F1 NIH_MGC 12 Homo sapiens cDNA clone IMAGE:3465905 5'
2950	12877	22875	0.92	9.8E-02	AV730747.1	EST_HUMAN	AY300747 HTP Homo sapiens cDNA clone HTBN005 5'
3229	13163	22952	1.16	9.8E-02	AF096810.1	NT	Homo sapiens neuron III-alpha gene, partial cds
4682	14472	24280	22.65	9.8E-02	BE574248.1	EST_HUMAN	7677612X1 NC1 CGAT L242 Homo sapiens cDNA clone IMAGE:3278938 3'
6151	15118	24802	7.86	9.8E-02	BE574248.1	EST_HUMAN	Aggrecan1, human BSO mRNA for BSLC101 S domain, complete cds
7332	17298	27440	1.56	9.8E-02	D33710.1	NT	Mus musculus phospholipid transfer protein (Plp), mRNA
651	10492		1.69	9.8E-02	X69338.1	NT	O salivary RAmysG gene for alpha-tryptase
1711	11612	21482	1.53	9.8E-02	4803224	NT	Homo sapiens cytochrome P450, sulfamylase (CYP2E1) mRNA
3108	13032	22827	3.28	9.8E-02	AF184271.1	NT	Daucus carota leucoanthonylin dihydroxylase 2 (LDOX) mRNA, LDOX-2 allele, complete cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
4131	14031	23605	0.07	9.5E-02	AF257329.1	NT	Leptothorax maculatus beta-tubulin mRNA, complete cds
4131	14031	23606	0.07	9.5E-02	AF257329.1	NT	Leptothorax maculatus beta-tubulin mRNA, complete cds
8755	17604	29148	2.1	9.5E-02	BF037421.1	EST_HUMAN	X0160735F1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:254788 3'
1328	11235	21062	1.19	9.7E-02	AB005608.1	NT	Alba albicincta mRNA for MDP-male enzyme, complete cds
1567	11471		0.86	9.7E-02	4603710	NT	Homo sapiens fibroblast growth factor receptor 3 (schachtdiopsis, then adophoric dwarfism) (FGFR3) mRNA
2214	12100	22004	2.37	9.7E-02	BE168900.1	EST_HUMAN	CEL-HT0516-070300-06-204 HT0516 Homo sapiens cDNA
3901	13811	25679	3.59	9.7E-02	BE168900.1	SWISSPROT	CEL SURFACE A33 ANTIGEN PRECURSOR (GLYCOPROTEIN A33)
5081	15572	25609	1.39	9.7E-02	AN054478.1	EST_HUMAN	EST366546 IMAGE:254788, MGC Homo sapiens cDNA
5321	18184	28345	4.27	9.7E-02	295118.1	NT	Bacillus subtilis complete genome (accession 16 of 21) from 2867771 to 3213440
8655	19335	26731	1.59	9.7E-02	127098.1	EST_HUMAN	X414083.1 Wistar-Kyoto Rat Embryo Kidney Homo sapiens cDNA clone IMAGE:254788 3'
8655	19335	26732	1.59	9.7E-02	127098.1	EST_HUMAN	X414083.1 Wistar-Kyoto Rat Embryo Kidney Homo sapiens cDNA clone IMAGE:254788 3'
7137	17044	27207	1.32	9.7E-02	A935984.1	EST_HUMAN	PERDYL-PROLYL-45S-TRANS ISOMERASE A (HUMAN)
8831	15403		1.97	9.7E-02	U6337.1	NT	Mus musculus Igkappa (Igk) mRNA, partial cds
1989	11882	21763	1.27	9.5E-02	U630721.1	EST_HUMAN	024711.1 x1 Soares NIH-MGC_51 Homo sapiens cDNA clone IMAGE:167485 3'
1989	11882	21764	1.27	9.5E-02	U630721.1	EST_HUMAN	024711.1 x1 Soares NIH-MGC_51 Homo sapiens cDNA clone IMAGE:167485 3'
4246	14147	23821	0.02	9.5E-02	U63062.1	NT	Protein mirabilis fibrillar operon, strain H1830
4632	14810	24759	0.64	9.5E-02	AB019620.1	EST_HUMAN	EST378303 IMAGE:254788, MGC Homo sapiens cDNA
5713	15321		2.72	9.5E-02	BE011039.1	EST_HUMAN	RC3-870254-031086-011-403 310254 Homo sapiens cDNA
7602	17371	27960	1.91	9.5E-02	AB019881.1	EST_HUMAN	X0160808F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:391803 5'
7077	17622	27685	1.84	9.5E-02	BE091695.1	EST_HUMAN	X0143008F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:391803 5'
7772	17622	27686	1.76	9.5E-02	AJ343211.1	NT	Homo sapiens DMBT1 candidate tumour suppressor gene, exons 1 to 85
7839	17689	27633	1.59	9.5E-02	AB019365.1	NT	Arthrinium majus transcript Tm3 pseudogene for transcriptase (in S-5 copy)
7839	17689	27634	1.59	9.5E-02	AB019365.1	NT	Arthrinium majus transcript Tm3 pseudogene for transcriptase (in S-5 copy)
7898	17736	27660	3.29	9.5E-02	P08174	SWISSPROT	COMPLEMENT DEACCELERATING FACTOR PRECURSOR (CD55)
8125	18013	26230	0.51	9.5E-02	276702.1	NT	Myobacterium tuberculosis H37Rv complete genome, segment 1027162
9897	16794	29056	1.8	9.5E-02	AA028755.1	EST_HUMAN	y019701.1 x1 Soares, testis, NIH Homo sapiens cDNA clone IMAGE:48362 3'
9759	19312		1.38	9.5E-02	HE14599.1	EST_HUMAN	y019701.1 x1 Soares, infant brain NIH Homo sapiens cDNA clone IMAGE:48363 3'
9846	19344	29212	1.26	9.5E-02	BE126718.1	EST_HUMAN	y019701.1 x1 Soares, infant brain NIH Homo sapiens cDNA clone IMAGE:3532808 5'
4012	13918	23894	2.25	9.5E-02	AN062365.1	EST_HUMAN	QW2-BN0023-050200-067-172 BN0023 Homo sapiens cDNA
5002	14932	24704	0.87	9.5E-02	U6337.1	NT	Lycopodium obscurum polygalacturonase isoenzyme 1 beta subunit, gene, complete cds

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expectation Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
6323	16186	29348	3.72	9.5E-02	A60034.73.1	NT	Timecourse liverdisea DNA for Phospholipase A2 inhibitor, complete cds
6467	16378	29454	7.46	9.5E-02	A611539.2	EST_HUMAN	Arachidonic (all)acid: NIH, MGC, 66 Homo sapiens cDNA clone IMAGE:3857243.8
6509	16479	28966	2.59	9.5E-02	E01033961.1	EST_HUMAN	8014536240F1 NIH, MGC, 66 Homo sapiens cDNA clone IMAGE:3857243.8
6566	16470	29067	2.69	9.5E-02	E01033961.1	EST_HUMAN	8014536240F1 NIH, MGC, 66 Homo sapiens cDNA clone IMAGE:3857243.8
6966	17627	29205	3.29	9.5E-02	E01033961.1	EST_HUMAN	8014536240F1 NIH, MGC, 66 Homo sapiens cDNA clone IMAGE:3857243.8
8066	17687	28267	3.28	9.5E-02	E01033961.1	EST_HUMAN	8014536240F1 NIH, MGC, 66 Homo sapiens cDNA clone IMAGE:3857243.8
1702	17693	21969	3.86	9.4E-02	E01033961.1	EST_HUMAN	8021508625F1 NIH, MGC, 61 Homo sapiens cDNA clone IMAGE:3857243.8
1820	17177	21997	2.197	9.4E-02	E01033961.1	NT	Capitellus parvulus 3'-hydroxysteroid sulfotransferase mRNA, complete cds
1820	17177	21998	0.96	9.4E-02	E01033961.1	NT	Capitellus parvulus 3'-hydroxysteroid sulfotransferase mRNA, complete cds
3804	13716	23804	4.34	9.4E-02	Z330494.1	NT	Macropodius DNA for CONTIC MC073
4990	14855	24621	0.99	9.4E-02	E783517	NT	Mac musculus coding region determinant-binding protein (C-deb), mRNA
6966	16976		2.62	9.4E-02	Z46893.1	NT	Kichnelelela sp. ocdm, lys3, rubA, rubB, eubB, coxR3, ptk, migA, ORF2 and ORF3 genes
8304	16538	26505	2.89	9.4E-02	Z748833.1	NT	Human BRCA1, Rho7 and xell genes, complete cds, and p185 ras, p185 ras
9083	19093		3.36	9.4E-02	U51815.1	NT	Rattus norvegicus calcium channel alpha1C subunit (RCA1C) mRNA, partial cds
9443	19411	25182	1.42	9.4E-02	U27699.1	NT	Human papilloma11, bovine-Qbeta transporter mRNA, complete cds
12601	12887		1.83	9.3E-02	4900296	NT	Human sapiens BAIT-associated protein 3 (BAUP3) mRNA
2963	12921		5.39	9.3E-02	6912826	NT	Human sapiens BAIT-associated protein 3 (BAUP3) mRNA
3278	13142	22946	2.03	9.3E-02	E01033961.1	EST_HUMAN	8021330406F1 NIH, MGC, 61 Homo sapiens cDNA clone IMAGE:3858269.9
1387	13847		1.98	9.3E-02	E01033961.1	EST_HUMAN	8021330406F1 NIH, MGC, 61 Homo sapiens cDNA clone IMAGE:3858269.9
4080	13962	23758	3.51	9.3E-02	BE391843.1	EST_HUMAN	8012986057F1 NIH, MGC, 44 Homo sapiens cDNA clone IMAGE:3807653.9
4000	13982	23739	3.51	9.3E-02	BE391843.1	EST_HUMAN	8012986057F1 NIH, MGC, 44 Homo sapiens cDNA clone IMAGE:3807653.9
4628	14916		1.88	9.3E-02	AV732224.1	EST_HUMAN	AV732224.1 H1F Homo sapiens cDNA clone HTFAUA03.0
7599	17496	27666	2.24	9.3E-02	BE462031.2	EST_HUMAN	80165888R1 NIH, MGC, 66 Homo sapiens cDNA clone IMAGE:3865991.3
7755	17705	27949	3.52	9.3E-02	Q15084	SWISSPROT	HYPOTEL-1 (HYPOTEL) protein KIAA0032
7855	17760		3.52	9.3E-02	Q15084	SWISSPROT	HYPOTEL-1 (HYPOTEL) protein KIAA0032
7913	17763	27950	3.74	9.3E-02	AW208117.1	EST_HUMAN	U01811-actin-05-DJ1-ET1 NC1, CGAP, Sub3 Homo sapiens cDNA clone IMAGE:2729553.3
9343	19527		1.85	9.3E-02	AJ249850.1	NT	Phorbolactone dimerase subsp. dimerase partial g7B3 gene for DNA gyrase S subunit
9704	19555		8.62	9.3E-02	AW48850.1	EST_HUMAN	nt289112.21 Scores, NFE..._T_GBC S1 Homo sapiens cDNA clone IMAGE:2911087.3
9806	19602		1.95	9.3E-02	AF100595.1	NT	Mus musculus major histocompatibility locus class II region; Fas-binding protein Daxx (DAXX) gene, partial cds, Bhrn1 (BING1), leucine (leasin), RAGG3s the factor (RLF), KE2 (KE2), BING4 (BING4), beta1, 3-galactosyl transferase (beta2-3-galactosyl tr
228	19197	20018	4.36	9.2E-02	U60315.1	NT	Molluscan contagium virus subtyp 1, complete genome
228	19197	20019	4.32	9.2E-02	U60315.1	NT	Molluscan contagium virus subtyp 1, complete genome
228	19197	20019	4.32	9.2E-02	U60315.1	NT	Molluscan contagium virus subtyp 1, complete genome
228	19197	20019	4.32	9.2E-02	U60315.1	NT	Molluscan contagium virus subtyp 1, complete genome

Table 4

Probe SEQ ID NO.	Even SEQ ID NO.	ORF SEQ ID NO.	Expression	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
2180	12687		2.2	9.2E-02	R61456.1	EST_HUMAN	y58007.1 Source infant brain INIB Homo sapiens cDNA clone IMAGE:47618.5'
3142	13087	22886	4.93	9.2E-02	Q26833	SWISSPROT	MAJOR EPIDIDYMUS SPECIFIC PROTEIN EA (EPIDIDYMAL PROTEIN BE-2)
3265	13368	22886	1.18	9.2E-02	A035434.1	EST_HUMAN	HFAO21.1 NCL CGAP_Col Homo sapiens cDNA clone IMAGE:528130.3
3357	13483		1.12	9.2E-02	6785218	NT	Mus musculus psc-1 rat antigen receptor alpha (P.rta) mRNA
4141	14048		1.34	9.2E-02	U02044.1	NT	Human preproinsulin I (beta 1-KD)-53, insulin-associated transcript; promoter region
4211	14109		1.02	9.2E-02	E529722.1	EST_HUMAN	B000438591 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:506070.5'
4538	14431	24213	1.86	9.2E-02	X09402.1	NT	C.gallus HSP gene
6670	16550	26748	1.86	9.2E-02	T16920.1	EST_HUMAN	y66009.1 Stratagene placenta (#637225) Homo sapiens cDNA clone IMAGE:68808.5' similar to similar to g-x56009 GUANINE NUCLEOTIDE-BINDING PROTEIN G(S), ALPHA SUBUNIT (HUMAN)
6760	16535	26823	2.07	9.2E-02	X09256.1	NT	H.vulgare xylose isomerase gene
4177	9884	19776	2.77	9.1E-02	A77966.1	NT	O. cuniculus T12 testis gene
2360	13583	22739	1.01	9.1E-02	P77868.5	SWISSPROT	R-PHOSPHOFRUCTOKINASE (PHOSPHOFRUCTOKINASE)
3678	13532		1.14	9.1E-02	A1W37869.1	EST_HUMAN	PM21073436-161595-007-E02 BT0340 Homo sapiens cDNA
4363	14279	24056	1.81	9.1E-02	AL161654.2	NT	Arbidopate Italiana DNA chromosome 4, contig fragment Nm_54
5807	15425	25487	1.73	9.1E-02	AF129756.1	NT	Homo sapiens MSH45 gene, partial cds; and CLC1, DDAH, Gdb, Gdb, Gdb, Gdb, BAT5, Gdb,
6372	16434	28383	11.80	9.1E-02	AW10068.1	EST_HUMAN	CSX28.5, BAT4, Gd, Apo M, BAT3, BAT2, AIF-1, 1C7, LST1, LTB, TNF, and 'LTA genes: complete cds
7956	17908		1.06	9.1E-02	T02984.1	EST_HUMAN	AY14065.1 Schaefer fetal brain 00004 Homo sapiens cDNA clone IMAGE:2751988.5'
2021	18615		1.29	9.1E-02	9633349.1	NT	BT016910 Fetal brain, Strathgery Homo sapiens cDNA clone BT016910 3' end
						NT	Bacteriophage M1, complete genome
9256	19832		1.82	9.1E-02	AA179601.1	EST_HUMAN	zwNTR12.51 Strathgery muscle 873209 Homo sapiens cDNA clone IMAGE:317783.3' similar to
9785	19548		5.63	9.1E-02	AJ201390.1	NT	SV-TRT3_HUMAN P45378 TROPONIN T, FAST SKELETAL MUSCLE, ISOFORM BETA ; Homo sapiens partial MYC3B gene for MYC3B much, exons 1-11
727	10650	20460	3.36	9.0E-02	P13328	SWISSPROT	FOLATE RECEPTOR ALPHA PRECURSOR (RR-ALPHA) (FOLATE RECEPTOR 1) (FOLATE RECEPTOR, ADULT) (ADULT FOLATE-BINDING PROTEIN) (FBP) (OVARIAN TUMOR-ASSOCIATED ANTIGEN MOV18) (KB cells FBP)
						EST_HUMAN	h036910.x1 NCL_CGAP_Lyx1 Homo sapiens cDNA clone IMAGE:3175842.3' similar to contains Aliu repetitive element;
1617	11821	21376	6.45	9.0E-02	BE220482.1	EST_HUMAN	HYV-1 pb0056-06 from USA envelope glycoprotein (env) gene, partial cds
2772	12634	22526	1.11	9.0E-02	AF136522.1	NT	HYV-1 pb0056-06 from USA envelope glycoprotein (env) gene, partial cds
2772	12634	22520	1.11	9.0E-02	AF136522.1	NT	Dyskalemia cloniding sperm coat structural protein SP55 (Gd) gene, complete cds
3294	13216	23016	0.92	9.0E-02	AF270195.1	NT	Corynebacterium diphtheriae glabinin (Salimti solvaceus-jarvis montages, linc. mRNAs, 1474 nt)
4202	14101	23983	0.8	9.0E-02	S68757.1	NT	Corynebacterium diphtheriae glabinin (Salimti solvaceus-jarvis montages, linc. mRNAs, 1474 nt)
4202	14101	23984	0.8	9.0E-02	S68757.1	NT	Corynebacterium diphtheriae glabinin (Salimti solvaceus-jarvis montages, linc. mRNAs, 1474 nt)
4321	14218	24001	1.2	9.0E-02	P65568	SWISSPROT	LAMININ BETA-2 CHAIN PRECURSOR (SLAMFINN)

Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Mean Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4558	14480	24248	1.79	9.0E-02	U65740.2	NT	Plasmodium falciparum P-type ATPase 3 gene
5142	13009	24790	1.06	9.0E-02	U24587	SWISSPROT	REGULATORY PROTEIN ZESTIE
5647	15590	25653	8.02	9.0E-02	U95037.1	EST_HUMAN	zsf88b2.11 Soares, Jial, Jinq, Noh-H, 19W Homo sapiens cDNA clone IMAGE:287694 5' similar to
5647	13428	25653	15.35	9.0E-02	U1431750	NT	PR-552171 Soares, Jial, Jinq, Noh-H, 19W Homo sapiens cDNA clone IMAGE:428561 5'
1419	11325	21189	2.15	8.6E-02	BF701953.1	EST_HUMAN	602125030F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:428561 5'
1419	11325	21190	2.15	8.6E-02	BF715953.1	EST_HUMAN	602125030F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:428561 5'
2338	12218	22117	1.41	8.6E-02	BE153572.1	EST_HUMAN	PMK-HT0339-251189-003-401 HT0339 Homo sapiens cDNA
4104	14004		1.71	8.6E-02	AF39055.1	NT	Antichem angustatum AtanFlaz protein (AtanFlaz) gene, partial cds
4834	14427	24208	0.92	8.6E-02	AA424887.1	EST_HUMAN	zsf33b3.41 Soares, NHIHUP, S1 Homo sapiens cDNA clone IMAGE:761190 3'
5565	15485	24559	3.3	8.6E-02	AW452123.1	EST_HUMAN	UHHB8-4b-0490-L1 s1 NCI_OGAP_S1b5 Homo sapiens cDNA clone IMAGE:3065294 3'
5565	15485	24559	3.3	8.6E-02	AW452122.1	EST_HUMAN	UHHB8-4b-0490-L1 s1 NCI_OGAP_S1b5 Homo sapiens cDNA clone IMAGE:3065294 3'
5576	15491	24559	3.13	8.6E-02	U1453478	NT	Homo sapiens similar to endoglycan (H. sapiens) (U0683107), mRNA
8270	18135	26290	1.56	8.9E-02	P47259	SWISSPROT	FOLD BIRINGTIONAL PROTEIN (INCLUDES: METHYLENTEFRAHYDROFOLATE
8460	18320	26290	1.83	8.9E-02	U70024.1	NT	DEHYDROGENASE: METHYLENTEFRAHYDROFOLATE CYCLOHYDROLASE]
8928	18976	27068	8.28	8.9E-02	AA302510.1	EST_HUMAN	H. sapiens flow-sorted chromosome 8 HindIII fragment, SC9P4.30F8
9238	18916		4.03	8.9E-02	BE090918.1	EST_HUMAN	EST180187 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' and
1351	11257	21113	1.25	8.9E-02	U27474	SWISSPROT	602125083F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285180 5'
3826	13740	24332	0.95	8.9E-02	AC36726.1	EST_HUMAN	PROGABILE DNA LIGASE (POLYDEOXYRIBONUCLEOTIDE SYNTHASE ATP)
3946	13866		3.24	8.9E-02	U00289	SWISSPROT	EST11566 Liver Homo sapiens cDNA 5' and
4205	14104		1.13	8.9E-02	450425	NT	TRANSCRIPTION INITIATION FACTOR TRID 135 KDA SUBUNIT (TAH135) (TAH130)
7195	17072	27260	1.83	8.9E-02	AA15187.21	EST_HUMAN	Homo sapiens period box gene 6 (aridra, Venalis) (PAX6), isoform b, mRNA
8481	18334	25697	3.19	8.9E-02	BE294485.1	EST_HUMAN	zsf88b3.11 Stratagene codon (60372A) Homo sapiens cDNA clone IMAGE:565288 3'
8481	18334	25697	3.19	8.9E-02	BE294485.1	EST_HUMAN	601191707F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:565288 3'
8895	18453	28722	10.63	8.9E-02	AL040726.1	EST_HUMAN	DNFZ73434D1313_1 434 (synonym: hies3) Homo sapiens cDNA clone DNFZ73434D1313 5'
9802	19001	25532	1.38	8.9E-02	U71861.1	NT	S. cerevisiae chromosome XIV reading frame ORF YNL286W
3639	13550	25337	3.02	8.7E-02	U83064.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28TS protein (XQ28ORF), and biglycan (BGN) genes, complete cds, and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
3639	13550	25339	3.02	8.7E-02	U83065.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28TS protein (XQ28ORF), and biglycan (BGN) genes, complete cds, and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Max Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3879	13790	23578	0.82	8.7E-02	M87641.1	EST_HUMAN	zfr56a/2.71 Soares, fetal liver, spleen, INHLS_S1 Homo sapiens cDNA clone IMAGE:417104 5' similar to cordless element MER12 repetitive element;
4609	14407	24296	1.22	8.7E-02	AF176936.1	NT	Mus musculus JNK interacting protein-3a (Jip3) mRNA, complete cds
5034	14906		1.09	8.7E-02	AE000605.1	NT	Melanoblastic thermotaxis factor from bases 1176187 to 1184005 (section 101 of 148) of the complete genome
5245	15177	24951	5.41	8.7E-02	AA286875.1	EST_HUMAN	z555905.at NC1 CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701438 3'
5255	15177	24952	5.41	8.7E-02	AA286875.1	EST_HUMAN	z555905.at NC1 CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701438 3'
8094	17965		2.56	8.7E-02	L04758.1	NT	Oryzopsis carolinensis cytochrome P-450 (CYP4A4) gene, 5' end
8831	18426	28770	1.77	8.7E-02	AJ007783.1	NT	Glucobacter oxydans RNA-ile and RNA-Ale genes
9263	18924		2.58	8.7E-02	X17116.1	NT	Human DNA for immunoglobulin alpha heavy chain from a case of alpha heavy chain disease
9484	19105		1.81	8.7E-02	697027	NT	Mus musculus nitroden 2 (N2d2), mRNA
1232	11139	20691	7.05	8.6E-02	AJ271795.1	NT	Homo sapiens Xu pseudobulbar region, segment 22
2197	12084	21086	2.22	8.6E-02	BE408507.1	EST_HUMAN	501804016F1 NIH MGCC 21 Homo sapiens cDNA clone IMAGE:3638443 5'
3191	13076	22676	2.94	8.6E-02	U04683.1	NT	Tribolium repleta beta-tubulin (tub2) gene, complete cds
3593	13907		3.07	8.6E-02	AF183862.1	NT	Drosophila melanogaster embryonic lethal (elb) gene, complete cds
4395	14261	24090	0.87	8.6E-02	U09178.1	NT	Oryzopsis carolinensis cytochrome-3 gene, unrelated exon and 5' flanking region
5709	15816	25718	4.89	8.6E-02	V10383.1	NT	Homo sapiens LON1b gene
5846	15752	25887	1.51	8.6E-02	U04401.1	NT	Mus musculus p34 chain gene, D region; D-352, mus switch region (part a)
5848	15752	25888	1.51	8.6E-02	U04401.1	NT	Mus musculus p34 chain gene, D region; D-352, mus switch region (part b)
6228	16308	25935	1.26	8.6E-02	5750096	NT	Homo sapiens Spz-related CBP activator protein (SROAP) mRNA
6228	16308	25936	1.26	8.6E-02	5750096	NT	Homo sapiens Spz-related CBP activator protein (SROAP) mRNA
8315	18192	28441	1.98	8.5E-02	AF208551.1	NT	Luciferia media cytochrome c oxidase subunit 1 gene, partial cds; mitochondrial gene for mitochondrial product
8315	18192	28441	1.98	8.5E-02	AF208551.1	NT	Luciferia media cytochrome c oxidase subunit 1 gene, partial cds; mitochondrial gene for mitochondrial product
8574	18442	28770	3.63	8.5E-02	BF069005.1	EST_HUMAN	501804337F1 NIH MGCC 17 Homo sapiens cDNA clone IMAGE:4198216 5'
8574	18442	28771	3.63	8.5E-02	BF069005.1	EST_HUMAN	501804337F1 NIH MGCC 17 Homo sapiens cDNA clone IMAGE:4198216 5'
8736	17867	28131	4.71	8.5E-02	AE001075.1	NT	Archaeobacter fulgidus section 34 of 172 of the complete genome
8858	18970	28658	1.79	8.5E-02	AF285960.1	NT	Bacillus stearothermophilus Esf1 methylase (Fim) and Esf1 restriction endonuclease (FIR) genes, complete cds
2347	12227	25124	2.87	8.5E-02	AE000652.1	NT	Helicobacter pylori 26995 section 130 of 134 of the complete genome
5901	15419		1.8	8.5E-02	P00089	SWISSPROT	W PROTEIN, SEROTYPE 6 PRECURSOR
5956	15370	25965	5.94	8.5E-02	AF233885.1	NT	Mus musculus phosphatase C-iso protein mRNA, partial cds
7003	16880	27072	1.63	8.5E-02	6754776	NT	Mus musculus myosin XV (Myo15), mRNA

Single Exon Probes Expressed in Heart
Table 4

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Max Similar EST/HT BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7661	17511	27737	3.07	8.3E-02	BE93054.1	EST_HUMAN	RC4-OT0037-260700-014-c05 OT0037 Homo sapiens cDNA
7661	17511	27738	3.07	8.3E-02	BE933054.1	EST_HUMAN	RC4-OT0037-260700-014-c05 OT0037 Homo sapiens cDNA
8406	18389		11.16	8.3E-02	AF155910.1	NT	Homo sapiens heparinase precursor, mRNA, complete cds
8512	18384	28649		8.3E-02	AB001562.1	NT	Streptococcus mutans gene for glucose-1-phosphate uridylyltransferase, complete cds
9847	18498		1.39	8.3E-02	AB000996.1	NT	Anthraxium majus mRNA for MYB-related transcription factor
9847	18339		3.26	8.3E-02	AA36234.1	EST_HUMAN	EST12726 Ovary II Homo sapiens cDNA 9' and
2632	12726	22831	4.24	8.4E-02	W69300.1	EST_HUMAN	244411-1 Soares, fetal, heart, NRH19W Homo sapiens cDNA clone IMAGE:343632 5'
5253	15175	26446	7.82	8.4E-02	BE267153.1	EST_HUMAN	501190439F1 NIH, MGC, 7 Homo sapiens cDNA clone IMAGE:3534393 5'
6019	15923	26053	1.71	8.4E-02	AK024483.1	NT	Homo sapiens mRNA for FLJ00050 protein, partial cds
6380	16500	26765	8.11	8.4E-02	BE069074.1	EST_HUMAN	565910-1 Barreled colon HP1687 Homo sapiens cDNA
7631	17761	28020	1.44	8.4E-02	AI735184.1	EST_HUMAN	Q88312 GQB-4, ;
1695	11859	21748	0.86	8.3E-02	5835680	NT	Isodias heteropus mitochondrion, complete genome
1695	11859	21748	0.86	8.3E-02	5835680	NT	Isodias heteropus mitochondrion, complete genome
3544	13480	23024	5.19	8.3E-02	P70334	SWISSPROT	HYPOTHETICAL PROTEIN UG399 HOMOLOG PRECURSOR
3567	13481	23271	0.88	8.3E-02	AI067097.1	EST_HUMAN	182295.1 Soares, NHMPL, S1 Homo sapiens cDNA clone IMAGE:2126210 3'
3567	13481	23272	0.88	8.3E-02	AI067097.1	EST_HUMAN	182295.1 Soares, NHMPL, S1 Homo sapiens cDNA clone IMAGE:2126210 3'
5840	13748	25866	2.83	8.3E-02	AF063893.1	NT	Homo sapiens proto-oncogene, 3' gene, exon 1
5853	15353	26778	3.42	8.3E-02	AF150787.1	NT	Rattus norvegicus dysembryonecton-related protein 2 A-form splice variant (Dn2) mRNA, complete cds
6871	16551		1.47	8.3E-02	AA95285.1	EST_HUMAN	965408.1 NC1, GQAP, 14615 Homo sapiens cDNA clone IMAGE:145422 3' similar to L1.1 L1 L1
8426	16708		1.42	8.3E-02	AA961873.1	EST_HUMAN	965408.1 NC1, GQAP, 14615 Homo sapiens cDNA clone IMAGE:145422 3' similar to L1.1 L1 L1
7468	17388	27573	1.44	8.3E-02	AF165503.1	EST_HUMAN	965408.1 NC1, GQAP, 14615 Homo sapiens cDNA clone IMAGE:145422 3' similar to L1.1 L1 L1
7506	17394		1.94	8.3E-02	AL101565.2	NT	965408.1 NC1, GQAP, 14615 Homo sapiens cDNA clone IMAGE:145422 3' similar to L1.1 L1 L1
9507	19698		1.66	8.3E-02	BE966498.1	EST_HUMAN	965408.1 NC1, GQAP, 14615 Homo sapiens cDNA clone IMAGE:145422 3' similar to L1.1 L1 L1
1367	11283		7.82	8.2E-02	U05170.2	NT	965408.1 NC1, GQAP, 14615 Homo sapiens cDNA clone IMAGE:145422 3' similar to L1.1 L1 L1
1480	11385	21248	1.21	8.2E-02	AF150777.2	NT	965408.1 NC1, GQAP, 14615 Homo sapiens cDNA clone IMAGE:145422 3' similar to L1.1 L1 L1
3092	12804		1.78	8.2E-02	AL103206.2	NT	965408.1 NC1, GQAP, 14615 Homo sapiens cDNA clone IMAGE:145422 3' similar to L1.1 L1 L1
3733	13946		1.26	8.2E-02	AL101483.2	NT	965408.1 NC1, GQAP, 14615 Homo sapiens cDNA clone IMAGE:145422 3' similar to L1.1 L1 L1
3626	13835	23616	1.11	8.2E-02	AL103206.2	NT	965408.1 NC1, GQAP, 14615 Homo sapiens cDNA clone IMAGE:145422 3' similar to L1.1 L1 L1
4187	14087	23862	5.36	8.2E-02	P44960	SWISSPROT	965408.1 NC1, GQAP, 14615 Homo sapiens cDNA clone IMAGE:145422 3' similar to L1.1 L1 L1
4187	14087	23863	5.36	8.2E-02	P44960	SWISSPROT	965408.1 NC1, GQAP, 14615 Homo sapiens cDNA clone IMAGE:145422 3' similar to L1.1 L1 L1
4187	14087	23864	5.36	8.2E-02	P44960	SWISSPROT	965408.1 NC1, GQAP, 14615 Homo sapiens cDNA clone IMAGE:145422 3' similar to L1.1 L1 L1

Single Exon Probes Expressed in Heart

Probe SEQ ID: NO:	Exon SEQ ID: NO:	CDS SEQ ID: NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top III Annotation No.	Top Hit Database Source	Top Hit Descriptor
5014	14988	24655	2.82	8.2E-02	U76090.1	NT	Mus musculus zinc transporter (Znt-3) gene, complete cds
5271	15193	24988	1.43	8.2E-02	B6807030.1	EST_HUMAN	Hs145709Ft NIH MGCC, 72 Homo sapiens cDNA clone IMAGE:392453 5'
5188	16073	26222	3.18	8.2E-02	AFC90565.1	NT	Bov testicular tissue growth factor precursor (GFH) gene, complete cds
7094	16071	27568	3.13	8.2E-02	X18167528.1	EST_HUMAN	RCP-TF0002-031252-011-005 PT0001 Homo sapiens cDNA
7536	17387	27958	5.33	8.2E-02	A04187.1	EST_HUMAN	Bact nematode yellow vein virus RNA-2
7628	17479	27660	2.11	8.2E-02	BE25493.8	EST_HUMAN	Hs119505Ft NIH MGCC, 16 Homo sapiens cDNA clone IMAGE:335558 5'
8314	19000	26336	4.13	8.2E-02	AE002248.2	EST_HUMAN	Chlamydia pneumoniae AR39, section 73 of the complete genome
9706	19490		1.84	8.2E-02	AF275366.1	NT	Mus musculus epididymal growth factor receptor (Egrf) gene, exons 5 through 28, and complete cds, alternatively spliced
1479	11384	21247	1.72	8.1E-02	AB071381.1	NT	Pseudomonas maltophilia decarboxylase gene cluster (mdcA, mdcB, mdcC, mdcD, mdcE, mdcG, mdmB, mdmC, and mdmM) genes, complete cds
7763	17653		1.85	8.1E-02	A7005150.1	NT	Human sarcoma osteoblastic glycoprotein luciferin precursor, gene, complete cds
8769	18004	28894	3.38	8.1E-02	AL163202.2	EST_HUMAN	Homo sapiens chromosome 21 segment HS21T002
5	12657	19784	3.28	8.0E-02	AF019483.1	EST_HUMAN	EST3366723 MAGE sequences, MAGE Homo sapiens cDNA
920	10844	20960	1.33	8.0E-02	U08316.1	NT	Mallacium conglagatum virus subtype 1, complete genome
1871	12701	21440	10.54	8.0E-02	D26536.1	NT	Human gene for dihydrobioamide succinyltransferase, complete cds (exon 1-15)
1871	12701	21440	10.54	8.0E-02	D26536.1	NT	Human gene for dihydrobioamide succinyltransferase, complete cds (exon 1-15)
1891	12701	21632	3.9	8.0E-02	BC040719.1	EST_HUMAN	PKB-BT0347-170300-001-508 BT0347 Homo sapiens cDNA
2323	12204	22103	1.01	8.0E-02	D00916.1	EST_HUMAN	Synchochrysis sp. PC05803 complete genome, 11/27, 2137256-2367256
2323	12204	22104	1.01	8.0E-02	D00916.1	EST_HUMAN	Synchochrysis sp. PC05803 complete genome, 11/27, 2137260-2267259
2221	12208	22241	4.08	8.0E-02	BF246744.1	EST_HUMAN	Hs105545Ft NIH MGCC, 57 Homo sapiens cDNA clone IMAGE:071810 5'
2221	12208	20833	0.91	8.0E-02	M23-49.1	NT	Dkysomycin-associated cyclic nucleotide phosphodiesterase gene, complete cds
2870	10991	21901	0.91	8.0E-02	AL445007.1	NT	Thermoplasma acidophilum complete genome, segment 3/5
2870	12707	22591	1.01	8.0E-02	AW098118.1	EST_HUMAN	EST3378101 MAGE sequences, MAGE Homo sapiens cDNA
3365	13657	23440	0.84	8.0E-02	AW098118.1	EST_HUMAN	Human spleen cAMP responsive element binding protein-like 2 (CREB2L2) mRNA
3940	13988		1.05	8.0E-02	45030324	NT	Mus musculus gene for galactinase B
4709	14595		5.92	8.0E-02	X27294.1	NT	Hepesvirus simrit transformation-associated protein (STP), and dihydrofolate reductase (DHFR) genes complete cds, and small nuclear RNAs (rRNAs)
4834	14716	24460	0.97	8.0E-02	M28371.1	NT	Homo sapiens ABGAT (ABCA1) gene, complete cds
5591	15500	25581	3.35	8.0E-02	AF275943.1	NT	Homo sapiens ABGAT (ABCA1) gene, complete cds
6291	15500	25581	1.03	8.0E-02	AF275943.1	NT	Butylytic chlamydia strain T4 cDNA library under conditions of nitrogen deprivation
8727	18507	28768	3.95	8.0E-02	AL1149083.1	NT	Hs145845Ft NIH MGCC, 14 Homo sapiens cDNA clone IMAGE:392453 5'
7401	17288	27471	1.49	8.0E-02	X74208.1	NT	Hs145845Ft NIH MGCC, 14 Homo sapiens cDNA clone IMAGE:392453 5'
7401	17288	27472	1.49	8.0E-02	X74208.1	NT	Hs145845Ft NIH MGCC, 14 Homo sapiens cDNA clone IMAGE:392453 5'

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Table 4
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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) ELASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
8172	19000	28310	7.42	8.0E-02	AF17796.1	NT	Homo sapiens SGO10 like-protein, histone-like protein NHL, M88, and ADP-ribosylation factor related protein 1 (ARFRP1) genes, complete cds
9344	19023	25300	2.94	8.0E-02	AJ005376.1	NT	Drosophila orna hunchback region
9821	13887		1.47	8.0E-02	4603034	NT	Homo sapiens cAMP responsive element binding protein-like 2 (CREB1.2) mRNA
9909	19654		3.04	8.0E-02	AJ274435.1	NT	Homo sapiens cAMP responsive element binding protein-like 2 (CREB1.2) mRNA
2127	12015	21913	3.98	7.9E-02	BE250038.1	EST_HUMAN	Homo sapiens cAMP responsive element binding protein-like 2 (CREB1.2) mRNA
2946	12875	22073	6.43	7.9E-02	AI582026.1	EST_HUMAN	ap8403.11 Barasid codon HPLRB7 Homo sapiens cDNA clone IMAGE:217846 3' similar to gb:Z58876
3176	13688	23471	3.31	7.9E-02	6681044	NT	Mus musculus colony stimulating factor 1 receptor (Csfr1), mRNA
3176	13688	23472	3.31	7.9E-02	6681044	NT	Mus musculus colony stimulating factor 1 receptor (Csfr1), mRNA
4625	14493	24269	1.08	7.9E-02	BF248454.1	EST_HUMAN	Arabidopsis thaliana RXW24L mRNA, partial cds
4706	14592		1.16	7.9E-02	AB030819.1	NT	Saccharomyces cerevisiae suppressor of Ulp2 Sm4p (SMT4) gene, complete cds
6632	16562	28756	3.25	7.9E-02	U37532.1	NT	Caenorhabditis elegans NCL_CGAP_B22 Homo sapiens cDNA clone IMAGE:1832465 3' similar to WPC37A2.2
7752	17612	27638	5.68	7.9E-02	AB01844.1	EST_HUMAN	CE08811
7752	17612	27638	5.68	7.9E-02	AB01844.1	EST_HUMAN	CE08811
1122	11102	20947	1.43	7.9E-02	AF193275.1	EST_HUMAN	CE08811
1122	11102	20947	1.43	7.9E-02	AF193275.1	EST_HUMAN	CE08811
4038	14574	24571	0.81	7.9E-02	BE33533.1	EST_HUMAN	CE08811
5019	13693		2.71	7.9E-02	BE250046.1	EST_HUMAN	CE08811
5197	15000	24826	1.04	7.9E-02	AA16320.1	EST_HUMAN	CE08811
7236	17113	27306	2.06	7.9E-02	AF23437.1	NT	CE08811
7236	17113	27306	2.06	7.9E-02	AF23437.1	NT	CE08811
7359	17307	27573	1.27	7.9E-02	AA06934.1	EST_HUMAN	CE08811
1378	12693	21159	1	7.7E-02	AF181897.1	NT	CE08811
3538	13454		2.09	7.7E-02	AJ236958.1	NT	CE08811
6915	16499	26982	4.4	7.7E-02	AA402946.1	EST_HUMAN	CE08811

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal Value	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
7660	7510	27736	4.92	7.7E-02	F38080	SWISSPROT	PROBABLE SERINE/THREONINE-PROTEIN KINASE YR089C
8376	78233	28504	5.24	7.7E-02	11422797	NT	Homo sapiens KIA00623 gene product (KIA00623), mRNA
9331	90981	32851	2	7.7E-02	11638569	NT	Homo sapiens intracran regulatory factor 7 (IR7), mRNA
9346	9331	23067	2.97	7.7E-02	B5514462.1	EST_HUMAN	8013616387 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3634903.5
3362	13281	23081	0.94	7.0E-02	A4289447.1	EST_HUMAN	81112214 Celacanth 1 Homo sapiens cDNA clone similar to similar to piodactin 43
3512	13428	23228	0.93	7.0E-02	A400877.1	NT	Homo sapiens ASG3.3 gene, CCEP1 gene, C11orf41 gene, C11orf16 gene and C11orf17 gene
4766	14650	27618	0.98	7.0E-02	A405944.1	EST_HUMAN	RC3-010347-10300-014-a05 C10347 Homo sapiens cDNA
7383	73711	27618	1.34	7.0E-02	A131010.1	NT	Homo sapiens SCL gene locus
7896	17548	27618	1.34	7.0E-02	A1330078.1	NT	Camptidactylid jutan NCTC11168 complete genome, segment 5/6
8927	18735	23028	2.45	7.0E-02	A1789645.1	EST_HUMAN	QY6-BN00405-150400-151-a04 BN00408 Homo sapiens cDNA
787	10668	20535	1.13	7.5E-02	59020693	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, glyco), member 9 (SLC6A9), mRNA
787	10668	20536	1.13	7.5E-02	59020693	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, glyco), member 9 (SLC6A9), mRNA
1878	11774	21649	0.87	7.5E-02	AL163378.2	NT	Homo sapiens chromosome 21 segment HS21C0378
4407	14931	24085	0.84	7.5E-02	A3015961.1	NT	Homo sapiens L-19 gene for interleukin-18, intron 1, and exon 2
6885	16734	28627	1.19	7.5E-02	A864367.1	EST_HUMAN	W62002.1 NC1_QGAP_Bmp23 Homo sapiens cDNA clone IMAGE:2428461.3 similar to gp.M1-4328 ALPHA ENOLASE (HUMAN)
6953	16831	27024	1.21	7.5E-02	A1167913.1	EST_HUMAN	AV116913 HEMAI1 Homo sapiens cDNA clone HEMAI100294.5
409	14041	20271	1.23	7.5E-02	AF163847.1	EST_HUMAN	RC61-T0064-260100-011-H09 T0064 Homo sapiens cDNA
1444	11949	20321	1.08	7.4E-02	AF530097.1	NT	Escheria coli strain NS95957, complete genome
2506	12410	23255	0.93	7.4E-02	67595069	NT	Mus musculus pated-like homeodomain transcription factor 1 (Pht1), mRNA
3546	13461	23255	0.80	7.4E-02	A807885.1	EST_HUMAN	W43391.1 Scores_NF1_GBC_S1 Homo sapiens cDNA clone IMAGE:2368388.3
4908	14464	24282	3.38	7.4E-02	L787810.1	NT	Homo sapiens ADP-ATP carrier protein (ANT-2) gene, complete cds
4987	14973	24270	2.66	7.4E-02	6978442	NT	Rattus norvegicus Adrenin receptor like kinase 1 (Aor1), mRNA
4868	14738	24618	1.7	7.4E-02	6979402	NT	Mus musculus Ubiquitin c terminal hydrolase related polypeptide (Ucnpr), mRNA
5913	15619	26778	1.75	7.4E-02	BT17477.1	EST_HUMAN	J974906.1 Scores Infant brain TNIB Homo sapiens cDNA clone IMAGE:32359.5
6012	16492	20978	1.7	7.4E-02	BE8880112.1	EST_HUMAN	8014933697 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:336204.5
6510	16628	20978	1.37	7.4E-02	U95086.1	NT	Human peroxidic tyrosinase protein 2 (PW2P) gene, exon 15 to 21, and complete cds
9271	18976	21882	2.08	7.4E-02	11528693	NT	Homo sapiens histone H2a desacylase 5 (NY-CC-9), mRNA
9527	19874	25242	2.82	7.4E-02	AW1378431.1	EST_HUMAN	CNH107245-081109-037-011 H10233 Homo sapiens cDNA
9978	10235	23542	1.81	7.4E-02	BF035006.1	EST_HUMAN	8014583137 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3387738.5
461	10405	20222	0.96	7.3E-02	BE504091.2	EST_HUMAN	8014583137 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3386203.3

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
7963	17593	28073	5.47	7.2E-02	BE565003.1	EST_HUMAN	60143026F1 NIH_MGC_S3 Homo sapiens cDNA clone IMAGE:368594.5'
7964	17594	28073	3.12	7.2E-02	BE530214.1	EST_HUMAN	60106519F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451559.5'
8235	18164	28407	4.3	7.2E-02	A7046674.1	EST_HUMAN	Ratio: no regions BLH1 transduction factor MIST (MIST) gene, complete cds
9178	18619	28346	1.44	7.2E-02	A4773696.1	EST_HUMAN	Ratio: no regions BLH1 transduction factor MIST (MIST) gene, complete cds
9179	18620	28346	1.44	7.2E-02	A4773696.1	EST_HUMAN	Ratio: no regions BLH1 transduction factor MIST (MIST) gene, complete cds
9273	18677	28410	3.13	7.2E-02	A4230798.1	EST_HUMAN	AJ230798 Homo sapiens library (Serafini) P1 Homo sapiens cDNA clone PS18306.5'
9274	18677	28410	1.44	7.2E-02	A3984466.1	EST_HUMAN	AD398468 NIH_MGC_P1 Homo sapiens cDNA clone IMAGE:1096593.3'
8532	19031	28321	1.62	7.2E-02	U52528.1	EST_HUMAN	Human alpha telomerase (ATM) gene, complete cds
8346	19033	28321	3.39	7.2E-02	AY190082.1	EST_HUMAN	CHM-HNT1006-200300-116-111 NN1009 Homo sapiens cDNA
1862	11769	21633	1.65	7.1E-02	U02290.1	NT	Human immunodeficiency virus type 1 (D9) proviral structural capsid protein (gag) gene, partial cds
2243	12127	22028	0.9	7.1E-02	AF048800.1	EST_HUMAN	Pseudomonas aeruginosa PA01, section 481 of 526 of this complete genome
2247	12131	22028	5.09	7.1E-02	BF098002.1	EST_HUMAN	AB072281F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:1092881.5'
6003	18844	20752	4.98	7.1E-02	BE504764.1	EST_HUMAN	AB1145974F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3051234.5'
517	14906	20720	1.23	7.0E-02	Q07092	SWISSPROT	COLLAGEN ALPHA 1(XV) CHAIN PRECURSOR
1484	11398	21496	1.46	7.0E-02	X06967.1	NT	Marifolia mellea 1 gene
1726	11616	21495	1.36	7.0E-02	AF048834.1	EST_HUMAN	269804.s1 Stratagene clone (H6372204) Homo sapiens cDNA clone IMAGE:506599.3'
2884	12822	22716	1.72	7.0E-02	A118162.1	EST_HUMAN	U1-H81-seq-07-Q1.s1 CT GAP Sub3 Homo sapiens cDNA clone IMAGE:2716020.3'
3822	13784	24823	1	7.0E-02	AA616488.1	EST_HUMAN	u65a12.s1 Soares_Jacobs_NHT Homo sapiens cDNA clone (1375679.3' similar to gK03002.60S)
1969	13866	28042	1.24	7.0E-02	BE570284.1	EST_HUMAN	RIBOSOMAL PROTEIN L32 (HUMAN);
4047	13969	27962	1.08	7.0E-02	A1707982.1	EST_HUMAN	Q14870407-289100-000-010 T0407 Homo sapiens cDNA
4121	14021	27899	1.27	7.0E-02	A767921.1	EST_HUMAN	CH0-UM0001-069300-270-012 UM0001 Homo sapiens cDNA
4248	14267	27410	7.1	7.0E-02	BF381887.1	EST_HUMAN	Cmns familiaris inducible nitric oxide synthase mRNA, complete cds
4759	17130	27329	1.25	7.0E-02	Q628113	EST_HUMAN	AB016261F1 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:1050071.5'
7259	17367	27329	1.25	7.0E-02	Q628113	EST_HUMAN	African swine fever virus, complete genome
7534	17395	27697	1.19	7.0E-02	K03201.1	NT	Rat g1 germline apical H-chain gene Cragin, 3' and
9079	18057	28860	2.39	7.0E-02	A4724295.1	EST_HUMAN	u65a105.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1327184.3' similar to gB1.4837
9083	18057	28860	5.34	6.9E-02	AL163210.2	NT	TIGHT JUNCTION PROTEIN ZO-1 (HUMAN);
503	10445	20257	5.34	6.9E-02	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3311	11217	28421	1.31	6.9E-02	4907968	NT	Homo sapiens regulator of Gs-selective protein signaling (ZOAP1) mRNA, and translated products
3724	13036	28421	1.42	6.9E-02	Q06364	SWISSPROT	265 PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 2107)
3724	13036	28422	1.42	6.9E-02	Q06364	SWISSPROT	265 PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 2107)
5100	14668	28422	1.05	6.9E-02	A1070906.1	NT	Rabies virus isolate b615 glycoprotein gene, partial cds

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6978	10855	27046	1.37	6.E-02 AF067455.1	EST_HUMAN		g0134069f1 NIH_MGC_S3 Homo sapiens cDNA clone IMAGE:3863030 F
6978	10855	27049	1.37	6.E-02 BC557455.1	EST_HUMAN		g0134069f1 NIH_MGC_S3 Homo sapiens cDNA clone IMAGE:3863030 F
6982	10830		3.95	6.E-02 AT734515.1	NT		X-linked XED2 mRNA for fork head protein
6983	10843		1.15	6.E-02 AP4423.1	SWISSPROT		HOMO TRANSPORT PROTEIN HOPG HOMOLOG
6986	10760		2.18	6.E-02 AF195033.1	NT		Protein sequence membrane-bound antiapoptosis P (SNRPEP2) gene, complete cds
6989	11736	21610	1.11	6.E-02 AA496739.1	EST_HUMAN		g00922 G-protein Wilms tumor Homo sapiens cDNA clone IMAGE:897330 S similar to gb:M22382
1839	11736	21611	1.11	6.E-02 AA496739.1	EST_HUMAN		MTCOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN)
1859	11761	21635	3.91	6.E-02 AF159673.1	NT		g00002 G-protein Wilms tumor Homo sapiens cDNA clone IMAGE:897330 S similar to gb:M22382
3062	12868	22760	1.23	6.E-02 AF181995.1	EST_HUMAN		Homo sapiens putative histone transcription factor (HIST5CFL1) gene, complete cds
3062	12868	22761	1.23	6.E-02 AF181995.1	EST_HUMAN		at3406.31 Soares_Jealls_NHT Homo sapiens cDNA clone J1316528.3
3062	12868	22762	1.23	6.E-02 AF181995.1	EST_HUMAN		at3406.31 Soares_Jealls_NHT Homo sapiens cDNA clone J1316528.3
4483	14347		0.92	6.E-02 BE141076.1	EST_HUMAN		NKX4-H1008b-07/1008-041-005 H1008b Homo sapiens cDNA
6315	19178	26337	7.71	6.E-02 AL163398.2	NT		Homo sapiens chromosome 21 segment HS21C086
6822	19178	26854	6.12	6.E-02 AJ246287.1	NT		Pycococcus abyssi complete genome, segment 36
6822	19178	26855	6.12	6.E-02 AJ246287.1	EST_HUMAN		F84A38 Fatal brain, Strangelye Homo sapiens cDNA clone F84A38.5 and similar to LINE-1
5011	19716		1.37	6.E-02 T03374.1	EST_HUMAN		hd0706.41 Soares_Jealls_NHT Homo sapiens cDNA clone J1320705.3
5194	19884	2260	2.89	6.E-02 AA738014.1	NT		Mad musculus latent TGF beta binding protein (LTgb), mRNA
9764	19924	2297	6.E-02	59106881	NT		Oncotrophic myxins TAP1 intran (Onmy/AP1) mRNA. Onmy/TAP1?01 allele, complete cds
1511	11747	21622	2.17	6.E-02 AF115536.1	EST_HUMAN		g00706.41 Soares_NEL_1_GIRC.S3 Homo sapiens cDNA clone IMAGE:1841400.3*
1851	11747	21622	2.5	6.E-02 AF120285.1	EST_HUMAN		g00706.41 Soares_NEL_1_GIRC.S3 Homo sapiens cDNA clone IMAGE:1841400.3*
3656	13570	23350	3.92	6.E-02 PT1728	SWISSPROT		HOMO-OBOX PROTEIN HOXB-D (CHOXA)
1326	11233	21089	1.05	6.E-02 AF738509.1	EST_HUMAN		at2a08.01 Bar-leiled axons HFLRB8 Homo sapiens cDNA clone IMAGE:3534920.3 similar to SWL/NIL_NTCOOX P09648 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.1
1347	11253	21169	1.5	6.E-02 AF284116.1	NT		Drosophila melanogaster ocellin mRNA, complete cds
2133	12021	21918	3.07	6.E-02 QJ296241.1	NT		Mus musculus Capn12 gene for calpain 12, exons 1-21, three alternative transcripts
3133	13068		1.32	6.E-02 QJ13885	SWISSPROT		MELANOTIN-RECEIVED RECEPTOR (H9)
3418	13335	23350	8.01	6.E-02 RF64306.1	EST_HUMAN		y1b5r0.01 Soares placenta B2bAP Homo sapiens cDNA clone IMAGE:139579.3*
3432	13349	23156	2.19	6.E-02	7100357	NT	Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA
3432	13349	23155	2.19	6.E-02	7100357	NT	Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA
3959	13890	23673	1.99	6.E-02 AF200225.1	NT		Homo sapiens Testis 2 and TESTIN 3 genes, complete cds, alternatively spliced
4904	14784	24568	8.4	6.E-02 Q61703	SWISSPROT		INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2)
4904	14784	24569	8.4	6.E-02 Q61703	SWISSPROT		INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2)

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Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF-SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6167	15033	24800	1.34	6.5E-02	AF204652.1	NT	Amsacta albistriga nucleopolydnavirus AcORF17 homolog gene, complete cds
6190	15033	24817	0.84	6.5E-02	AE004346.1	NT	Vibrio cholerae chromosome 1, section 2 of 93 of the complete chromosome
5938	15073	25568	3.05	6.5E-02	X00411.1	NT	P. vulgaris mRNA for chalcone synthase
6309	15099	29105	2.93	6.5E-02	AI243326.1	EST HUMAN	gH41d01.X1 Soares, NFL_T_OBC S1 Homo sapiens cDNA clone IMAGE:1647233 3'
6335	15615	29706	1.48	6.5E-02	AF555872.1	NT	Homo sapiens chemokine receptor CXCR4 gene, promoter region and complete cds
7606	17656	27884	1.27	6.5E-02	V07848.1	NT	Homo sapiens EWS, gcr22, mp22 and bcr22 genes
8330	18207	28467	1.26	6.5E-02	BF574348.1	EST HUMAN	MR1-SN0084-07000-009-412 SN0084 Homo sapiens cDNA
5953	19176		2.08	6.5E-02	66076941	NT	Mus musculus DIPB gene (Dipb), mRNA
5852	19326	29313	1.48	6.5E-02	AF107430.1	NT	Rattus norvegicus cytochrome P450 2E1 (CYP2E1) gene, 5' flanking region
607	19506	30743	1.91	6.5E-02	BF627539.1	EST HUMAN	901871048F1.NH, MGSC_20 Homo sapiens cDNA clone IMAGE:3844776 5'
677	19595	30743	1.75	6.5E-02	7703068	NT	Homo sapiens Espr-like protein (LOC51270), mRNA
1359	11275	21131	4.17	6.5E-02	U47624.1	NT	Xenopus laevis alpha(E)-catenin mRNA, complete cds
1702	11503	21474	2.16	6.5E-02	AE000764.1	NT	Aquifex sedulius section 96 of 108 of the complete genome
8413	15333	23583	1.76	6.5E-02	AA43394.1	EST HUMAN	sub12.31 Soares (very low) NIH-07 Homo sapiens cDNA clone IMAGE:166743 3' similar to gb:M20038
8335	17927	28173	3.61	6.5E-02	AA165248.1	EST HUMAN	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-5 BETA, CHAIN (HUMAN)
9334	18623		3.53	6.5E-02	AF14563.1	NT	Rabbit histocompatible protein hydrolase
9383	19051		3.73	6.5E-02	AF10583.1	NT	Neurin hematopoietic kinase related protein 2 (NRP2) gene, complete cds
951	19501	23307	1.53	6.5E-02	X01649.1	NT	A. castaneae precursor of peritrophin-chorion-like protein (PCP) gene
4802	12068	22708	1.35	6.5E-02	5969523	NT	Mus musculus histone H4acetylase 5 (H4ac5), mRNA
5180	15044		8.78	6.5E-02	6969523	NT	Mus musculus histone H4acetylase 5 (H4ac5), mRNA
5348	15207	28064	1.4	6.5E-02	A114956.1	EST HUMAN	9076071.X1 Soares, beta2, N1H7 Homo sapiens cDNA clone IMAGE:175249 3' similar to contains LTRB.53
5718	15025	25727	7.56	6.5E-02	AF05733.1	NT	Heterodera glycines beta-1,4-mannoglucanase-1 precursor (HG-ang-1) gene, complete cds
5718	15025	25728	7.58	6.5E-02	AF05733.1	NT	Heterodera glycines beta-1,4-mannoglucanase-1 precursor (HG-ang-1) gene, complete cds
6079	19092	28210	5.23	6.5E-02	BE574448.1	EST HUMAN	901880292F2.NH, MGSC_33 Homo sapiens cDNA clone IMAGE:390503 3'
6863	19732		2.57	6.5E-02	6763323	NT	Mus musculus chaperonin subunit 6a (p60) (Cib5a), mRNA
7034	19911	27099	4.12	6.5E-02	AA003006.1	EST HUMAN	K14193.seq F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
7803	17454	27698	2.02	6.5E-02	AB011128.1	NT	Homo sapiens mRNA for RAG3B54 protein, partial cds
8946	16754	28049	1.89	6.5E-02	U01328.1	NT	Human hereditary hemochromatosis region, histone 2A-like protein gene, hereditary hemochromatosis (HLA-H) gene, Rofei gene, and sodium phosphate transporter (NPT3) gene, complete cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8546	18754	29050	1.86	6.4E-02	U91323.1	NT	Human hereditary haemochromatosis (HLA-H) gene, RefSeq gene, and sodium phosphate transporter (NPT3) gene, complete cds
5289	19635		3.05	6.4E-02	AF107600.1	NT	Homo sapiens muscle 53 (MLC53) gene, partial cds
8537	19017	25295	2.27	6.4E-02	A.127174.1	NT	Drosophila melanogaster mRNA for mod(mdg4)31.4 protein
1720	11921	21490	2.43	6.3E-02	AF109505.1	NT	Mus musculus major histocompatibility locus class III region H2a70 gene, partial cds, enRNP, G7A, NG23, MADS homolog, CLCP, NG24, NG25, and NG29 genes, complete cds, and unknown genes
3542	13467		2.09	6.3E-02	P37062	SWISSPROT	HEAT SHOCK PROTEIN 70 HOMOLOG
7752	17002	27825	3.14	6.3E-02	AF010192.1	NT	Haplophilus sp. virus RNA for polyprotein (NS5A region), partial cds, strain: OWR-152
8068	15937	25741	3.29	6.3E-02	BF210736.1	EST_HUMAN	00178319FT.NH.MSC. 54 Homo sapiens cDNA clone IMAGE:4097469.5'
9373	19039		1.46	6.3E-02	P13276	SWISSPROT	TRANSFERRIN RECEPTOR ALGinate-binding protein (ALG3)
4157	14407	23831	3.37	6.2E-02	AL161572.2	NT	A. nidulans: human DNA chromosome 4, contig fragment No. 68
4243	14142		1.11	6.2E-02	AF21235.1	NT	Rattus norvegicus differentiation-associated Nucleotide-dependent inorganic phosphate cotransporter (DNPI) mRNA, complete cds
4479	14373		5.41	6.2E-02	Q62191	SWISSPROT	32 KD RO PROTEIN (SODIUM SYNDROME TYPE A ANTIGEN (SS-A)) (ROISS-A)) (ROSS2)
4693	14697		1.23	6.2E-02	AF070570.1	EST_HUMAN	AF070570.1 AOB Homo sapiens cDNA clone AOB8A803.5'
7459	17319	27625	1.21	6.2E-02	AF070570.1	EST_HUMAN	Mus musculus thymal cell derived factor receptor 2 (Sdf2), mRNA
8555	18343	28827	1.84	6.2E-02	A.042735.1	NT	Mesothelium thymal cell derived factor receptor 2 (Sdf2), mRNA
9128	19752		3.33	6.2E-02	AF007650.1	NT	Aquilar cardiac section 82 of 108 of the complete genome
9541	19742	25285	1.98	6.2E-02	BF112399.1	EST_HUMAN	733909.31 Spaca, NSF, FL, 91W, OT, PL, P, S1 Homo sapiens cDNA clone IMAGE:3622815.5' similar to
286	10222	20358	4.33	6.1E-02	U10471.1	NT	TR-09A456.09/456 HYPOTHETICAL 30.3 KD PROTEIN [1];
3989	18219		2.05	6.1E-02	D73325.1	NT	Human mRNA, 5' terminal portion
5150	15017	24785	1.01	6.1E-02	A5040697.1	NT	Arabidopsis thaliana Kcs1-like voltage-gated potassium channel protein (AKC1) gene, complete cds
8659	16988	28877	3.46	6.1E-02	X59268.1	NT	Homo sapiens mRNA for KIM1560 protein, partial cds
81-2	18002	28248	5.44	6.1E-02	BC117843.1	EST_HUMAN	Homo sapiens mRNA for p21H DNA binding protein
8658	16970		7.17	6.1E-02	X70989.1	EST_HUMAN	L3-H10816-110500-108-C08 H10816 Homo sapiens cDNA
9783	19256		3.6	6.1E-02	AF163077.2	NT	S. japonicum mRNA for serine-enzyme
1241	11148	20957	1.41	6.1E-02	AE001777.1	NT	Homo sapiens chromosome 21 segment H521C07
2641	12508	22399	1.57	6.0E-02	AF089848.1	EST_HUMAN	Thermoplasma maritima section 89 of 130 of the complete genome
2745	12607		1.22	6.0E-02	A5031289.1	EST_HUMAN	EST336524 IMAGE resequencing, MAGI Homo sapiens cDNA
2906	10076	19892	1.61	6.0E-02	A4186720.1	EST_HUMAN	Mesostoides corti mitochondrial DNA, NADH dehydrogenase subunit 4, RNA-Gln, RNA-Phe, RNA-Ileu, A1Pase subunit 6, and NADH dehydrogenase subunit 2
			1.42	6.0E-02	A4186720.1	EST_HUMAN	ap7904.H1 Stratifigene Hella cell c3 937218 Homo sapiens cDNA clone IMAGE:630510.5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2005	10076	19803	1.22	6.0E-02	AA188730.1	EST_HUMAN	zfp7604.r1 Stratagene HeLa cell c3 937218 Homo sapiens cDNA clone IMAGE:620310 5'
3191	13116	22921	1.2	6.0E-02	AA372376.1	EST_HUMAN	EST184396 Odon adenocarcinoma IV Homo sapiens cDNA 5' end similar to tissue-specific protein
3191	13116	22922	1.2	6.0E-02	AA372376.1	EST_HUMAN	EST184396 Odon adenocarcinoma IV Homo sapiens cDNA 5' end similar to tissue-specific protein
3593	13467	22922	0.9	6.0E-02	BE094443.2	EST_HUMAN	601650150R1 NF1_MGC_98 Homo sapiens cDNA clone IMAGE:3876060 3'
4893	14773	24551	1.17	6.0E-02	267739.2	NT	Spirochaete pneumoniae parC, parE and transposase genes and ORF DNA
5514	15235	24648	3.46	6.0E-02	AW370211.1	EST_HUMAN	RC3-B70233.01189-013-3041 B70233 Homo sapiens cDNA
6172	15129	24648	2.86	6.0E-02	5174638	NT	Homo sapiens stimulated trans-acting factor (50 Cbp) (STAF50) mRNA
6172	15129	24649	2.86	6.0E-02	5174638	NT	Homo sapiens stimulated trans-acting factor (50 Cbp) (STAF50) mRNA
6265	16130	25304	1.97	6.0E-02	BF382476.1	EST_HUMAN	601515274P2 NF1_MGC_98 Homo sapiens cDNA clone IMAGE:4049226 5'
9524	16333	25652	2.05	6.0E-02	A1242476.1	EST_HUMAN	qf5905.x1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:1754199 3'
7540	17235	27403	1.19	6.0E-02	A1231467.1	EST_HUMAN	h75400.x1 NCI CGAP G05 Homo sapiens cDNA clone IMAGE:2237362 3'
7540	17235	27407	1.19	6.0E-02	A1231467.1	EST_HUMAN	h75400.x1 NCI CGAP G05 Homo sapiens cDNA clone IMAGE:2237362 3'
7411	17278	27465	1.78	6.0E-02	A245355.1	NT	Adipocyte basal partial (BLV) gene for immunoglobulin light chain variable region, exon 1-2
7411	17278	27467	1.78	6.0E-02	A245355.1	NT	Adipocyte basal partial (BLV) gene for immunoglobulin light chain variable region, exon 1-2
9538	19016	25304	1.95	6.0E-02	11451702	NT	Homo sapiens DNA-dependent protein kinase catalytic subunit-interacting protein 2 (KIP2) mRNA
9715	16296		1.84	6.0E-02	A169673.1	EST_HUMAN	w69003.x1 Soares, JFL T_OBC_S1 Homo sapiens cDNA clone IMAGE:2300805 3' similar to TR-C09298
229	10196	20011	3.42	5.9E-02	AW554791.1	EST_HUMAN	CG286 (KIA03591) PROTEIN, 1
2955	12852	22681	2.59	5.9E-02	AF160593.1	EST_HUMAN	RC1-D7001-25010-012-410 D7001 Homo sapiens cDNA
4770	14955	24443	0.88	5.9E-02	AF00504.1	NT	Mus musculus p53 tumor suppressor gene, exon 10 and 11, partial cds, alternatively spliced
7008	18885	27077	1.87	5.9E-02	9055249	NT	Saccharomyces cerevisiae protein tyrosine phosphatase (PTP) gene, complete cds
6165	18053		2.72	5.9E-02	6670670	NT	Mus musculus toroquin related homeobox 3 (Toro3) (Trox) mRNA
8393	18260	28509	3.15	5.9E-02	11493356	NT	Mus musculus toll-like receptor 1 (TLR1) mRNA
8842	18955		1.06	5.9E-02	A240733.1	NT	Homo sapiens nhrin (LOC351169), mRNA
917	10841		4.35	5.8E-02	D00110.1	NT	Gallus gallus HCR9 telomere junction
2930	12759		1.1	5.8E-02	AJ229921.1	NT	Thiodiculus ferroxidase mcrC, mcrA genes and URF-1
3913	13527	23314	1.44	5.8E-02	AE001775.1	NT	Populus trichocarpa CoAOMT1 gene, exon 1 to exon 5
4257	14156	23551	4.36	5.8E-02	AW051027.1	EST_HUMAN	Thermoplasma maritima section 87 of 138 of the complete genome
4257	14156	23552	4.36	5.8E-02	AW051027.1	EST_HUMAN	w24402.x1 NCI CGAP K4R1 Homo sapiens cDNA clone IMAGE:2544678 3'
4257	14156	23552	4.36	5.8E-02	AW051027.1	EST_HUMAN	w24402.x1 NCI CGAP K4R1 Homo sapiens cDNA clone IMAGE:2544678 3'
4447	14341	24132	4.21	5.8E-02	A247905.1	EST_HUMAN	qf59001.x1 Soares, fetal liver, spleen, INFLS_S1 Homo sapiens cDNA clone IMAGE:1848897 3' similar to
4447	14341	24133	4.21	5.8E-02	A247905.1	EST_HUMAN	qf59001.x1 Soares, fetal liver, spleen, INFLS_S1 Homo sapiens cDNA clone IMAGE:1848897 3' similar to
4471	14355		2.04	5.8E-02	AF060284.1	NT	gM13142 COAGULATION FACTOR XI PRECURSOR (HUMAN); gM13142 COAGULATION FACTOR XI PRECURSOR (HUMAN); Gallus gallus Yroline kinase JAK1 (JAK1) mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6523	13302	26560	2.79	5.9E-02	M6150.1	NT	Human polymorphic microsatellite DNA
6523	13302	26561	2.79	5.9E-02	M6150.1	NT	Human polymorphic microsatellite DNA
9227	19048		2.34	5.9E-02	AF220177.1	NT	Drosophila melanogaster male fruitless type-A1 (fru) mRNA, complete cds
9518	19739		4.59	5.9E-02	A4404289.1	EST HUMAN	nc67541.1 nt1 CGAP_AAT Homo sapiens cDNA clone IMAGE:1113984.3'
3038	12946	22738	1.34	5.7E-02	A081644.1	EST HUMAN	cd63605.1 nt1 CGAP_B22 Homo sapiens cDNA clone IMAGE:1632468.3' similar to WP-C37A2.2
3038	12946	22738	1.34	5.7E-02	A081644.1	EST HUMAN	CE08911.1
3731	13543	23428	4.8	5.7E-02	AF191917.1	EST HUMAN	Homo sapiens dopamine transporter (SLO6A) gene, complete cds
8740	18619	29808	1.42	5.7E-02	A1230069.1	NT	EST378605 IMAGE rescues, MAGI Homo sapiens cDNA
8824	18326	29681	3.86	5.7E-02	A173385.1	EST HUMAN	Rattus norvegicus mRNA for potassium channel, alpha subunit (Kv2.2 gene)
8524	18326	29682	3.86	5.7E-02	A173385.1	EST HUMAN	cn18603.v1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn18608 random
8437	19538		5.55	5.7E-02	D59328.1	NT	cn18603.v1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn18608 random
8682	19330		2.47	5.7E-02	AF217499.1	NT	Pig DNA (cc SPAL2) complete cds
9798	19727		3.82	5.7E-02	AF261280.1	NT	Homo sapiens fragile 180 cido calcitriol (FOR) gene, exon 8, and partial cds
1510	11415	21274	0.86	5.9E-02	AF084455.1	NT	Pan troglodytes apolipoprotein-E gene, complete cds
4540	14433	24215	1.26	5.9E-02	AB015100.1	NT	Hydroxylase reticulolysis rheosomal protein L16 (pr16) gene, intron, chloroplast gene for chloroplast product
4588	14488	24272	1.14	5.9E-02	AA29599.1	EST HUMAN	Lycopodium obscurum LE_4C3S mRNA for 4-aminopyridoxalase-1, carboxylate synthase, complete cds
6008	15913	28940	4.74	5.9E-02	AW172708.1	EST HUMAN	2345201.1 nt1 CGAP_C02 Homo sapiens cDNA clone IMAGE:7035416.3'
6247	19107	26258	2.88	5.9E-02	BE000001.1	EST HUMAN	Q37-BN0747-250400-214-g07 BN0147 Homo sapiens cDNA
7110	19937	27178	2.29	5.9E-02	BE542683.1	EST HUMAN	001067758F1 NIH_MGC-10 Homo sapiens cDNA clone IMAGE:3453278.5'
7110	19937	27179	2.29	5.9E-02	BE542683.1	EST HUMAN	001067758F1 NIH_MGC-10 Homo sapiens cDNA clone IMAGE:3453278.5'
7647	17487	27719	1.15	5.9E-02	AA482894.1	EST HUMAN	nf45007.1 nt1 CGAP_AMT Homo sapiens cDNA clone IMAGE:933345 similar to TR-G768859 G768859
8650	18962	22375	2.18	5.9E-02	AF200235.1	NT	LAMINA ASSOCIATED POLYPEPTIDE 1C.1
2818	12486	22375	8.10	5.9E-02	X67986.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
3178	13104	22609	3.0	5.9E-02	67655001	NT	Hi sapiens gene encoding La autoantigen
4777	14051	24448	0.81	5.9E-02	AF161286.1	NT	His musculus SH3 domain protein 4B (SH3a1B), mRNA
5472	13302	25438	3.47	5.9E-02	Q01174	SWISSPROT	Murray Valley encephalitis virus strain MVE-1431, complete genome
5971	15302	25438	4.31	5.9E-02	Q01174	SWISSPROT	TROPOMYOSIN ALPHA CHAIN, NON MUSCLE

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6305	10228	26338	1.58	5.5E-02	6756902	NT	Mus musculus tafazzin 1 (Taf1), mRNA
7666	17417	27632	1.3	5.5E-02	10947034	NT	Human sapiens eff-4e-transporter (4E-7), mRNA
7666	17417	27633	1.3	5.5E-02	10947034	NT	Human sapiens eff-4e-transporter (4E-7), mRNA
7619	17470	27689	1.48	5.5E-02	U94942.1	NT	Mus musculus second IL11 receptor alpha chain (IL11Ra2) gene, exons 1 and 2
8382	18259	28608	11.58	5.5E-02	U69771.1	NT	Cleavage of frondil DSM 30040 cyclopropane fatty acid synthase (cfa) gene, partial cds, dihydroxyacetone kinase (dhak), glycerol dehydrogenase (dhac), transcriptional activator (dhac), 1,3-propanediol dehydrogenase (dhac), glycerol dehydrogenase (dhac), >
2066	12914		0.95	5.4E-02	AJ277468.1	NT	Oryza sativa tdk3-1 gene for putative Bowman-Birk trypsin inhibitor
3375	15076		6.34	5.4E-02	BC073498.1	EST_HUMAN	RC3-570558-140200-012-C03 B70559 Homo sapiens cDNA
4908	14787	24663	0.92	5.4E-02	U63528.1	NT	Xenopus laevis homeobox protein (Xac-1) mRNA, complete cds
5108	14678	24761	1	5.4E-02	N68761.1	NT	Mus musculus p-glycoprotein (mdr1a) gene, exons 1 and 2
8083	17074	28223	1.78	5.4E-02	U02700.1	NT	Neurospora crassa ubiquitin-cyclochrome c oxidoreductase subunit VIII (QCR8) mRNA, complete cds
8523	18522		1.55	5.4E-02	U44984.1	NT	Bara calicheirina heat shock protein 30 (HSP30) mRNA, complete cds
1037	10855	20797	1.02	5.5E-02	AF0391248.1	EST_HUMAN	Q10-570213-021269-052-056 STC213 Homo sapiens cDNA
1037	10855	20798	1.02	5.5E-02	AF0391248.1	EST_HUMAN	Q10-570213-021269-052-056 STC213 Homo sapiens cDNA
1489	11394	21265	18.21	5.3E-02	T04739.1	EST_HUMAN	h4 CLASS II HISTOCOMPATIBILITY ANTIGEN, DR(1) (ALPHA CHAIN (HLA-A)),
2447	12324	22222	3.14	5.3E-02	AJ279463.1	NT	Procardinase pulvis BPS gene
2912	12839	22638	3.91	5.3E-02	U58417.1	NT	Oncocytin mediator kinase B2 gene, complete cds
2912	12839	22639	3.91	5.3E-02	U58417.1	NT	Oncocytin mediator kinase B2 gene, complete cds
3113	13038	22834	4.89	5.3E-02	AJ279406.1	NT	Procardinase pulvis BPS gene
4908	14399	24185	1.22	5.3E-02	AJ011048.1	NT	Procardinase pulvis BPS gene
6021	14894	24662	7.28	5.3E-02	U69465.1	NT	Arabidopsis thaliana tdk gene, exon 1 (1)
5288	15180	24965	1.79	5.3E-02	AJ000627.1	NT	Mus musculus caudal type homeobox (Cdx-1) gene, complete cds
5288	15180	24966	1.79	5.3E-02	AJ000627.1	NT	Helicobacter pylori 26895 section 5 of 134 of the complete genome
6115	16009	25145	3.87	5.3E-02	9696413	NT	Lymphocyte disease virus 1, complete genome
6363	16016		1.94	5.3E-02	S78221.1	NT	Nuclear protein TIF1 isoform 1, complete cds
7276	17153	27349	1.78	5.3E-02	X03127.1	NT	Procardinase pulvis BPS gene
2239	12123		4.88	5.2E-02	6031008	NT	Procardinase pulvis BPS gene
3076	13003	22793	2.34	5.2E-02	AJ276651.1	NT	Human sapiens partial LMOT1 gene for LIM domain only 1 protein, exon 1
3076	13003	22794	2.34	5.2E-02	AJ276651.1	NT	Human sapiens partial LMOT1 gene for LIM domain only 1 protein, exon 1
4181	14081	23854	3.35	5.2E-02	U07132.1	NT	Human atrophomodulin receptor Nef-1 mRNA, complete cds
4633	14521	24311	1.04	5.2E-02	383246.1	NT	Drosophila melanogaster filament protein homolog (Sept) gene, complete cds

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Probe SEQ ID NC:	Exon SEQ ID NC:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5714	15622		1.73	5.2E-02	A830965.1	EST_HUMAN	W6004.41 NC1 CGAP Lym12 Homo sapiens cDNA clone IMAGE:2409150.3' similar to contains MER18.61
5716	16647		2.23	5.2E-02	AI163294.2	NT	MER16 repetitive element;
7610	17461	27077	2.03	5.2E-02	D10827.1	NT	Homo sapiens chromosome 21 segment HS21.0004
7610	17461	27078	2.03	5.2E-02	D10827.1	NT	Tumip msclo virus genomic RNA for Capsid protein, complete cds
9561	19167		1.63	5.2E-02	Q03090	SWISSPROT	Tumip msclo virus genomic RNA for Capsid protein, complete cds
2313	12164	24520	1.02	5.1E-02	A112407.1	EST_HUMAN	OXA10A20C10E12 DECARBOXYLASE ALPHA CHAIN
4076	14864		1.12	5.1E-02	BE57423.2	EST_HUMAN	BT026470973.11 547 (exon): h101 Homo sapiens cDNA clone DKFZ547D07.6
9556	15103	24571	1.65	5.1E-02	BF37626.1	EST_HUMAN	BT026470973.11 547 (exon): h101 Homo sapiens cDNA clone IMAGE:3930381.3'
9556	15103	24570	1.43	5.1E-02	A112407.1	EST_HUMAN	BT026470973.11 547 (exon): h101 Homo sapiens cDNA clone IMAGE:3930381.3'
7646	17465	27164	0.32	5.1E-02	A112407.1	EST_HUMAN	BT026470973.11 547 (exon): h101 Homo sapiens cDNA clone IMAGE:3930381.3'
7946	17666	27164	0.32	5.1E-02	A112407.1	EST_HUMAN	BT026470973.11 547 (exon): h101 Homo sapiens cDNA clone IMAGE:3930381.3'
8204	16568	26339	2.42	5.1E-02	A112407.1	EST_HUMAN	BT026470973.11 547 (exon): h101 Homo sapiens cDNA clone IMAGE:3930381.3'
8204	16568	26340	2.42	5.1E-02	A112407.1	EST_HUMAN	BT026470973.11 547 (exon): h101 Homo sapiens cDNA clone IMAGE:3930381.3'
9456	19168		1.81	5.1E-02	A112407.1	EST_HUMAN	BT026470973.11 547 (exon): h101 Homo sapiens cDNA clone IMAGE:3930381.3'
474	10416	20234	1.81	5.0E-02	A112407.1	EST_HUMAN	BT026470973.11 547 (exon): h101 Homo sapiens cDNA clone IMAGE:3930381.3'
1196	11966	20642	7.11	5.0E-02	269104.1	NT	BT026470973.11 547 (exon): h101 Homo sapiens cDNA clone IMAGE:3930381.3'
1947	11642	21726	4.27	5.0E-02	202610	SWISSPROT	BT026470973.11 547 (exon): h101 Homo sapiens cDNA clone IMAGE:3930381.3'
2768	10894	20749	1.84	5.0E-02	U17242.1	NT	BT026470973.11 547 (exon): h101 Homo sapiens cDNA clone IMAGE:3930381.3'
3256	13277		1.17	5.0E-02	730510	NT	BT026470973.11 547 (exon): h101 Homo sapiens cDNA clone IMAGE:3930381.3'
3526	13543	22530	5.53	5.0E-02	U17242.1	NT	BT026470973.11 547 (exon): h101 Homo sapiens cDNA clone IMAGE:3930381.3'
4890	14770	24448	0.86	5.0E-02	A1168530.1	NT	BT026470973.11 547 (exon): h101 Homo sapiens cDNA clone IMAGE:3930381.3'
6450	15811	25477	10.61	5.0E-02	A1168530.1	NT	BT026470973.11 547 (exon): h101 Homo sapiens cDNA clone IMAGE:3930381.3'
7658	17708	27654	1.32	5.0E-02	A1168530.1	NT	BT026470973.11 547 (exon): h101 Homo sapiens cDNA clone IMAGE:3930381.3'
8762	18597	26866	2.47	5.0E-02	U67800.1	NT	BT026470973.11 547 (exon): h101 Homo sapiens cDNA clone IMAGE:3930381.3'
9006	18653		2.81	5.0E-02	Q04417	SWISSPROT	BT026470973.11 547 (exon): h101 Homo sapiens cDNA clone IMAGE:3930381.3'
216	10166		28.96	4.9E-02	A112407.1	NT	BT026470973.11 547 (exon): h101 Homo sapiens cDNA clone IMAGE:3930381.3'
365	10321	20143	2.57	4.9E-02	A112407.1	NT	BT026470973.11 547 (exon): h101 Homo sapiens cDNA clone IMAGE:3930381.3'
365	10321	20144	2.57	4.9E-02	A112407.1	NT	BT026470973.11 547 (exon): h101 Homo sapiens cDNA clone IMAGE:3930381.3'
3261	13174	22972	1.87	4.9E-02	F51268	SWISSPROT	BT026470973.11 547 (exon): h101 Homo sapiens cDNA clone IMAGE:3930381.3'
3522	13436		0.87	4.9E-02	AA118640.1	EST_HUMAN	BT026470973.11 547 (exon): h101 Homo sapiens cDNA clone IMAGE:3930381.3'
3543	13469	22922	1.16	4.9E-02	AA400514.1	EST_HUMAN	BT026470973.11 547 (exon): h101 Homo sapiens cDNA clone IMAGE:3930381.3'

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Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3543	13459	23263	1.10	4.8E-02	AA400914.1	EST HUMAN	277603.11 Soares. Italia. NHT Homo sapiens cDNA clone IMAGE/28428 3'
4733	14618	24404	1.89	4.8E-02	AW167821.1	EST HUMAN	x656910.11 NC1 CGAP. U14 Homo sapiens cDNA clone IMAGE/263286 3'
4733	14618	24405	1.89	4.8E-02	AW167821.1	EST HUMAN	x656910.11 NC1 CGAP. U14 Homo sapiens cDNA clone IMAGE/263286 3'
5338	16220	25923	1.94	4.8E-02	L00122.1	NT	Rat diacylglycerol 11 gene, exon 6
5338	16220	25924	1.94	4.8E-02	L00122.1	NT	Rat diacylglycerol 11 gene, exon 6
8703	18523	28895	3.78	4.8E-02	AF006003.1	NT	Homo sapiens progesterone receptor TGF-beta gene, complete cds
9490	19107		2.25	4.8E-02	8623846	NT	Homo sapiens CS box-containing WD protein (LOC55884). mRNA
9751	19276		3.87	4.8E-02	M16984.1	NT	Human gamma-B-crystallin (gamma 1-2) and gamma-C-crystallin (gamma 2-1) genes, complete cds
327	10287	20104	1.43	4.8E-02	D16471.1	NT	Human mRNA. Ya terminal portion
338	10287	20104	1.97	4.8E-02	D16471.1	NT	Human mRNA. Ya terminal portion
480	10424	20259	7.54	4.8E-02	AF03100.1	NT	Human mRNA. Ya terminal portion
2227	12112	22614	1.92	4.8E-02	W61683.1	EST HUMAN	483603.1 Soares. Italia. NHT Homo sapiens cDNA clone IMAGE/325611 3' similar to
3172	13087	22603	2.12	4.8E-02	X17144.1	NT	483603.1 Soares. Italia. NHT Homo sapiens cDNA clone IMAGE/325611 3' similar to
4572	14484		1.97	4.8E-02	Z52801.1	NT	26140638 LUPUS K1 AUTOANTIGEN PROTEIN P66 (HUMAN);
5078	14648	24722	1.28	4.8E-02	U09141.1	NT	26140638 LUPUS K1 AUTOANTIGEN PROTEIN P66 (HUMAN);
6731	16611	26801	1.31	4.8E-02	AW338497.1	EST HUMAN	26140638 LUPUS K1 AUTOANTIGEN PROTEIN P66 (HUMAN);
4940	14818	24586	0.78	4.7E-02	6891351	NT	26140638 LUPUS K1 AUTOANTIGEN PROTEIN P66 (HUMAN);
6085	10030	28170	3.41	4.7E-02	W01163.1	EST HUMAN	26140638 LUPUS K1 AUTOANTIGEN PROTEIN P66 (HUMAN);
6134	15681	28117	1.85	4.7E-02	M62762.1	NT	26140638 LUPUS K1 AUTOANTIGEN PROTEIN P66 (HUMAN);
8800	16679	28688	9.71	4.7E-02	X15543.1	NT	26140638 LUPUS K1 AUTOANTIGEN PROTEIN P66 (HUMAN);
7179	17056	27245	1.18	4.7E-02	X89211.1	NT	26140638 LUPUS K1 AUTOANTIGEN PROTEIN P66 (HUMAN);
7189	17066		2.03	4.7E-02	A0206678.1	NT	26140638 LUPUS K1 AUTOANTIGEN PROTEIN P66 (HUMAN);
7321	17107	27397	7.44	4.7E-02	X15543.1	NT	26140638 LUPUS K1 AUTOANTIGEN PROTEIN P66 (HUMAN);
8136	18024	28270	1.76	4.7E-02	6754595	NT	26140638 LUPUS K1 AUTOANTIGEN PROTEIN P66 (HUMAN);
5935	19740		2.35	4.7E-02	AV846521.1	EST HUMAN	26140638 LUPUS K1 AUTOANTIGEN PROTEIN P66 (HUMAN);
9552	19743		2.35	4.7E-02	P29561	SWISSPROT	26140638 LUPUS K1 AUTOANTIGEN PROTEIN P66 (HUMAN);
9881	19365		1.39	4.7E-02	AJ277662.1	NT	26140638 LUPUS K1 AUTOANTIGEN PROTEIN P66 (HUMAN);
722	10654	20484	2.74	4.8E-02	AE000445.1	NT	26140638 LUPUS K1 AUTOANTIGEN PROTEIN P66 (HUMAN);
1270	11177		1.05	4.8E-02	AD14255.1	EST HUMAN	26140638 LUPUS K1 AUTOANTIGEN PROTEIN P66 (HUMAN);

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Table 4
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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1336	11242	21100	2.74	4.8E-02	AV27059.1	EST_HUMAN	AV27059 HTC Homo sapiens cDNA clone HTCSW/C01 5'
2438	12316	22212	2.51	4.8E-02	AJ29023.1	EST_HUMAN	xi24003.t1 NCI CGAP_K041 Homo sapiens cDNA clone IMAGE:3864663 3' similar to SW-GRF1_HUMAN
2777	10256	20053	1.51	4.8E-02	BE153683.1	EST_HUMAN	Q12848 C-RICH SEQUENCE FACTOR-1;
2777	12604	27703	0.98	4.8E-02	BE153683.1	EST_HUMAN	PMO-HT0339-251199-003-003 HT0339 Homo sapiens cDNA
3461	12804	27703	0.98	4.8E-02	BE153683.1	EST_HUMAN	PMO-HT0339-251199-003-003 HT0339 Homo sapiens cDNA
4033	13636	27703	1.22	4.8E-02	AF220368.1	EST_HUMAN	PMO-HT0339-251199-003-003 HT0339 Homo sapiens cDNA
3777	15684	25792	3.94	4.8E-02	AF220368.1	NT	Mus musculus nuclear RNA helicase II (dazl) gene, complete cds
3777	15684	25793	3.94	4.8E-02	AF220368.1	NT	C-metadiaz II (dazl) mRNA
6070	19083	25200	1.31	4.8E-02	AJ148574.1	EST_HUMAN	C-metadiaz II (dazl) mRNA
7029	19506	27097	3.65	4.8E-02	BE154006.1	EST_HUMAN	PMO-HT0339-251199-003-003 HT0339 Homo sapiens cDNA
6707	18524	25808	3.35	4.8E-02	AJ015328.1	EST_HUMAN	Q27509.31 Source: MCL_3, GBC, S1 Homo sapiens cDNA clone IMAGE:1524737 3'
6633	19748		1.34	4.8E-02	L11692.1	NT	Oryzopsis ventralis macrophage scavenger receptor type II mRNA, complete cds
6845	19343		2.98	4.8E-02	AF27008.1	NT	Human pro-endothelin-1 protein, partial cDNA clone
439	10383	20207	1.84	4.8E-02	P22448	SWISSPROT	REININ-ACID RECEPTOR BETA (RAR-BETA)
1200	11110	20645	0.85	4.8E-02	AF007790.1	NT	Mercury virus strain MS-Africa/Johns Hopkins 1035 (Oasis VP25 gene, complete cds)
1200	11110	20646	0.85	4.8E-02	AF007790.1	NT	Mercury virus strain MS-Africa/Johns Hopkins 1035 (Oasis VP25 gene, complete cds)
1763	11662	21635	3.55	4.8E-02	P32182	SWISSPROT	HEPATOCYTE NUCLEAR FACTOR-3B (HNF-3B)
2083	11663	21680	2.04	4.8E-02	AE003904.1	NT	Xyella fastidiosa, section T10 of 228 of the complete genome
3652	13576	23354	3.83	4.8E-02	AF163278.2	NT	Homo sapiens chromosome 21 segment H521C076
5778	19665	25794	1.54	4.8E-02	AJ400877.1	NT	Homo sapiens ASO3 gene, CCEP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
6861	19770	25956	2.3	4.8E-02	AF036964.1	NT	Arabidopsis thaliana GCAT box binding factor HAP3 homolog gene, complete cds
7718	17568	27793	4.43	4.8E-02	AA332516.1	EST_HUMAN	EST28157 Corallorhiza II Homo sapiens cDNA 3' end similar to neuro-D4 protein
9331	19000	29331	1.74	4.8E-02	11418013	NT	Homo sapiens rd finger protein-like 3 (RFLP3), mRNA
9331	19037	29009	3.41	4.8E-02	AA191097.1	EST_HUMAN	201811.1 T1 Stragelene INT, neuron (9937233) Homo sapiens cDNA clone IMAGE:83498 5'
213	10184		4.79	4.8E-02	BE972793.1	EST_HUMAN	60165154P1 NH, MGC, R2 Homo sapiens cDNA clone IMAGE:383388 5'
1008	10026	20770	1.29	4.8E-02	P31658	SWISSPROT	Drocephila melanogaster extracellular (EXO) mRNA, complete cds
2049	11940		6.15	4.8E-02	P31658	SWISSPROT	HYPOPHYSICAL PROTEIN (OCT 2380)
2440	12317	22214	1.29	4.8E-02	AF075475.1	EST_HUMAN	GV2-P10012-010300-070-p02 P10012 Homo sapiens cDNA
3688	13502	23291	1.86	4.8E-02	AF169100.1	NT	Myocytosarcoma cell sarcoma/Myocytosarcoma cell sarcoma (P107.0) gene, complete cds
4627	14420	24203	1.08	4.8E-02	AF106607.1	NT	Homo sapiens S164 gene, partial cds; P51 and hypothetical protein genes, complete cds; and S171 gene, partial cds

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Probe SEQ ID NO:	Even SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4527	14420	24294	1.08	4.4E-02 AF109007.1	NT		Homo sapiens S104 gene, partial cds; F51 and hypothetical protein genes, complete cds, and S171 gene,
4537	14526		3.12	4.4E-02 AJ228693.1	NT		One gene, CCM4, cathepsin B binding protein, partial cds
7084	16361	27164	1.86	4.4E-02 AF193698.1	EST_HUMAN		hw16361.x1 NC1_CGAP_S51 Homo sapiens cDNA clone IMAGE:2269221 5'
8428	18207	28452	4.11	4.4E-02 AF069389.1	NT		Hsp40L1 E. tritric autar HEV US2 polypeptide (ORF1), (ORF3), and capsid protein (ORF2) genes, complete
8533	18405	28670	2.39	4.4E-02 AF069389.1	EST_HUMAN		hsc400.11 Gascas Wilms tumor Homo sapiens cDNA clone IMAGE:397631 5'
8920	19020		1.38	4.4E-02 AB043628.1	NT		Homo sapiens mRNA for UTM1490 protein, partial cds
9270	19753		1.44	4.4E-02 BF212583.1	EST_HUMAN		0016788P1 NH_3052, 36 Homo sapiens cDNA clone IMAGE:407418 5'
9284	10965	20532	3.74	4.3E-02 AF032348.1	NT		Myosin subclass myosin heavy chain TM3A (TM3A) mRNA, complete cds
2521	12285		1.23	4.3E-02 AF104378.1	EST_HUMAN		AY04878 AB3 Homo sapiens cDNA clone A040408 5'
3383	13301	23101	7.04	4.3E-02 AF104378.1	EST_HUMAN		Homo sapiens chromosome 21 segment HS21C010
3493	13523		1.07	4.3E-02 AF069598.1	NT		Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds
6141	15008	24779	0.92	4.3E-02 AF069598.1	SWISSPROT		Pea P4 grain specific gene
8514	18520	25941	4.83	4.3E-02 P30427	SWISSPROT		PLECTIN
8914	18520	25945	4.83	4.3E-02 P30427	SWISSPROT		PLECTIN
8242	18722	28572	2.48	4.3E-02 AL170121	NT		Rat T33327 NT29M2 Homo sapiens cDNA clone NT29M200020 5'
905	10734	20571	2.05	4.2E-02 AL123327.1	EST_HUMAN		AY04337 NT30M2 Homo sapiens cDNA clone NT29M200020 5'
8448	10776		1.83	4.2E-02 AL123327.1	EST_HUMAN		w049491.x1 NC1_CGAP_F41 Homo sapiens cDNA clone IMAGE:3545594 3' similar to TR:Q33267 Q33267
878	10804	20654	0.83	4.2E-02 AF000445.1	EST_HUMAN		11 RETROPOSON, ORF21 mRNA, contains 1.13.1.1.1 repetitive element;
1850	11892		1.21	4.2E-02 AF040068.1	NT		Thermoplasma acidophilum complete genome; segment 4/5
3117	13042	22388	0.9	4.2E-02 AF054721	EST_HUMAN		99580F02.x1 NC1_CGAP_P3m25 Homo sapiens cDNA clone IMAGE:2019787 3' similar to gp135718
5172	15093		1.07	4.2E-02 D03484.1	NT		Homo sapiens mRNA for KIAA0160 gene, partial cds
6444	16305	28370	4.45	4.2E-02 AF276752.1	NT		Legionella pneumophila catalase-peroxidase (katA) gene, complete cds
7114	16901	27183	3.88	4.2E-02 P06055	SWISSPROT		ALPHA-ACTININ 3, NON MUSCULAR (F-ACTIN CROSS LINKING PROTEIN)
7946	17696	27941	1.28	4.2E-02 P10690	SWISSPROT		T-BRAIN-1 PROTEIN (T-BOX BRAIN PROTEIN 1) (TBR-1) (TFES-56)
8627	18462	28754	2.33	4.2E-02 BE519522.1	EST_HUMAN		PNG-BN0174-256500-009-010 BN0174 Homo sapiens cDNA
8827	18462	28756	2.33	4.2E-02 BE519522.1	EST_HUMAN		PNG-BN0174-256500-009-010 BN0174 Homo sapiens cDNA
8795	19699	28900	1.73	4.2E-02 AF176448.1	NT		PRRS isolate PRRSV26 envelope glycoprotein gene, complete cds
9563	19981		2.69	4.2E-02 AB082494.1	EST_HUMAN		w041010.x1 NC1_CGAP_Pant1 Homo sapiens cDNA clone IMAGE:2510850 3'
2943	12710	22401	0.97	4.1E-02 EC207230.2	NT		Chromylin/mucin, section 60 of 86 of the complete genome
3324	13788	23528	0.86	4.1E-02 EC207230.2	EST_HUMAN		001177607F1 NH_3052, 17 Homo sapiens cDNA clone IMAGE:333353 5'

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Probe SEQ ID NCBI	Exon SEQ ID NCBI	ORF SEQ ID NCBI	Expression Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
3824	13736	23827	0.86	4.1E-02	SE027238.1	EST_HUMAN	30117001F1 NIH_MGC_17 Homo sapiens cDNA, clone IMAGE355353.9
4372	14268		0.37	4.1E-02	A1959349.1	EST_HUMAN	Q1Y1NN0012-18400-104-06 UN00721 Homo sapiens cDNA
6436	16297	28466	1.84	4.1E-02	7628247	NT	Homo sapiens Kufs03.087 protein (P040387), mRNA
6895	16423	28604	2.44	4.1E-02	AF209188.1	NT	Fugu subunit protein cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds; putative protein 1 (PUT1) gene, partial cds; mitotic-specific chromosome segregation protein SMC1 homolog (SMC1) gene, complete cds; and calcium channel alpha-1 subunit
8973	19882	24884	12.83	4.1E-02	A1271009.1	NT	Brassica napus gln gene for plastid glutamine synthetase, exon 1-12
3206	13130	22852	2.88	4.0E-02	A5043904.1	NT	Homo sapiens mRNA for KIAA1471 protein, partial cds
8304	18228	28026	4.92	4.0E-02	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 4 (CYP3A4) gene, partial cds; cytochrome P450 polypeptide 5 (CYP3A5) gene, complete cds; and cytochrome P450 polypeptide 6 (CYP3A6) gene, partial cds
6628	15387	25867	5.89	4.0E-02	L23838.1	NT	Strongylocentrotus purpuratus homolog of human bone morphogenetic protein 1 (subunit) mRNA, complete cds
7036	16888	27126	2.8	4.0E-02	P08940	SWISSPROT	GLUCAMYLASE S162 PRECURSOR (GLUCAM 1',ALPHA-D-GLUCOSIDASE) (1'4-ALPHA-D-GLUCAN GLUCOHYDROLASE)
7572	17423	27638	2.42	4.0E-02	A000944.1	NT	Methanocaldococcus thermophilus strain Marburg, Thioltransferase reductase subunit A
8683	18788		1.94	4.0E-02	AJ001018.1	NT	Kluyveromyces fragilis gene for Caa+ ATPase
8160	18906	25193	4.96	4.0E-02	AJ001056.1	NT	Osteonin mRNA for osteocalcin-carboxylase
1104	11020	21082	2.77	3.8E-02	BF516149.1	EST_HUMAN	U1-HW1-exon-03-01-UT1 nt1_CGAP_Sub7 Homo sapiens cDNA clone IMAGE308473.4 3'
1322	11229	21084	3.46	3.8E-02	AF141047	SWISSPROT	PAS ANTIGEN LIGAND
1918	11813	21091	3.04	3.8E-02	AJ403380.1	NT	Musculus DNA for deamin-binding fragment Dcsd7
2671	12536		2.26	3.8E-02	4506652	NT	Homo sapiens succinate dehydrogenase complex, subunit C, integral membrane protein, 15kD (SD-HC) mRNA
5165	14973	24748	0.88	3.9E-02	8024519	NT	Homo sapiens hypothetical protein PRO1163 (PRO1163), mRNA
5105	14973	24748	0.98	3.9E-02	8924019	NT	Homo sapiens hypothetical protein PRO1163 (PRO1163), mRNA
6591	16461	28654	1.22	3.9E-02	BF238613.1	EST_HUMAN	01900848F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE4134779.5
9056	18044		5.45	3.9E-02	AB042593.1	NT	Falls culture G-CSF gene for granulocyte colony-stimulating factor, complete cds
6967	19248		1.57	3.9E-02	U66361.1	NT	Human germline T cell receptor beta chain (TCRBV17S1A1, TCRBV251, TCRBV10S1P, TCRBV26S1P, TCRBV10S1P, TCRBV19S11, HVB nile, TCRBV26S1P, TCRBV34S1, TCRBV14S1, TCRBV33S1, TCRBV45A1M1, TRV4, TRV5, TRV6, TRV7, TRCBB1, TCRBV1S1, TCRBV1S2+)
9811	19556		7.38	3.9E-02	AL049866.2	NT	Mus musculus chromosome X contig; X-linked lymphocyte regulated 5 gene; Zinc finger protein 275, Zinc finger protein 92, nmix28bfr
1009	11824	21883	0.94	3.9E-02	BE885137.1	EST_HUMAN	00151089F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE3912215.9

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Single Exon Probes Expressed in Heart
Table 4

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6331	10194	26355	1.74	3.5E-02	8005700	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA
7033	10810	29185	1.39	3.5E-02	M60575.1	NT	Human von Willebrand factor gene, exons 23 through 34
8045	17936	29185	2.45	3.5E-02	AF143652.2	NT	Homo sapiens PELOTA (PELOTA) gene, complete cds
976	10869	20746	4.59	3.7E-02	P10137	SWISSPROT	LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN)
1396	11272	21128	0.9	3.7E-02	14591.1	NT	Homo sapiens plasma membrane calcium ATP-ase isoform 1 (ATP2B1) gene, alternative splice products, partial cds
2190	12071	21982	6.3	3.7E-02	A69406.1	EST_HUMAN	w8505.x1 NCPI, Kdr11 Homo sapiens cDNA clone IMAGE:2494502 3'
2533	12407	22269	0.91	3.7E-02	AB015261.1	NT	Homo sapiens mRNA for KIAA0718 protein, partial cds
3012	12940	22733	0.8	3.7E-02	F76944	SWISSPROT	EXOMEODERMIN
3013	12941	22734	3.45	3.7E-02	BF11295.1	EST_HUMAN	Mus musculus potassium large conductance pH-sensitive channel, subfamily M, alpha member 3 (Kcnnk3), mRNA
3408	13325	25119	1.1	3.7E-02	6680541	NT	60176217F1 NIH, MGC -70 Homo sapiens cDNA clone IMAGE:4024673 5'
5995	18957	25093	1.63	3.7E-02	11418392	NT	Homo sapiens scabiosin carrier family 22 (organic cation transporter), member 1 (SLC22A1), mRNA
8755	19520	25093	1.63	3.7E-02	11418392	NT	H. vulgare Sst1 gene for sucrose synthase
3504	13518	23308	0.85	3.5E-02	A73221.1	NT	Homo sapiens genomic region containing hypoxanthine phosphoribosyl transferase chromosome 10 (q28.3) of Homo sapiens
3612	13526	23313	0.8	3.5E-02	AL039803.1	NT	Homo sapiens genomic region containing hypoxanthine phosphoribosyl transferase chromosome 10 (q28.3) of Homo sapiens
5135	19002	24773	0.84	3.5E-02	AL039810.1	NT	OMZ-EN0073-110500-102-510 EN0073 Homo sapiens cDNA
6028	19632	26062	5	3.5E-02	AF145516.1	EST_HUMAN	OMZ-EN0073-110500-102-510 EN0073 Homo sapiens cDNA
6028	19632	26063	5	3.5E-02	AF145516.1	EST_HUMAN	Chetium murexium salivary gland protein C12 precursor (cp2) gene, complete cds
6214	10080	26229	1.82	3.5E-02	AF129552.1	NT	m2060531 NC1, CGAP -10080 Homo sapiens cDNA clone IMAGE:1241024 3' similar to gp.000314_m2
6324	10197	26340	2.83	3.5E-02	AAT14521.1	EST_HUMAN	TUBULIN BETA-51 CHAIN (HUMAN);
7402	17269	27473	2.08	3.5E-02	J200608.1	NT	Diclyptelium discoidium unknown spore germination-specific protein-like protein, orf1, orf2 and orf3 genes, complete cds
7402	17269	27474	2.08	3.5E-02	J200608.1	NT	Diclyptelium discoidium unknown spore germination-specific protein-like protein, orf1, orf2 and orf3 genes, complete cds
877	10803	20653	1.15	3.5E-02	U09006.1	NT	Orosphila melanogaster legitin mRNA, complete cds
892	10913	20758	1.53	3.5E-02	AF253417.1	NT	Homo sapiens microsome epoxide hydrolase (EPHX1) gene, complete cds
1544	11449	21309	1.49	3.5E-02	BF176065.1	EST_HUMAN	Homo sapiens microsome epoxide hydrolase (EPHX1) gene, complete cds
1544	11449	21310	1.49	3.5E-02	BF176065.1	EST_HUMAN	902085130F1 NIH, MGC -83 Homo sapiens cDNA clone IMAGE:4268377 5'
1544	11449	21310	1.49	3.5E-02	BF176065.1	EST_HUMAN	902085130F1 NIH, MGC -83 Homo sapiens cDNA clone IMAGE:4268377 5'
4120	14020	23798	2.01	3.5E-02	AE001773.1	NT	Thermoplasma maritima section 85 of 136 of the complete genome

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Table 4

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Probe SEQ ID NO.	Exon SEQ ID NO.	GRF SEQ ID NO.	Expression Signal	Most Similar Top Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1705	11606		1.28	3.3E-02	AE00700.1	NT	Aquifer sedicus section 32 of 108 of the complete genome
2038	11029		2.77	3.3E-02	RG0112.1	EST_HUMAN	V25c08.1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:127688.5
4086	11625	21393	2.24	3.3E-02	AF110763.1	NT	Homo sapiens skeletal muscle LM-protein 1 (HLT) gene, complete cds
4366	14262	24047	1.85	3.3E-02	6755952	NT	Mus musculus tumor rejection antigen gp98 (Trat), mRNA
5976	15781	29002	18.26	3.3E-02	BF24566.1	EST_HUMAN	601553910F1 NIH MGCC 571 Homo sapiens cDNA clone IMAGE:4073787.5
5975	15781	29002	18.26	3.3E-02	BF24566.1	EST_HUMAN	601553910F1 NIH MGCC 571 Homo sapiens cDNA clone IMAGE:4073787.5
8463	18337	28901	3.39	3.3E-02	BF691107.1	EST_HUMAN	60224717F1 NIH MGCC 821 Homo sapiens cDNA clone IMAGE:4332497.5
9260	18931		1.78	3.3E-02	T06543.1	EST_HUMAN	ye4811.1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:121101.5
9441	18078		1.50	3.3E-02	M81800.1	NT	Human interleukin 11 (L11) gene, complete mRNA
127	10101	19223	1.13	3.3E-02	AJ002005.1	NT	Cryptosporidium parvum gene encoding ileal sodium-dependent bile acid transporter
1110	11026	20967	12.7	3.3E-02	AF096273.1	NT	Drosophila melanogaster head shock protein 68 (hap68) gene, hap68d allele, complete cds
1110	11026	20968	12.7	3.3E-02	AF096273.1	NT	Drosophila melanogaster head shock protein 68 (hap68) gene, hap68d allele, complete cds
1734	11836	21503	1.14	3.3E-02	AF12864.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 7-16 and complete cds
2072	11932		0.91	3.3E-02	P26935	SWISSPROT	LARGE TEGUMENT PROTEIN
2859	10101	19923	1.15	3.3E-02	AJ002005.1	NT	Cryptosporidium parvum gene encoding ileal sodium-dependent bile acid transporter
3095	13022	22817	10.71	3.3E-02	BE667353.1	EST_HUMAN	59142431F1 NIH MGCC 851 Homo sapiens cDNA clone IMAGE:3848727.5
3883	13697	20554	1.05	3.3E-02	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4124	14034		12.30	3.3E-02	304708.1	NT	H sapiens REP3 gene (XLRP gene 3)
4658	14544	24333	2.88	3.3E-02	AF114824.1	NT	Saccharomyces cerevisiae (yeast) gene, chloroplast gene encoding chloroplast protein, partial cds
5359	15318	23359	1.40	3.3E-02	X87108.1	NT	S. glycolicoides wHG-Su gene
5359	15318	23359	1.40	3.3E-02	X87108.1	NT	S. glycolicoides wHG-Su gene
5851	15536	25656	2.25	3.3E-02	NS2497.1	NT	Rat polyoma virus PTA-1 junction in cell line W8-14
5832	15837		26.54	3.3E-02	T63897.1	EST_HUMAN	Y03811.2 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:110087.5 similar to contains
5968	15951	28013	3.72	3.3E-02	AF17846.1	NT	Alu repetitive element contains L1/T1 repetitive element
6390	16768	25802	3.48	3.3E-02	6603955	NT	Sagittaria latifolia tissue kallikrein gene, complete cds
7766	17636		3.82	3.3E-02	AA176795.1	EST_HUMAN	245461.21 Soares: pituitary gland NDRHG Homo sapiens cDNA clone IMAGE:397151.3 similar to
9552	19467		1.38	3.3E-02	AB02184.1	NT	gp108H41 CYTOSOLIC CHROMOSOME C OXIDASE POLYPEPTIDE III (HUMAN);
1239	11146		2.05	3.3E-02	4503416	NT	Mercurialis polymorpha genes for 26S rRNA, 5S rRNA, 18S rRNA, and 26S rRNA
1283	11191	21043	1.28	3.3E-02	P18845	SWISSPROT	Homo sapiens cdu specificity phosphatase 4 (CDS4) mRNA
1850	11746	21621	1.35	3.3E-02	6671564	NT	NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-3 CHAIN PRECURSOR (GF-ALPHA-3)
1931	11826		1.09	3.3E-02	250097.1	NT	Mus musculus adaptor-related protein complex AP-3, delta subunit (Ap3delta), mRNA
							Drosophila melanogaster mRNA for hecidiase protein

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Table 4
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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4132	14032		0.82	3.1E-02	AF119006.1	EST_HUMAN	AUT18000 HEMBA1 Homo sapiens cDNA clone HEMBA1004842 5'
4757	14652	24440	0.99	3.1E-02	AF083513.1	EST_HUMAN	OVAL-T0014-250200-126-009 T0014 Homo sapiens cDNA
5200	15211		2.39	3.1E-02	AA278478.1	EST_HUMAN	2881463.1 NCI CGAP CG81 Homo sapiens cDNA clone IMAGE 703959 5'
7765	17616	27843	2.62	3.1E-02	AF034778.1	NT	Enterococcus faecalis surface protein precursor, gene, complete cds
1608	11911		2.82	3.0E-02	AF187125.1	NT	Polydiphosphate synthase (cytochrome oxidase) gene, partial cds, mitochondrial gene for mitochondrial product
2541	12416	22305	1.07	3.0E-02	AA402242.1	EST_HUMAN	269503.11 Swain, beta, NHT Homo sapiens cDNA clone IMAGE 727253 5'
3518	18434	23234	1.07	3.0E-02	AF01765.1	NT	Saccharomyces cerevisiae stem loop initiation suppressor SSI2, gene, complete cds
3603	13617	23305	2.61	3.0E-02	AF217644.1	NT	Pseudomonas fluorescens frtII, beta-lactamase gene, complete cds
3695	13693		0.99	3.0E-02	AF020233.1	EST_HUMAN	EST17430 Pnta1 (beta) II Homo sapiens cDNA
3696	13777		1.18	3.0E-02	AF083023.1	EST_HUMAN	EST17430 Pnta1 (beta) II Homo sapiens cDNA 8' and
4779	14657	24444	0.89	3.0E-02	AF020233.1	EST_HUMAN	60177203 F1NF.MGC.07 Homo sapiens cDNA clone IMAGE 3875603 5'
4933	14859	24624	6.02	3.0E-02	AF251074.1	NT	Homo sapiens neuropilin 2 (NP2) gene, complete cds, alternatively spliced
4933	14859	24625	6.02	3.0E-02	AF251074.1	NT	Homo sapiens neuropilin 2 (NP2) gene, complete cds, alternatively spliced
8312	12333		2.89	3.0E-02	AF049703.1	NT	Homo sapiens mRNA for KIAA1573 protein, partial cds
8096	10050	26196	2.71	3.0E-02	AJ242063.1	NT	Cyprinus carpio mRNA for inducible nitric oxide synthase (iNOS) gene
8127	15974	26109	3.59	3.0E-02	BE88948.1	EST_HUMAN	60151200 F1NF.MGC.71 Homo sapiens cDNA clone IMAGE 3813948 5'
8127	15974	26110	3.59	3.0E-02	BE88948.1	EST_HUMAN	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
8207	15987	26101	1.79	3.0E-02	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
8207	15987	26102	1.79	3.0E-02	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
9202	19160	26311	1.54	3.0E-02	AF06624.1	NT	Human dystrophin gene
7106	19583		2.11	3.0E-02	AF27664.1	NT	Omithrhythmus anellatus coagulation factor X mRNA, complete cds
7978	17828	28089	1.71	3.0E-02	AE001797.1	NT	Thermoplasma maritima section 100 of 139 of the complete genome
8562	18432	28701	3.09	3.0E-02	AF01387.1	NT	Human coagulation factor VII (F7) gene exon 1 and factor X (F10) gene, exon 1
8571	18745	29039	7.7	3.0E-02	AA163216.1	EST_HUMAN	m87604.s1 NCI CGAP_K071 Homo sapiens cDNA clone IMAGE 911283
9396	19730	24909	1.66	3.0E-02	R32019.1	EST_HUMAN	Y65904.s1 Soares placenta NB2HP Homo sapiens cDNA clone IMAGE:134407 3'
9740	19273		4.67	3.0E-02	AF058565.1	EST_HUMAN	OVAL-N0008-270-400-187-H05 NN0038 Homo sapiens cDNA
9790	19723		2.09	3.0E-02	AF048867.1	NT	Rattus norvegicus UDP-Gal 4-epimerase beta-1,4-galactosyltransferase mRNA, complete cds
2385	12720	22167	1.1	2.9E-02	AF257703.1	NT	Homo sapiens mitochondrial glutathione reductase and cytosolic glutathione reductase (GRU1) gene, alternatively spliced
2662	12850	22687	1.07	2.9E-02	BE59664.1	EST_HUMAN	60133342 F1NF.MGC.53 Homo sapiens cDNA clone IMAGE 3690059 5'

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Protein Accession NO.	Exon Seq ID NO.	ORF Seq ID NO.	Expression Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Distance Source	Top Hit Description
2902	13890	20868	1.07	2.8E-02	BE569244.1	EST_HUMAN	60133242BT NIH_MGC_59 Homo sapiens cDNA clone IMAGE:358064 5'
3851	13762	20855	0.92	2.0E-02	AF172905.1	EST_HUMAN	u07010.1 Scores full liver sapiens T1NF5 Homo sapiens cDNA clone IMAGE:231130 5'
4650	14627	21630	1.32	2.0E-02	X6137.1	NT	S. vulgaris p400 genes for PEP carboxylase
4950	14627	21630	1.32	2.0E-02	X6137.1	NT	S. vulgaris p400 genes for PEP carboxylase
5790	15705	20817	1.47	2.0E-02	AF032233.1	EST_HUMAN	60145359BT NIH_MGC_60 Homo sapiens cDNA clone IMAGE:358568 5'
6236	16152	20819	1.03	2.0E-02	BE271430.1	EST_HUMAN	60140738BT NIH_MGC_58 Homo sapiens cDNA clone IMAGE:304850 5'
7908	17419	27635	1.34	2.0E-02	AF187978.1	EST_HUMAN	CMS-17001-1-071235-05T-c04 P10014 Homo sapiens cDNA
7908	17419	27635	1.34	2.0E-02	AF187978.1	EST_HUMAN	CMS-17001-1-071235-05T-c04 P10014 Homo sapiens cDNA
563	10464	23046	1.37	2.0E-02	AF197015.1	EST_HUMAN	EST362234 IMAGE resistances, TACR6 Homo sapiens cDNA
3321	13241	23046	1.27	2.0E-02	AF196083.1	NT	Homo sapiens retinal tacin (FSN2) gene, exon 2
3321	13241	23047	1.27	2.0E-02	AF196083.1	NT	Homo sapiens retinal tacin (FSN2) gene, exon 2
4214	14714	23347	0.98	2.0E-02	893757.1	NT	Fetus notegous microtubule-associated protein tau (Map1) mRNA
5373	15293	25140	11.41	2.0E-02	BE714083.1	EST_HUMAN	60180407BT NIH_MGC_59 Homo sapiens cDNA clone IMAGE:304807 5'
6547	16720	26620	1.33	2.0E-02	AA069520.1	NT	Orderadigma plasmidgen mRNA for homeodomain leucine zipper protein (hbc-1)
9674	19674	27635	1.51	2.0E-02	AF069651.1	EST_HUMAN	u07010.1 Scores full liver sapiens T1NF5 Homo sapiens cDNA clone IMAGE:126376 5'
9980	19237	27635	1.33	2.0E-02	X06322.1	NT	Yeast GNC30 chromosome III RH45 DNA (right arm transcription hot-spot)
1473	11378	21242	1.26	2.7E-02	U60609.1	NT	TCRBV135R135S>
3385	13303	23103	2.07	2.7E-02	AF161494.2	EST_HUMAN	Arbidopole Italiane DNA chromosome 4, contig fragment No. 6
4307	14007	23763	2.07	2.7E-02	N47258.1	EST_HUMAN	Y69HJ21 Scores, multiple sclerosis, ZNF4MSP Homo sapiens cDNA clone IMAGE:280487 5'
4307	14007	23764	2.07	2.7E-02	N47258.1	EST_HUMAN	Y69HJ21 Scores, multiple sclerosis, ZNF4MSP Homo sapiens cDNA clone IMAGE:280487 5'
6205	15995	20809	1.9	2.7E-02	AA568377.1	EST_HUMAN	069003.31 Scores, total leuko, N30H8 5w Homo sapiens cDNA clone IMAGE:1924861 3'
9548	16900	25134	1.52	2.7E-02	BF154856.1	EST_HUMAN	UHH BW1-161-105-0 UL1 NCL CGAP Sub7 Homo sapiens cDNA clone IMAGE:3082520 3'
559	10490	20306	1.14	2.0E-02	AF169282.1	NT	Homo sapiens chromosome 21 segment HS21D82
1346	11281	22093	1.04	2.0E-02	AA806915.1	EST_HUMAN	L3-CT0219-280100-062-C08 012019 Homo sapiens cDNA
2315	12196	22093	2.9	2.0E-02	AA480021.1	EST_HUMAN	L3-CT0219-280100-062-C08 012019 Homo sapiens cDNA
2206	22005	22005	2.86	2.0E-02	6754241	NT	u072002.1 Shiga toxin like retinoblastoma 872070 Homo sapiens cDNA clone IMAGE:358595 3'
2317	12198	22006	2.86	2.0E-02	6754241	NT	Mus musculus histidine rich calcium binding protein (Hrc) mRNA
2317	12198	22006	2.86	2.0E-02	6754241	NT	Mus musculus histidine rich calcium binding protein (Hrc) mRNA
2885	12012	22006	1.95	2.0E-02	AF106906.1	NT	Mus musculus MHC class II region RD gene, partial cds; B1, C2, G9A, N322, G9, HSP70, HSP70, HSC70, and anrmp genes, complete cds; G7A gene, partial cds; and unknown genes
3853	13764	23046	1.13	2.0E-02	AF161916.1	EST_HUMAN	Y69HJ21 Scores, multiple sclerosis, ZNF4MSP Homo sapiens cDNA clone IMAGE:280487 5'
4517	14314	23046	1.13	2.0E-02	BE569244.1	EST_HUMAN	60180407BT NIH_MGC_59 Homo sapiens cDNA clone IMAGE:358568 5'

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4811	16695	24481	3.09	2.0E-02	L12032.1	NT	Chicken desmin-1 mRNA, complete cds
4993	14873	24637	1.67	2.0E-02	AE002041.1	NT	Dendroica rubicunda R1 section 151 of 229 of the complete chromosome 1
5025	14698	24667	2.06	2.0E-02	AW204154.1	EST_HUMAN	h5204.x1 NCI CGAP_Sarc Homo sapiens cDNA clone IMAGE:3073038 3' similar to SW17059_HUMAN
5771	15978		6.95	2.0E-02	AI009030.1	EST_HUMAN	Q18041 HYPOTHETICAL PROTEIN KIAA0069
5870	15776	25805	2.08	2.0E-02	BE821748.1	EST_HUMAN	q92711.1 NCI CGAP_K48 Homo sapiens cDNA clone IMAGE:176237 3'
6130	15971	26113	6.09	2.0E-02	6891271	EST_HUMAN	Q1492473.1 NH_MGC_70 Homo sapiens cDNA clone IMAGE:3995678 3'
7398	17308	27512	1.19	2.0E-02	11422020	NT	Rattus norvegicus Nerve growth factor receptor, fast (Ngfr), mRNA
7948	17798	28038	4.87	2.0E-02	AL163303.2	EST_HUMAN	Homo sapiens KIAA1070 protein (KIAA1070), mRNA
8662	18579		2.1	2.0E-02	AA270351.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C103
8848	18600	28949	1.89	2.0E-02	AW500547.1	EST_HUMAN	2384402.01 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:704162 5'
9320	19715	24906	1.58	2.0E-02	BF343827.1	EST_HUMAN	U1HF.BNO-4H+10.0.U1.1 NH_MGC_50 Homo sapiens cDNA clone IMAGE:3077468 5'
521	10483	20274	1.45	2.0E-02	AT093130.1	EST_HUMAN	90201560.F1 NCI CGAP_Brm4 Homo sapiens cDNA clone IMAGE:4159444 5'
521	10483	20274	1.45	2.0E-02	AT093130.1	EST_HUMAN	902006.05 NCI CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1657427 5'
792	10721	20562	12.83	2.0E-02	BE974314.1	EST_HUMAN	9018003852.NH_MGC_83 Homo sapiens cDNA clone IMAGE:3950668 3'
881	10778	20638	4.77	2.0E-02	BE974314.1	EST_HUMAN	9018003852.NH_MGC_83 Homo sapiens cDNA clone IMAGE:3950668 3'
2735	12697		2.59	2.0E-02	U12571.1	NT	Rattus norvegicus zap70b-3A, mRNA, complete cds
2028	12653	22462	4.4	2.0E-02	X09697.1	NT	H. carassius mRNA for farnesyl transferase binding protein, Fop1
2028	12653	22463	4.4	2.0E-02	X09697.1	NT	H. carassius mRNA for farnesyl transferase binding protein, Fop1
3959	16700	23643	1.09	2.0E-02	BE701165.1	EST_HUMAN	PM2.NM0128-007070-001-x12.NM0128 Homo sapiens cDNA
3959	16700	23644	1.09	2.0E-02	BE701165.1	EST_HUMAN	PM2.NM0128-007070-001-x12.NM0128 Homo sapiens cDNA
4111	14011	23768	5.97	2.0E-02	AB262141.1	EST_HUMAN	h554008.x1 Sordex.NE1_1_C5C_5.11 Homo sapiens cDNA clone IMAGE:3924015 3'
5759	15697		4.48	2.0E-02	BE670128.1	EST_HUMAN	7480008.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284008 3' similar to contains L1.N1.1 repetitive element 1
5767	15674		3.86	2.0E-02	BE740888.1	EST_HUMAN	901870339.F1 NH_MGC_9 Homo sapiens cDNA clone IMAGE:3928054 5'
6519	16378	26585	1.57	2.0E-02	BF520721.1	EST_HUMAN	90201662.F1 NCI CGAP_Brm4 Homo sapiens cDNA clone IMAGE:4213408 5'
6519	16378	26586	1.57	2.0E-02	BF520721.1	EST_HUMAN	90201662.F1 NCI CGAP_Brm4 Homo sapiens cDNA clone IMAGE:4213408 5'
8185	18071	28520	2.45	2.0E-02	Q10339	SWISSPROT	HYPOTHETICAL 487 MD PROTEIN C19310.05 IN CHROMOSOME 1
8185	18071	28521	2.45	2.0E-02	Q10339	SWISSPROT	HYPOTHETICAL 487 MD PROTEIN C19310.05 IN CHROMOSOME 1
8238	18118	28570	3.39	2.0E-02	AL237036.1	NT	Bos taurus partial alpha gene, exons 17-19
8255	18135		3.39	2.0E-02	AF050167.1	NT	Mus musculus major histocompatibility class II region, major histocompatibility protein class II alpha chain (Mudpup) and major histocompatibility protein class II beta chain (Ebeta) genes, complete cds; bryophyllin-like (NCG), bryophyllin-like
8978	18783		1.74	2.0E-02	AB007546.1	NT	Homo sapiens gene for LECT2, complete cds

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8280	19037		2.19	2.5E-02	11420078	NT	Homo sapiens similar to ALEX3 protein (H. sapiens) LOC93834, mRNA
8403	19028		1.63	2.5E-02	11433220	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 13 (MAPKKK13), mRNA
8581	19107	28271	2.39	2.5E-02	BE979327.1	EST HUMAN	5018526582 NIH MGSC B2 Homo sapiens cDNA clone IMAGE:393618 3'
167	10109	19056	1.01	2.4E-02	AG78936.1	EST HUMAN	1672007.AT Scores: NHHMPU, S1 Homo sapiens cDNA clone IMAGE:211149 5'
1580	11484	21344	1.89	2.4E-02	H65964.1	EST HUMAN	W76111.AT Scores: fetal liver spleen INRLS Homo sapiens cDNA clone IMAGE:2707156 3'
1698	12770	21784	2.22	2.4E-02	P01901	SWISSPROT	H-2 CLASS HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
1698	12770	21785	2.22	2.4E-02	P01901	SWISSPROT	H-2 CLASS HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
4372	14171	29648	1.4	2.4E-02	J06110.1	NT	T. thermophilus calcium-binding 28 kDa (TCBP 28) protein mRNA, complete cds
4426	14314	24059	1.03	2.4E-02	P01901	SWISSPROT	H-2 CLASS HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
4426	14314	24100	1.43	2.4E-02	P01901	SWISSPROT	H-2 CLASS HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
5119	14857		11.51	2.4E-02	AL161596.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 91
8802	18640	27032	10.39	2.4E-02	N89143.1	EST HUMAN	383501.AT Scores: fetal liver spleen INRLS Homo sapiens cDNA clone IMAGE:284466 3' similar to
7643	17463	27714	2.17	2.4E-02	AV062954.1	EST HUMAN	g81020900RATSR7K Rat (RNA) containing ASR b1 A3R repetitive element ;
7734	17594	27808	2.98	2.4E-02	AA463804.1	EST HUMAN	W07012.1 NC1 C2AP Thy1 Homo sapiens cDNA clone IMAGE:943593 similar to contains Alu repetitive element/contains element PTF5 repetitive element ;
8857	18889	28856	1.96	2.4E-02	AF105005.1	NT	Mus musculus major histocompatibility locus class III regions H-2D1 genes, partial cds; anRNP, G7A, NG23, MafB homolog, CLCP, NG24, NG25, and NG28 genes, complete cds, and unknown genes
8857	18889	28857	1.96	2.4E-02	AF105005.1	NT	Mus musculus major histocompatibility locus class III regions H-2D1 genes, partial cds; anRNP, G7A, NG23, MafB homolog, CLCP, NG24, NG25, and NG28 genes, complete cds, and unknown genes
9080	18896		1.95	2.4E-02	657969	NT	Bacteriophage B107, complete genome
9224	18847	25337	2.72	2.4E-02	9753653	NT	Mus musculus DnaD homolog 1 (L. coli) (DnaS), mRNA
9282	18864	25326	2.03	2.4E-02	BE528686.1	EST HUMAN	NR017-107175-310800-200-406 OT175 Homo sapiens cDNA
9398	19036		1.27	2.4E-02	AF105864.1	NT	Homo sapiens SPCA isoform (SPCA) gene, complete cds, alternatively spliced
9505	19120		3.87	2.4E-02	AB008969.1	NT	Ceanothoides elegans mRNA, for non-sulfur subunit of mitochondrial succinate dehydrogenase, complete cds
9532	19138		1.6	2.4E-02	NA2390.1	EST HUMAN	Y005605.UT Scores: melanocyte 28kDa Homo sapiens cDNA clone IMAGE:270610 5'
9538	19141		1.38	2.4E-02	BF079477.1	EST HUMAN	160215281F1 NIH MGSC B3 Homo sapiens cDNA clone IMAGE:4294718 5'
9977	19007		1.59	2.4E-02	P04643	SWISSPROT	SPORE COAT PROTEIN SP07 PRECURSOR (PL3 PROTEIN)
1826	11726		5.78	2.3E-02	W65340.1	EST HUMAN	288768.AT Scores: fetal lung, NHL15W Homo sapiens cDNA clone IMAGE:290264 5'
1844	11740		7.89	2.3E-02	U61865.1	NT	4 Homo sapiens mammary tumor-associated protein INT6 (INT6) gene, exon 4
2302	12183	22081	2.52	2.3E-02	Z74263.1	NT	S. cerevisiae chromosome IV reading frame ORF YOL2456

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Probe Seq ID NO.	Exon Seq ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Distance Score	Top Hit Description
3628	15842	23329	4.79	2.5E-02	Z3037.1	EST_HUMAN	HSAATC3DH2P Human fetal Brain Whole tissue Homo sapiens cDNA
4057	13569	23735	1.19	2.3E-02	Z47195.1	NT	Gallus gallus connective AS6 (Cvds 6) gene, complete cds
4097	13569	23735	1.19	2.3E-02	Z47195.1	NT	Gallus gallus connective AS6 (Cvds 6) gene, complete cds
4323	14249	24002	1.26	2.3E-02	AF1986107.1	EST_HUMAN	U441NN368.350-003.100-350.NN0350 Homo sapiens cDNA
4347	14244	24027	0.81	2.3E-02	BE365225.1	EST_HUMAN	CAC-MIT0118-070900-318-907.MT0118 Homo sapiens cDNA
4347	14244	24028	0.81	2.3E-02	BE365225.1	EST_HUMAN	CAC-MIT0118-070900-318-907.MT0118 Homo sapiens cDNA
4347	14244	24029	0.84	2.3E-02	AF1959983.1	EST_HUMAN	2526083.81 NC1 CGAP- D2 Homo sapiens cDNA clone IMAGE2770871.3
4348	15072	24029	0.84	2.3E-02	AF1959983.1	EST_HUMAN	2526083.81 NC1 CGAP- D2 Homo sapiens cDNA clone IMAGE2770871.3
4348	15072	24030	0.84	2.3E-02	BC143150.1	EST_HUMAN	80167.227997.NH1.MGC_20 Homo sapiens cDNA clone IMAGE3563398.5
4472	14399	24155	1.75	2.3E-02	BC143150.1	EST_HUMAN	80167.227997.NH1.MGC_20 Homo sapiens cDNA clone IMAGE3563398.5
4490	14384	24171	2.39	2.3E-02	BF024987.1	EST_HUMAN	916762203.3 NC1 CGAP- K4H1 Homo sapiens cDNA clone IMAGE2028588.3
4490	14384	24172	2.39	2.3E-02	BF024987.1	EST_HUMAN	916762203.3 NC1 CGAP- K4H1 Homo sapiens cDNA clone IMAGE2028588.3
4948	14825	24591	1	2.3E-02	AF793177.1	EST_HUMAN	9256035.3 NC1 CGAP- K4H1 Homo sapiens cDNA clone IMAGE2028588.3
4948	14825	24592	1	2.3E-02	AF793177.1	EST_HUMAN	9256035.3 NC1 CGAP- K4H1 Homo sapiens cDNA clone IMAGE2028588.3
6302	18223	25027	3.57	2.3E-02	U63303.1	NT	Cardiac-specific topoisomerase IV P-ant substrate (pate) gene, complete cds, and propionyl-CoA carboxylase beta chain (pcbb) homologous genes, partial cds
6990	16895	26018	4	2.3E-02	AF161505.2	NT	Arabidopsis thaliana DNA chromosome 1, contig fragment NC_17
6998	16478	26055	5.57	2.3E-02	U63010.1	NT	Human plectin (PLEC1) gene, exons 3-32, and complete cds
7764	17614	27941	1.51	2.3E-02	AC030119.1	NT	Escherichia coli K-12 MG1655 section 88 of 400 of the complete genome
7764	17614	27942	1.51	2.3E-02	AC030119.1	NT	Escherichia coli K-12 MG1655 section 88 of 400 of the complete genome
8162	18050	28302	2.16	2.3E-02	P06849	SWISS-PROT	GLUCOAMYLASE STIS2 PRECURSOR (GLUCAN 1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)
9201	19512	2	4.41	2.3E-02	BE278331.1	EST_HUMAN	80117950871.NH1.MGC_21 Homo sapiens cDNA clone IMAGE3545667.5
9713	10254	25210	1.94	2.3E-02	U63934.1	NT	Siniperla kneri sp. alpha-1,3/4-fucosidase precursor gene, complete cds
9767	19759	1	2.27	2.3E-02	U11077.1	NT	Dicystostellum discoideum extracellular signal-regulated protein kinase (ERK1) mRNA, complete cds
9951	18609	1	1.27	2.3E-02	U11423989.1	NT	Homo sapiens dead nigar (Cnophilophylla) beta 1 (ORL1), mRNA
720	10852	20482	3.09	2.2E-02	AF193297.1	NT	Columbia lima nucleoside diphosphate kinase (NDPK) gene, nuclear gene encoding mitochondrial protein, complete cds
1713	11104	1	1.53	2.2E-02	4957448	NT	Homo sapiens chromodomain helicase DNA binding protein 2 (CHD2) mRNA
1908	11891	21752	1.78	2.2E-02	Z52001.1	NT	S. pneumoniae psdA gene and open reading frame
2230	12248	22448	1.4	2.2E-02	AF109633.1	NT	Mus musculus rat variant protein ERB1 gene, exons 1 through 4
3395	13305	23595	1.93	2.2E-02	AA577785.1	EST_HUMAN	MT26024.01 NC1 CGAP- Gier1 Homo sapiens cDNA clone IMAGE1094782.3
3595	13509	1	3.27	2.2E-02	AF168094.1	NT	Infectious bacterial disease virus segment B strain I-4 VP1 gene, complete cds
3779	18477	23477	1.05	2.2E-02	AW103137.1	EST_HUMAN	BM0-8170340-770100-404303.B T0340 Homo sapiens cDNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3844	13705	29549	0.99	2.2E-02	Z71293.1	NT	S.cerevisiae chromosome IV reading frame ORF YOL245c
6297	16751	29318	3.78	2.2E-02	AF166072.1	EST_HUMAN	AV699721 GKG Homo sapiens cDNA clone GKGAND03.3
6876	16755	29552	2.26	2.2E-02	AF161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
6876	16755	29553	2.26	2.2E-02	AF161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
7855	17436	27651	2.33	2.2E-02	AB023983.1	NT	Homo sapiens DNA, DLEC1 to ORC1L4 gene region, section 1/2 (DLEC1, ORC1L3, ORC1L4 genes, complete cds)
7855	17436	27652	2.33	2.2E-02	AB023983.1	NT	Homo sapiens DNA, DLEC1 to ORC1L4 gene region, section 1/2 (DLEC1, ORC1L3, ORC1L4 genes, complete cds)
9466	19098		2.24	2.2E-02	AA024593.1	EST_HUMAN	hesh707.1 NCI CGAP_C3b Homo sapiens cDNA clone IMAGE500541.3 similar to contains Alu repetitive element
413	10359		5.56	2.1E-02	AF167692.1	EST_HUMAN	Dipstickium discolorum histidine kinase C (DHK) mRNA, complete cds
441	10359		7.99	2.1E-02	AF029728.1	NT	Bacillus subtilis coeLUM cluster, Cok (cok), Cok (cok), and spore coat protein CokM (cokM) genes, complete cds
1242	11149	29998	7.43	2.1E-02	U72073.1	NT	Bacillus subtilis macrophage migration inhibitor factor (MIF) gene, 5' flanking region and partial cds
1365	11270	21125	1.91	2.1E-02	AF200395.1	NT	Mus musculus macrophage migration inhibitor factor (MIF) gene, 5' flanking region and partial cds
1365	11270	21126	1.91	2.1E-02	AF200395.1	NT	Mus musculus macrophage migration inhibitor factor (MIF) gene, 5' flanking region and partial cds
1920	11815	21664	0.95	2.1E-02	AF160899.1	NT	Trypanosoma brucei major surface glycoprotein precursor (MSP) mRNA, complete cds
2785	10963	20590	3.98	2.1E-02	N52698.1	EST_HUMAN	Y45897.1 Scores: melanocyte 213441 Homo sapiens cDNA clone IMAGE234541.5
3110	11883	21776	0.85	2.1E-02	BE072546.1	EST_HUMAN	PI2C-810546:120100-301111 BT0546 Homo sapiens cDNA
3535	13451	21777	0.85	2.1E-02	BE072546.1	EST_HUMAN	PI2C-810546:120100-301111 BT0546 Homo sapiens cDNA
4038	13941	23247	1.23	2.1E-02	AA461271.1	EST_HUMAN	263409.1 Scores: beta_2_mig_H2bP6_5w Homo sapiens cDNA clone IMAGE769121.5
4342	14239	24022	0.89	2.1E-02	U49141.1	NT	S.cerevisiae chromosome IV reading frame ORF YOL245c
4351	14247	24033	1.61	2.1E-02	U49141.1	NT	S.cerevisiae chromosome IV reading frame ORF YOL245c
4611	14499	24286	1.03	2.1E-02	Y08591.1	EST_HUMAN	A.thaliana mitochondrial genome, part A
4714	14600	24386	4.05	2.1E-02	AB24332.1	EST_HUMAN	W614405.1 NCI CGAP_K3H1 Homo sapiens cDNA clone IMAGE2394528.3
7553	17404	27618	0.89	2.1E-02	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
7553	17404	27619	1.8	2.1E-02	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
9440	15095		4.99	2.1E-02	Y19213.1	NT	Homo sapiens putative pathHBA pseudogene for hair keratin, exons 2 to 7
9837	19348	25184	3.33	2.1E-02	AF183913.1	NT	Azospirillum brasilense major outer membrane protein OmsA precursor (omsA) gene, complete cds
17	10004	19795	1.35	2.0E-02	BF002862.1	EST_HUMAN	7561d08.x1 NCI CGAP_P729 Homo sapiens cDNA clone IMAGE3309598.3 similar to contains MER1.9 MER1 repetitive element
18	10005	19796	7.86	2.0E-02	AF185655.1	EST_HUMAN	GV4-NN0038-270400-187-H05 NN0038 Homo sapiens cDNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
259	10256	20040	2.83	2.0E-02	6753953	EST_HUMAN	Mus musculus D181 knockdown 1 (E. coli) (D181), mRNA
262	10258	20077	2.62	2.0E-02	AA489538.1	EST_HUMAN	art18010.1 Scores: NHHJPUA_S1 Homo sapiens cDNA clone IMAGE:81307.5
781	10711	20550	1.75	2.0E-02	6753953	NT	Mus musculus D181 knockdown 1 (E. coli) (D181), mRNA
1071	10987	20830	0.97	2.0E-02	AL098600.1	NT	Homo sapiens genomic region containing hypervariable minisatellite chromosomes (1) (p98.38) of Homo sapiens
1181	11092	21038	1.61	2.0E-02	6022391	NT	Homo sapiens hypophyseal protein PL10379 (FL10379), mRNA
1181	11092	20939	1.61	2.0E-02	6022391	NT	Homo sapiens hypophyseal protein PL10379 (FL10379), mRNA
1181	11092	20939	1.61	2.0E-02	6022391	NT	Homo sapiens hypophyseal protein PL10379 (FL10379), mRNA
1830	11727	21600	2.31	2.0E-02	6022493	NT	Homo sapiens hypophyseal protein PL10486 (FL10486), mRNA
1830	11727	21601	2.31	2.0E-02	6022493	NT	Homo sapiens hypophyseal protein PL10486 (FL10486), mRNA
2788	12830	22600	1.75	2.0E-02	AL015322.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
3040	10004	19795	1.95	2.0E-02	BF002932.1	EST_HUMAN	7P107i08.x1 NCI_GCAP_P28 Homo sapiens cDNA clone IMAGE:330069.8 similar to contains MEN1, 18 MER1 repetitive element
3105	13031		1.16	2.0E-02	7305474	NT	Mus musculus delta domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 88 (Semaph), mRNA
3189	13114		3.33	2.0E-02	AF065588.1	NT	Arabidopsis thaliana C2H2 zinc finger protein (ZFP) mRNA, complete cds
3925	13834	23614	1.5	2.0E-02	AI18095.1	NT	P. vulgaris hydroxyproline-rich glycoprotein (HFG) mRNA, 3' and
4075	14549	24725	0.96	2.0E-02	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C0378
5085	14635	24730	0.90	2.0E-02	AA489538.1	EST_HUMAN	art18010.1 Scores: NHHJPUA_S1 Homo sapiens cDNA clone IMAGE:81307.5
7676	17520		1.8	2.0E-02	U74008.1	NT	Japanese encephalitis virus envelope protein mRNA, partial cds
7930	17600	28019	1.39	2.0E-02	AF040342.1	EST_HUMAN	wet17062.x1 NCI_GCAP_Kd11 Homo sapiens cDNA clone IMAGE:298815.3
8037	17629	28715	2.01	2.0E-02	U73996.1	NT	Myobacterium tuberculosis H37Rv complete genome, segment 931/102
8676	18566	28849	2.55	2.0E-02	D88184.1	NT	Equus caballus DNA for Taphin-hydroxylase17.2-lyase, complete cds
8931	18739	29031	3.06	2.0E-02	10947055	EST_HUMAN	Homo sapiens ankyrin 3, node of Ranvier (ankyrin G) (ANK3), transcript variant 1, mRNA
8931	18739	29032	3.09	2.0E-02	AA489538.1	EST_HUMAN	Homo sapiens ankyrin 3, node of Ranvier (ankyrin G) (ANK3), transcript variant 1, mRNA
9016	14855	24730	1.41	2.0E-02	AL163282.1	EST_HUMAN	art18010.1 Scores: NHHJPUA_S1 Homo sapiens cDNA clone IMAGE:81307.5
9481	14920	24730	1.58	2.0E-02	AL163282.1	EST_HUMAN	art18010.1 Scores: NHHJPUA_S1 Homo sapiens cDNA clone IMAGE:81307.5
9608	19530		1.72	2.0E-02	BE785959.1	EST_HUMAN	801478819P1 NIH MGCC 69 Homo sapiens cDNA clone IMAGE:3881477.5
9955	19404		4.08	2.0E-02	TB0037.1	EST_HUMAN	yH4C001.1 Scores infant brain T1818 Homo sapiens cDNA clone IMAGE:24675.5
578	10011	20432	1.98	1.9E-02	AA572784.1	EST_HUMAN	r19407.x1 NCI_GCAP_P41 Homo sapiens cDNA clone IMAGE:914198 similar to contains L1, L1 L1 repetitive element
1559	11594	21364	0.84	1.9E-02	F18488	SWISS-PROT	EMPTY SPINRACLES HOMEOTIC PROTEIN
1963	11887	21770	2.32	1.9E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
1963	11887	21770	2.32	1.9E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
1963	11887	21770	2.32	1.9E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2459	12305	22760	0.97	1.9E-02	AL161580.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 50

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2875	12802	22606	7.08	1.9E-02	AA13856.1	EST_HUMAN	inv406.5 x1 NCL CGAP_S1 Homo sapiens cDNA clone IMAGE:238337 3'
2923	12850	22650	1.93	1.9E-02	AV46698.1	EST_HUMAN	AV46698 GLC Homo sapiens cDNA clone GLCBLN07 3'
3022	13146		0.82	1.9E-02	AB03691.1	NT	Utricularia talpoides mitochondrial gene for cytochrome b, complete cds
3160	13474		1.26	1.9E-02	NE2250.1	EST_HUMAN	X2250.2.1 Soares, multiple isoforms_2N6HNSP Homo sapiens cDNA clone IMAGE:264331 3'
3644	13858		5.76	1.9E-02	BE73908.1	EST_HUMAN	69157359FT.NH.MGC.57 Homo sapiens cDNA clone IMAGE:333954 5'
3654	13868	23355	0.98	1.9E-02	A391183.1	EST_HUMAN	g94467.x1 NCL CGAP_Lu6 Homo sapiens cDNA clone IMAGE:11897260 3' similar to contains Alu1 repetitive element;
3981	13988	23646	1.14	1.9E-02	AF141940.1	EST_HUMAN	Mycoplasma肺炎e VHA1 precursor (VHA1) and VHA2 precursor (VHA2) genes, partial cds
4096	13999	23777	1.47	1.9E-02	P09091	SWISSPROT	HOMEOTIC BICOID PROTEIN (PRD-4)
4099	13999	23778	1.47	1.9E-02	P09091	SWISSPROT	HOMEOTIC BICOID PROTEIN (PRD-4)
4441	14335	24125	2.51	1.9E-02	AA45299.1	EST_HUMAN	346904.x1 Soares, NSF RB_9V_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2144561 3' similar to contains Alu1 repetitive element;
4844	12355	22250	1.3	1.9E-02	AF151630.2	NT	Xc2b0935 ratella DNA chromosome 4, contig fragment No. 50
5396	15276	25106	1.28	1.9E-02	AF7572.1	NT	Mus musculus galloanser parvovirus 2 (PNU2) mRNA, complete cds
6095	16862		1.29	1.9E-02	AF157452.1	NT	Mus musculus parvovirus A strain Zs91 complete genome, segment 3/7
7377	17248	27482	1.47	1.9E-02	BF376120.1	EST_HUMAN	301586139FT.NH.MGC.49 Homo sapiens cDNA clone IMAGE:4126482 5'
7777	17827	27859	1.31	1.9E-02	BF695832.1	EST_HUMAN	301552359FT.NH.MGC.56 Homo sapiens cDNA clone IMAGE:407258 5'
8234	18516	25137	2.55	1.9E-02	AF101095.1	NT	Thyudo medialis thermatidis filamentous glauin mRNA, complete cds
343	10302	20117	1.44	1.9E-02	AW771104.1	EST_HUMAN	int0206.x1 NCL CGAP_C67 Homo sapiens cDNA clone IMAGE:3027274 3' similar to contains element MER20 repetitive element;
670	10604	20421	1.14	1.9E-02	BF308122.1	EST_HUMAN	301594359FT.NH.MGC.17 Homo sapiens cDNA clone IMAGE:4139583 5'
1144	11057	20900	1.34	1.9E-02	X17684.1	NT	h1144c301 mRNA for myelin basic protein (MBP)
1417	11323	21187	1.23	1.9E-02	AF243382.1	NT	Drosophila melanogaster cytoplasmic protein ezrin (ezc) mRNA, complete cds
2845	12512	22403	1.51	1.9E-02	AL004544.1	NT	Pseudomonas aeruginosa PAO1, section 106 of 639 of the complete genome
3174	13099		0.89	1.9E-02	AB06829.1	EST_HUMAN	655206.x1 Soares, NTL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2060268 3'
3812	13724	23513	1.09	1.9E-02	AW67972.1	EST_HUMAN	MRI-010011-289300-009.g04 OT0011 Homo sapiens cDNA
3812	13724	23514	1.15	1.9E-02	AW67972.1	EST_HUMAN	MRI-010011-289300-009.g04 OT0011 Homo sapiens cDNA
3960	13903		1.15	1.9E-02	AA691446.1	EST_HUMAN	48241004.x1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:1408935 3'
4332	14229	24011	1.44	1.9E-02	AW69393.1	EST_HUMAN	QV44700021-301299-071-b11 OT0021 Homo sapiens cDNA
4873	14753	24532	1.05	1.9E-02	O69810	SWISSPROT	HYPOPHYSICAL PROTEIN D.945024.2
4877	14767	24543	1.06	1.9E-02	AI28570.1	EST_HUMAN	g9706504.x1 NCL CGAP_Lu6 Homo sapiens cDNA clone IMAGE:1881007 3'
8075	16056	26207	3.96	1.9E-02	P14310	SWISSPROT	HYPOPHYSICAL 7.8 KD PROTEIN IN RWY REGION
7590	17411		2.49	1.9E-02	AA97543.1	EST_HUMAN	460708.x1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:1394621 3' similar to gbl11672 ZINC FINGER PROTEIN PH (HUMAN);

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Disease Source	Top Hit Descriptor
501	10443		1.58	1.0E-02	AI021829.1	NT	Myocardial infarction 137RV complete genome; segment 13/162
1635	11539	21369	1.13	1.0E-02	Y18899.1	NT	Tropomyosin alphaB2, flab3, and flab4 genes for flagellin subunit proteins and CAP protein homologues
2202	12089	21990	1.13	1.0E-02	Q34176	SWISSPROT	LIVER CARBOXYL ESTERASE 22 PRECURSOR (EGCASYN) (ESTERASE-22)
2202	12089	21991	1.13	1.0E-02	Q34176	SWISSPROT	LIVER CARBOXYL ESTERASE 22 PRECURSOR (EGCASYN) (ESTERASE-22)
2618	12392	22294	0.88	1.0E-02	AJ008346.1	NT	Homo sapiens KULDT1 gene
2618	12474	22368	1.47	1.0E-02	AJ434872.1	EST_HUMAN	h891806.81 NC1 CGAP Ex1 Homo sapiens cDNA clone IMAGE:910387
2652	12529		1.14	1.0E-02	AB014534.1	NT	Homo sapiens h8903 for KUL0354 protein, partial cds
3431	13397	23202	3.83	1.0E-02	AW806952.1	EST_HUMAN	U3-C10218-160200-038-C07 010218 Homo sapiens cDNA
4034	13988		2.16	1.0E-02	AF110520.1	NT	Mus musculus major histocompatibility complex antigen NG27 N328, P8528, NADH oxidoreductase, NG29, h4PC1, Fc-gamma binding protein, B1NG1, Hepatin, RelG25-like, KE2, BING4, beta 1.3-galactosyl transferase, and P8518 genes, complete cds, 5' UTR, 3' UTR, partial cds
4203	14102	23365	0.94	1.0E-02	AW875407.1	EST_HUMAN	QY2-F10012-140100-030-07 P10012 Homo sapiens cDNA
5435	15377	25437	1.31	1.0E-02	AB015281.1	NT	Mus musculus C3H antigen (C3), mRNA
6003	15900	25032	2.11	1.0E-02	AB015281.1	NT	Candida albicans CAC030 gene, complete cds
6758	16637		4.01	1.0E-02	X01516.1	NT	Human apc-ii gene for preprocalcitonin C-ii
7773	17623		2.71	1.0E-02	AF079764.1	NT	Drosophila melanogaster enhancer of polyomavirus (E(P)) mRNA, complete cds
7954	17804	29044	1.47	1.0E-02	AA572818.1	EST_HUMAN	h19903.31 NC1 CGAP P11 Homo sapiens cDNA clone IMAGE:914260 similar to SW:TELO_7481T
7954	17804	29045	1.47	1.0E-02	AA572818.1	EST_HUMAN	h19903.31 NC1 CGAP P11 Homo sapiens cDNA clone IMAGE:914260 similar to SW:TELO_7481T
8280	18473	28401	2.17	1.0E-02	Z94828.1	NT	P52934 TELONIN, [1]
8544	18416	28663	2.52	1.0E-02	AI.161508.2	NT	Gallus microsatellite DNA (E0250) (at 161E11)
8544	18416	28664	2.52	1.0E-02	AI.161508.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
8891	18615	28665	1.91	1.0E-02	AJ373558.1	EST_HUMAN	q56107.x1 Scores, pregnant, uterus NDHPU Homo sapiens cDNA clone IMAGE:204242.3
9211	12080	21860	1.35	1.0E-02	Q64176	SWISSPROT	LIVER CARBOXYL ESTERASE 22 PRECURSOR (EGCASYN) (ESTERASE-22)
9211	12080	21861	1.35	1.0E-02	Q64176	SWISSPROT	LIVER CARBOXYL ESTERASE 22 PRECURSOR (EGCASYN) (ESTERASE-22)
9577	19163	21981	2.35	1.0E-02	X32731.1	NT	R nonnegative gene for choline acetyltransferase, exon 1 (non coding)
9973	19433		1.42	1.0E-02	11417966	NT	Homo sapiens SEG14 (S. cerevisiae) like 2 (SEC14L2), mRNA
754	10666		24.6	1.0E-02	8823734	NT	Homo sapiens transcription factor (HSA130894), mRNA
2058	11984	21870	3.91	1.0E-02	N39321.1	EST_HUMAN	Y57407.41 Scores, fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:248925.3
2128	12016	21914	2.86	1.0E-02	AI.161594.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 90
3023	12581	22743	1.44	1.0E-02	AJ008216.1	NT	Homo sapiens CACNA1F gene, exons 1 to 48
3023	12581	22744	1.44	1.0E-02	AJ008216.1	NT	Homo sapiens CACNA1F gene, exons 1 to 48

Table 4

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3663	13577	23365	0.8	1.E-02 BF06242.1	EST_HUMAN	EST_HUMAN	MR4-TN015-080303-201-1312 TN015 Homo sapiens cDNA
4049	13851	23727	1.28	1.E-02 AF100987.1	EST_HUMAN	EST_HUMAN	29400.10.1 Stratum NEST neuron (6337233) Homo sapiens cDNA clone IMAGE:633228 5'
4387	13983	24048	0.91	1.E-02 AF200226.1	EST_HUMAN	EST_HUMAN	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
5601	15707	25819	1.91	1.E-02 CG6711	SWISSPROT	SWISSPROT	HYPOHEMICAL CALCIUM-BINDING PROTEIN C18B11.04 IN CHROMOSOME I
6332	16195	26195	1.66	1.E-02	EST_HUMAN	EST_HUMAN	Oncogene paracrine signaling, complete genome
6377	16230	26309	1.35	1.E-02	EST_HUMAN	EST_HUMAN	Homo sapiens KIA11009 protein (KIA11009) mRNA
6566	16716	26864	1.93	1.E-02 AL163303.2	NT	NT	Homo sapiens chromosome 21 segment HS21C103
6900	16460	26960	3.44	1.E-02	EST_HUMAN	EST_HUMAN	Homo sapiens vgl-HRNA synthetase 2 (VARS2) mRNA
7136	17030	27105	1.20	1.E-02 BF44554.1	EST_HUMAN	EST_HUMAN	60201915BF1 N1 CGAP 5067 Homo sapiens cDNA clone IMAGE-5154004 5'
7520	17530	27454	2.07	1.E-02 D12406.1	NT	NT	Saccharomyces cerevisiae chromosome VI plasmid (GAP)
7646	17468	27171	1.35	1.E-02 R32697.1	EST_HUMAN	EST_HUMAN	454540.10.1 Soares placenta N242P Homo sapiens cDNA clone IMAGE:133531 5'
7646	17468	27171	1.35	1.E-02 R32697.1	EST_HUMAN	EST_HUMAN	454540.10.1 Soares placenta N242P Homo sapiens cDNA clone IMAGE:133531 5'
8509	18390	28647	2.5	1.E-02 AL06930.1	NT	NT	Pleuroctenid telopodum (strain F100-071-131) CN0059 Homo sapiens cDNA
9428	18550		1.32	1.E-02 AF752034.1	EST_HUMAN	EST_HUMAN	366009.01 N1 CGAP GUT1 Homo sapiens cDNA clone IMAGE:2575763 5'
9460	19437		1.47	1.E-02 AF015473.01	EST_HUMAN	EST_HUMAN	AI134730 FLICE1 Homo sapiens cDNA clone IMAGE:10030374 5'
11021	11018	20060	3.98	1.E-02 AC002030.2	NT	NT	Chromopoporus plerianus AR35, section 18 of 41 of the complete genome
11021	11018		3.98	1.E-02	7769860	NT	Homo sapiens NES1 protein (LOC31723), mRNA
1238	11473		1.35	1.E-02 U82930.1	NT	NT	Haemophilus influenzae Rd section 110 of 103 of the complete genome
1276	11184		2.82	1.E-02 U3776.1	NT	NT	Xenopus laevis neurogenin related 16 (XNRNL-16) mRNA, complete cds
1374	11260		0.84	1.E-02 AC210684.1	NT	NT	Homo sapiens headpin genes, complete cds
1507	11495		0.86	1.E-02 AF723785.1	EST_HUMAN	EST_HUMAN	AY22785 H1B Homo sapiens cDNA clone HTB4H11 5'
3176	13101	22005	1.9	1.E-02 AF160699.2	NT	NT	Bifidobacterium longum Nc-H+, antiporter (hlaB), cytosolic deaminase, and alpha-galactosidase (galL) genes, complete cds
3352	13272	22074	0.89	1.E-02 AF074212.1	EST_HUMAN	EST_HUMAN	3060609.01 N1 CGAP GUT1 Homo sapiens cDNA clone IMAGE:2575763 5'
3439	13356	23161	5.21	1.E-02 AL101686.2	NT	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82
3439	13356	23162	5.21	1.E-02 AL101686.2	NT	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82
3476	13392	23197	0.88	1.E-02	4530628	NT	Homo sapiens coagulation factor XI (Hageman factor) (F12), mRNA
3906	13302	23308	8.16	1.E-02	6930619	NT	Mus musculus histocompatibility 2, complement component factor B (H-2B), mRNA
4387	14283	24062	7.29	1.E-02 AW82498.1	EST_HUMAN	EST_HUMAN	EST374761 MAGE rescues, MAGS Homo sapiens cDNA
4387	14283	24063	7.29	1.E-02 AW82498.1	EST_HUMAN	EST_HUMAN	EST374761 MAGE rescues, MAGS Homo sapiens cDNA
4776	14659	24445	6.7	1.E-02 BF673342.1	EST_HUMAN	EST_HUMAN	00156740037 NIH_MGC_231 Homo sapiens cDNA clone IMAGE:3842280 5'
4776	14659	24446	6.7	1.E-02 BF673342.1	EST_HUMAN	EST_HUMAN	00156740037 NIH_MGC_231 Homo sapiens cDNA clone IMAGE:3842280 5'

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5562	15768	25837	4.52	1.4E-02	AA55030.1	EST_HUMAN	hH1G04.s1 NCQ1 GCAP_B21 Homo sapiens cDNA clone IMAGE:1026860 3' similar to contains Alu repetitive element;
5602	15768	25598	4.52	1.4E-02	AA55030.1	EST_HUMAN	Myocardium tuberculothel H37RV complete genome; segment 80/162
6732	16612	27481	1.82	1.4E-02	AL022078.1	NT	001075236.F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3464241 5'
7408	17276	27481	2.07	1.4E-02	BE64459.1	EST_HUMAN	Human IFNAR gene for interferon alpha/beta receptor
8126	18895	20750	4.79	1.4E-02	X90459.1	NT	Arabidopsis thaliana P2L39.2 mRNA, complete cds
8476	19102		1.55	1.4E-02	AF324685.1	NT	Arabidopsis thaliana P2L39.2 mRNA, complete cds
8753	19277		1.89	1.4E-02	11428668	NT	Homo sapiens telomere associated antigen 7 (SPAG7) mRNA
1821	11718		0.86	1.3E-02	BE73023.1	EST_HUMAN	001550402.F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3326335 5'
1972	11937	21634	2.41	1.3E-02	AL05201.2	NT	Homo sapiens chromosome 21 segment HS21C001
3177	13102	22508	1.99	1.3E-02	BF60709.1	EST_HUMAN	002132478.F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4295203 5'
3177	13102	22507	1.99	1.3E-02	BF60709.1	EST_HUMAN	002132478.F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4295203 5'
3558	13799		1.41	1.3E-02	AF026293.1	NT	Mus musculus beta-satellite gamma, complete cds
5178	11807	21684	1	1.3E-02	AL16201.2	NT	Homo sapiens chromosome 21 segment HS21C001
5212	15195	24884	1.36	1.3E-02	AL048982.2	NT	Mus musculus chromosome X contigB; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 82, mrx202b7
5212	15195	24885	1.36	1.3E-02	AL048982.2	NT	Mus musculus chromosome X contigB; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 82, mrx202b7
6165	15114	24856	1.35	1.3E-02	AL161546.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 48
6165	15114	24857	1.35	1.3E-02	AL161546.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 48
6473	16332	25489	4.77	1.3E-02	AI031993.1	EST_HUMAN	0000055.x1 Soares, parathyroid, tumor, N0HFA; Homo sapiens cDNA clone IMAGE:164072.9 similar to contains Alu repetitive element;
6639	16817	27010	1.74	1.3E-02	AF15961.1	NT	Homo sapiens human endogenous retrovirus W gag(3.37 G gag) gene, complete cds
7692	17712	27895	1.97	1.3E-02	M63707.1	NT	Human kidney androgen-regulated protein (KARP) gene, complete cds
8300	18237	28464	4.39	1.3E-02	AW28593.1	EST_HUMAN	0034603.x1 Soares, NFL_T_GBC; S1 Homo sapiens cDNA clone IMAGE:2815006 3'
8300	18237	28446	4.39	1.3E-02	AW28593.1	EST_HUMAN	0034603.x1 Soares, NFL_T_GBC; S1 Homo sapiens cDNA clone IMAGE:2815006 3'
9102	19705		2.62	1.3E-02	X51780.1	NT	Yeast ARP1 gene for actin binding protein
9482	19664		1.6	1.3E-02	299117.1	NT	Bacillus subtilis complete genome (section 14 of 21); from 2894851 to 2812870
9595	19170		1.8	1.3E-02	8633006	NT	Human herpesvirus 68, complete genome
9780	19483		28.64	1.3E-02	AF016228.1	NT	Homo sapiens Vrb vesepresin receptor (VPRR) gene, complete cds
9949	19744	24812	1.32	1.3E-02	AF009176.1	NT	Oryza sativa replication protein A1 (Oa-RPA1) mRNA, complete cds
206	10177		0.94	1.2E-02	X67844.1	NT	H.sapiens DNA, HLA-A*21, B*22, L*2P1, TAP2, DOB, DOB2 and RING9, 9, 13 and 14 genes

Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) HT BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
352	10310	20126	1.74	1.2E-02	A408299.1	EST_HUMAN	45601.1 Soares relax N24-4R Homo sapiens cDNA clone IMAGE:301840.9 similar to contains element L.1.1.1.1
445	10389	20710	1.48	1.2E-02	P33858	SWISSPROT	HYPOPHOSPHATASE 1, K03 PROTEIN IN PURS 3REGION
721	10683	20463	2.98	1.2E-02	A118592.1	EST_HUMAN	q68612.1 Soares_beta1_HHT Homo sapiens cDNA clone IMAGE:1734670.3 similar to contains L.1.1.1.1 negative element.
2130	12018	21918	1.96	1.2E-02	A118523.2	NT	Homo sapiens chromosome 21 segment HS21C013
2383	12271	22167	1.23	1.2E-02	A117350.1	EST_HUMAN	307080.1 Soares_NFL_1_C80.31 Homo sapiens cDNA clone IMAGE:2856432.3
2448	12233	22223	1.11	1.2E-02	B65393.10	EST_HUMAN	307080.1 Soares_NFL_1_C80.31 Homo sapiens cDNA clone IMAGE:354598.8
2448	12325	22224	1.11	1.2E-02	B65393.10	EST_HUMAN	307080.1 Soares_NFL_1_C80.31 Homo sapiens cDNA clone IMAGE:354598.8
2596	12271	22167	1.27	1.2E-02	A117350.1	EST_HUMAN	307080.1 Soares_NFL_1_C80.31 Homo sapiens cDNA clone IMAGE:2856432.3
3063	12690	24071	0.18	1.2E-02	A407541.1	EST_HUMAN	HT6803.1.1 Stratagene ovarian cancer (H93721.0) Homo sapiens cDNA clone IMAGE:546020.5
3250	13173	22971	1.89	1.2E-02	R62860.1	EST_HUMAN	HT6803.1.1 Stratagene N20-4P Homo sapiens cDNA clone IMAGE:138903.3
4830	14172	24495	2.04	1.2E-02	A011328.1	NT	Human hereditary haemochromatosis region, Heline 2A-like protein, gene, hereditary haemochromatosis (H4-H4) gene, Hctet, gene, and sodium phosphate transporter (NPT3) gene, complete cds
4974	14849		1.73	1.2E-02	A8019786.1	NT	Cnops pythagostris Gub3a1 mRNA, partial cds
5017	14891	24559	2.12	1.2E-02	AV731104.1	EST_HUMAN	AT371704.HTF Homo sapiens cDNA clone HTB14011.5
5516	15434	25497	1.96	1.2E-02	D76899.1	NT	Rana temporaria mRNA for carboxidin, complete cds
6190	16060	26216	5.33	1.2E-02	A117541.2	NT	Mus musculus DNA methyltransferase (Dnmt3), exons 2, 3, 4, and 5
6327	16190	26352	6.37	1.2E-02	AV72093.1	EST_HUMAN	AT372093.HTF Homo sapiens cDNA clone HTB14011.5
6865	16546	26742	2.11	1.2E-02	Q11205	SWISSPROT	CMP-NAACE1 YLEURAMINATE-BETA-GALACTOSAMIDE-ALPHA-2,3-SIALYLTRANSFERASE (BETA-GALACTOSE ALPHA-2,3-SIALYLTRANSFERASE (ALPHA 2,3-ST) (GALNAAC8) (GAL-BETA-1,3-GALNAAC-ALPHA-2,3-SIALYLTRANSFERASE) (ST3GALA.2) (SIAT4.8)
6765	16644	26932	1.22	1.2E-02	A119301.2	NT	Homo sapiens fringe protein mRNA, partial cds
6765	16644	26933	1.22	1.2E-02	A119301.2	NT	Homo sapiens fringe protein mRNA, partial cds
7152	17029	26933	1.17	1.2E-02	T76397.1	EST_HUMAN	yf2208.51 Soares fetal liver spleen INHLS Homo sapiens cDNA clone IMAGE:113774.3
7557	17408	27623	2.45	1.2E-02	A8031013.1	NT	Noncell-like virus group209 2 gene for capsid protein, complete cds
7575	17426	27640	1.23	1.2E-02	AJ240603.1	NT	Homo sapiens Spast gene for spastin protein
8177	18918	28346	1.78	1.2E-02	Q11534	SWISSPROT	PERIOD CIRCADIAN PROTEIN 1 (CIRCADIAN PACEMAKER PROTEIN RIGU) (HPER)
9888	19267	29546	1.51	1.2E-02	P11739	SWISSPROT	COLLAGEN ALPHA 1(VI) CHAIN PRECURSOR
9765	19296		3.47	1.2E-02	A118119.1	EST_HUMAN	C18119.Homo placenta cDNA (17Jwure) Homo sapiens cDNA clone GEN-567066.5
1248	11181	21451	1.32	1.1E-02	AA070394.1	EST_HUMAN	zm66511.1 Stratagene neuroepithelium (H93723) Homo sapiens cDNA clone IMAGE:530924.3
1679	11881	21451	1.99	1.1E-02	X75491.1	NT	H.sapiens LIPA gene, exon 4
1679	11881	21452	1.99	1.1E-02	X75491.1	NT	H.sapiens LIPA gene, exon 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E- Value	Top Hit Accession No.	Top Hit Database Source
1992	11866	21778	4.35	1.E-02 BF342603.1	EST_HUMAN	G02016031 F1 NCL CGAP B-Het Homo sapiens cDNA clone IMAGE:415308.5
2648	12776	21778	3.33	1.E-02 NG6623.1	EST_HUMAN	Z64065.1 Soares fetal liver spleen INRHS Homo sapiens cDNA clone IMAGE:285040.5
2033	12590	22660	10.39	1.E-02 AF050506.1	NT	Homo sapiens NCI-GC Class 1 region
3478	13344	23200	2.48	1.E-02 AF065506.1	EST_HUMAN	IG650.10.41 NCL CGAP C-Het Homo sapiens cDNA clone IMAGE:221653.9 similar to SWJXP-F_HUMAN
3937	13364	21778	0.87	1.E-02 BE114439.1	EST_HUMAN	C02689.HDA-REPAIR PROTEIN COMPLEMENTING XP-C CELL:
4016	13631	21778	0.87	1.E-02 AWB13796.1	EST_HUMAN	PAG-HIT0177-123200-011 G51 ST10187 Homo sapiens cDNA
4723	14600	24360	1.81	1.E-02 AL048393.2	EST_HUMAN	KCFZ-5068E0092.4 (f61) (synonym: huter) Homo sapiens cDNA clone DKFZ5386E0024
4821	14704		0.92	1.E-02 AG020281.1	EST_HUMAN	DY-012036-100300-028-011 S10258 Homo sapiens cDNA
6460	16330	26050	2.26	1.E-02 BE1146911.1	EST_HUMAN	RCH-HIT0266-100300-018-007 H070255 Homo sapiens cDNA
7160	17037	27230	6.97	1.E-02 Q31982	SWISSPROT	NEUROGENIC LOCUS NOTCH 3 PROTEIN
7710	17550	27765	2.25	1.E-02 AA063276.1	EST_HUMAN	zn24a01.1 Stratiogene neuroepithelium NT2RAM1 g97234 Homo sapiens cDNA clone IMAGE:548328.5
7810	17590	27760	4.1	1.E-02 AAO31486.1	EST_HUMAN	EST1186494 Colon carcinoma (HCC) cell line H1 Homo sapiens cDNA 5' end
8347	18224	28476	3.38	1.E-02 I1435906	NT	Homo sapiens T-Box 3 (TBX3), mRNA
8064	18845		2.23	1.E-02 AA968239.1	EST_HUMAN	ab71711.s1 Stratiogene fetal retina g37202 Homo sapiens cDNA clone IMAGE:550305.3 similar to containe
5	8992	19785	3.65	1.E-02 ANV467120.1	EST_HUMAN	MFG-CT0176-11092-030-410 GT0176 Homo sapiens cDNA
1506	11411	21770	0.81	1.E-02 ANV38126.1	EST_HUMAN	Q32-HIT0177-741068-017-A12 HT0177 Homo sapiens cDNA
2625	12598		1.2	1.E-02 AA033369.1	EST_HUMAN	c22308.s1 NCL CGAP C-B1 Homo sapiens cDNA clone IMAGE:135449.3
3051	12878	22771	2.37	1.E-02 AB033555.1	EST_HUMAN	RPO-PN025-256049-012 FN0035 Homo sapiens cDNA
3226	13150	22860	0.98	1.E-02 AE059586.1	EST_HUMAN	F60-5569/751 NH_1MGC_74 Homo sapiens cDNA clone IMAGE:33835669.3
3464	13390		1.18	1.E-02 ANV45421.1	EST_HUMAN	MRO-CT0030-01050-005-110 CT0030 Homo sapiens cDNA
3805	13717	23030	0.78	1.E-02 AA050956.1	EST_HUMAN	PA0521 Human foetal liver cDNA library Homo sapiens cDNA
4057	14553	24345	4.26	1.E-02 G763521	NT	Mus musculus corticosterone releasing hormone receptor 2 (Chr2), mRNA
4736	14821	24407	2.38	1.E-02 RG6667.1	EST_HUMAN	Y5-4901.1 Soares fetal liver spleen INRHS Homo sapiens cDNA clone IMAGE:196033.5
4965	14870	24407	0.95	1.E-02 AFZ18910.1	NT	Homo sapiens atrial natriuretic precursor (ATNP) gene, exon 25 and complete cds, alternatively spliced
5140	15016		0.82	1.E-02 BF076539.1	EST_HUMAN	B0146286BF1 NH_1MGC_69 Homo sapiens cDNA clone IMAGE:5388608.0
5751	15303		2.74	1.E-02 ANV577115.1	EST_HUMAN	MK4-BT0309-070100-301-H01 BT03558 Homo sapiens cDNA
5751	15560	26787	2.74	1.E-02 ANV577115.1	EST_HUMAN	MK4-BT0309-070100-301-H01 BT03558 Homo sapiens cDNA
6054	16037	26787	2.06	1.E-02 Z29642.1	NT	Z-myo1 UtsarRNA pseudogene
7403	17270	27715	4.65	1.E-02 BF036331.1	EST_HUMAN	B01459570F1 NH_1MGC_66 Homo sapiens cDNA clone IMAGE:3963177.5
7403	17270	27715	4.65	1.E-02 BF036331.1	EST_HUMAN	B01459570F1 NH_1MGC_66 Homo sapiens cDNA clone IMAGE:3963177.5

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF-SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Describer
8696	18454		2.1	1.0E-02	AF157559.1	NT	Citridhase fasciculata 27 kDa guido RNA-binding protein mRNA, complete cds; mitochondria gene for
8674	19502	28646	2.03	1.0E-02	AV760016.1	EST_HUMAN	mitochondrial product
8142	19792		1.7	1.0E-02	Q62023	SWISSPROT	ALCOHOL DEHYDROGENASE ASSOCIATED PROTEIN 82 (SAP 62) (SPLICING FACTOR 3A SUBUNIT 27) (SF3A66)
8202	19535	29001	2.95	1.0E-02	AF035521.1	EST_HUMAN	RC2-D70007.120200.016-h02.D70007 Homo sapiens cDNA
8217	19500		5.22	1.0E-02	S703030.1	EST_HUMAN	Homo sapiens renal dipeptidase (RDP) gene, complete cds
8745	18845		2.44	1.0E-02	X63554.1	NT	H.sapiens gene for Mcd97CD83 antigen
876	18901	20651				EST_HUMAN	W42093.1 NC1 CGAP R4011 Homo sapiens cDNA clone IMAGE2383433.3 similar to contains element
876	18901	20651	1.7	9.0E-03	AF09126.1	EST_HUMAN	MER22 MER22 repetitive element;
1243	11150		1.97	9.0E-03	BE761889.1	EST_HUMAN	501170242P21 NH MGC 57 Homo sapiens cDNA clone IMAGE3373346.5
2340	12220	22123	3.26	9.0E-03	AL161589.2	NT	A rabbit alpha human DNA chromosome 4, contig fragment No. 59
2593	12463	22315	1.08	9.0E-03	AL243727.1	NT	Oncorhynchus nerka proviral gypsy retrotransposon partial reverse transcriptase and protease genes (pol gene)
2593	12463	22315	1.08	9.0E-03	AL243727.1	NT	Oncorhynchus nerka proviral gypsy retrotransposon partial reverse transcriptase and protease genes (pol gene)
2876	12603	22357	0.33	9.0E-03	AL251744.1	EST_HUMAN	q06009.x1 Soares_NHL_T_CGC 351 Homo sapiens cDNA clone IMAGE1854281.3
2876	12603	22358	0.33	9.0E-03	AL251744.1	EST_HUMAN	q06009.x1 Soares_NHL_T_CGC 351 Homo sapiens cDNA clone IMAGE1854281.3
3677	13531	23317	0.92	9.0E-03	U05154.1	NT	3. subclonized hemoglobin gene, complete cds
4914	14783	24568	1.17	9.0E-03	BE47346.1	EST_HUMAN	544010.1 NC1 CGAP BamHI Homo sapiens cDNA clone IMAGE228456.5
5181	15048		2.96	9.0E-03	AF137260.1	NT	Sardegna1002 mixed lineage leukemic-like protein (ML) gene, partial cds
5597	19502		4.17	9.0E-03	BE74556.1	EST_HUMAN	601075438F1 NH MGC 57 Homo sapiens cDNA clone IMAGE334732.5
5687	16477		1.19	9.0E-03	AL038991.1	EST_HUMAN	DNK2763543.121.1 491 (Spontaneous) Homo sapiens cDNA clone DKF26434.0412.5
7673	17523	27749	1.47	9.0E-03	P29608	SWISSPROT	COLLAGEN ALPHA 1(V) CHAIN PRECURSOR
8354	18231		1.86	9.0E-03	Y19000.1	EST_HUMAN	Homo sapiens N72 gene
9352	19783		1.34	9.0E-03	BF35114.1	EST_HUMAN	PM1-HT0452.291299-001-c09.HT0452 Homo sapiens cDNA
9557	19789		11.59	9.0E-03	BE34385.1	EST_HUMAN	PM176093.1 NC1 CGAP L1024 Homo sapiens cDNA clone IMAGE3103161.3
9552	18045		1.27	9.0E-03	AF137260.1	NT	Sardegna1002 mixed lineage leukemic-like protein (ML) gene, partial cds
9649	18215	25259	1.62	9.0E-03	AL163297.2	NT	Homo sapiens chromosome 21 segment H327C067
9943	18341		27.64	9.0E-03	BF35114.1	EST_HUMAN	PM1-HT0452.291299-001-c09.HT0452 Homo sapiens cDNA
493	19436		3.2	9.0E-03	AA72007.1	EST_HUMAN	233003.x1 Soares_jaked_N81.F0 Homo sapiens cDNA clone IMAGE413606.3 similar to contains
978	18597	20744	45.2	9.0E-03	AF106556.1	NT	Alu repetitive element
2113	12002	21900	2.38	9.0E-03	AL103283.2	NT	Homo sapiens adenylosuccinate lyase gene, complete cds
							Homo sapiens chromosome 21 segment H327C083

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2930	12857		0.86	8.0E-03	U47048.1	NT	Escherichia coli microtubule 24 region, DNA binding protein (mdaB), immunity protein (mif), microtubule 24 (mtfS), and microtubule transport protein (mtfA, mtfB) genes, complete cds
3270	13191	22690	0.97	8.0E-03	BE171226.1	EST_HUMAN	RC1-HIT0545-170200-011-009 HIT0545 Homo sapiens cDNA
3314	13235	23039	0.89	8.0E-03	AJ131016.1	NT	Homo sapiens SCL gene locus
3702	13704		1.07	8.0E-03	AF068784.1	NT	Xeropus laevis bone morphogenetic protein 4 (BMP-4) gene, complete cds
4290	14195	23066	5.12	8.0E-03	BF363327.1	EST_HUMAN	CNNM119-300000-222-505 NN0119 Homo sapiens cDNA
5391	15310	25164	2.7	8.0E-03	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RP528, NACH oxidoreductase, NG29, XIFC1, Fas-binding protein, BING1, lipase, FALGOS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RP518 genes, complete cds; Samc21 gene, partial
5701	16463	25775	1.35	8.0E-03	AP000002.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 287001-544000 nt position (2/7)
6048	15961	26081	4.52	8.0E-03	P05577	SWISSPROT	PROBABLE PEPTIDASE YAMA
6279	16143	26299	2.19	8.0E-03	M17197.1	NT	A. californica (marine gastropod mollusc) neuropeptide gene (big cell), exon 1, 5' end
6453	16314	27235	1.86	8.0E-03	AB036267.1	NT	Tursiops truncatus mRNA for p40-plox, complete cds
7166	17043	27235	3.81	8.0E-03	AY069892.1	EST_HUMAN	MRL-ST0111-11199-011-H06 S10111 Homo sapiens cDNA
7717	17567		4.72	8.0E-03	BC086509.1	EST_HUMAN	QV1-BT0877-040400-131-g03 B10677 Homo sapiens cDNA
8148	18036	28234	1.92	8.0E-03	BE768441.1	EST_HUMAN	8914766197 NH, LMC, 68 Homo sapiens cDNA clone IMAGE:3874405 5'
8253	18230	28234	2.78	8.0E-03	Z46652.1	NT	S. cerevisiae chromosome X, reading frame, ORF Y1R152v
8697	18575	28458	1.75	8.0E-03	AJ428517.1	EST_HUMAN	cd8b2a.41 NC1_CGAP_O2 Homo sapiens cDNA clone IMAGE:374322
8697	18575	28458	1.75	8.0E-03	AJ428517.1	EST_HUMAN	cd8b2a.41 NC1_CGAP_O2 Homo sapiens cDNA clone IMAGE:374322
8693	18700	29063	4.53	8.0E-03	AF004599.1	NT	Homo sapiens nucleosome-associated antigen (NAGE/C5) gene, complete cds
9075	18852		1.34	8.0E-03	U69035.1	NT	Cytoskeleton-aff-2a kinase mRNA, complete cds
9121	18882		3.36	8.0E-03	AB039161.1	NT	Homo sapiens ABCG1 gene for ABC transporter (ATP-binding cassette, sub-family G (WHITE), member 1), complete cds
679	10612	20453	11.58	7.0E-03	AF071631.1	NT	Cryptosporidium parvum HC-10 gene, complete cds
679	10612	20454	11.58	7.0E-03	AF071631.1	NT	Cryptosporidium parvum HC-10 gene, complete cds
691	10894	20732	2.01	7.0E-03	AI243763.1	NT	Cytine max guaiatone S-transferrase GST 21 mRNA, partial cds
1100	11016	20968	2.6	7.0E-03	AY347121.1	EST_HUMAN	AV371212 HTF Homo sapiens cDNA clone HTAF210 5'
1341	11247		1.19	7.0E-03	Q51080	SWISSPROT	FORKHEAD BOX PROTEIN D3 (PITF3/3H TRANSCRIPTION FACTOR GENESIS) (HEPATOCYTE
1373	11279	21139	13.73	7.0E-03	AJ468298.1	EST_HUMAN	NUCLEAR FACTOR 3 FORKHEAD HOMOLOG 2 (NFK-2)
1486	11391	21251	4.6	7.0E-03	AY303396.1	EST_HUMAN	3679609.91 Strangens fetal retina 937202 Homo sapiens cDNA clone IMAGE:583145 3'
2210	12715	22001	2.24	7.0E-03	P04629	SWISSPROT	X21B02.21 Soares, NLY_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813739 3'
3702	13816	23400	1.27	7.0E-03	AW444663.1	EST_HUMAN	HITDIN6-RICH GLYCOPROTEIN PRECURSOR
							UH-HB3-rib-c-10-5-U1-AT NC1_CGAP_S5b5 Homo sapiens cDNA clone IMAGE:2739891 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3208	13132		2.06	6.0E-03	U75690.1	EST_HUMAN	Y77H04.L1 Scores fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:211381 5'
3264	13187		0.82	6.0E-03	AF190338.1	NT	Notodens sp. cytochrome c oxidase subunit II gene, partial cds; mitochondrial gene for mitochondrial product
3336	13256	23062	1.24	6.0E-03	U60880.1	NT	Fugu rufipes zinc finger protein, isoform, fatty acid binding protein, sepiapterin reductase and vasodilator
3336	13256	23063	1.24	6.0E-03	U60880.1	NT	Fugu rufipes zinc finger protein, isoform, fatty acid binding protein, sepiapterin reductase and vasodilator
3429	13416		1.05	6.0E-03	U37595.1	EST_HUMAN	zr13a11.7 Scores parathyroid tumor NHHPA Homo sapiens cDNA clone IMAGE:322172 5'
3610	13524	23311	3.62	6.0E-03	BF510665.1	EST_HUMAN	U-H-BH4-apm-c-05-011.51 NCI CGAP Sub8 Homo sapiens cDNA clone IMAGE:3087764 3'
3711	13624	23407	1.26	6.0E-03	67540238	NT	Mus musculus glucosamine-6-phosphate deaminase (Gnp), mRNA
3846	13767	23551	0.93	6.0E-03	AW847284.1	EST_HUMAN	60084290.F1 NCI MGCL 15 Homo sapiens cDNA clone IMAGE:2954913 5'
3873	13784		1.16	6.0E-03	BE256108.1	EST_HUMAN	RCO-CT0204.210069-021-370 CT0204 Homo sapiens cDNA
4231	14129		0.87	6.0E-03	NS5946.1	EST_HUMAN	Y62910.1 Scores multiple sclerosis 2NH-NSP Homo sapiens cDNA clone IMAGE:278176 3'
4337	14166		1.37	6.0E-03	AA32424.1	EST_HUMAN	o33c11.1 Scores testis NHT Homo sapiens cDNA clone IMAGE:1639724 3'
4697	14485	24271	6.82	6.0E-03	AA32424.1	EST_HUMAN	ES127116 Corneal epithelium II Homo sapiens cDNA 5' and similar to EST containing Alu repeat
5115	14693	24756	1.83	6.0E-03	AL43261.2	EST_HUMAN	495503.1 Scores parathyroid tumor NHHPA Homo sapiens cDNA clone IMAGE:1404258 3'
5129	14698	24767	0.89	6.0E-03	AL43261.2	EST_HUMAN	Homo sapiens telomerase reverse transcriptase (TER) gene, exon 7-16 and complete cds
6006	16865	26442	1.97	6.0E-03	AF126864.1	NT	ov13a3.41 Scores parathyroid tumor NHHPA Homo sapiens cDNA clone IMAGE:1646970 3' similar to
6556	16468	26857	7.04	6.0E-03	AL33380.1	EST_HUMAN	cor13a3.41 Scores parathyroid tumor NHHPA Homo sapiens cDNA clone IMAGE:1646970 3' similar to
6653	16530	26724	2.44	6.0E-03	AY179537.1	EST_HUMAN	ROUJMK051-210305-033-021 UM051 Homo sapiens cDNA
6659	16559		1.41	6.0E-03	BF303195.1	EST_HUMAN	8014501.BF1 NH MGCL20 Homo sapiens cDNA clone IMAGE:3856226 5'
7509	17257	27506	8.21	6.0E-03	D10548.1	NT	Substrate extruding parameciophyllus (SPE) virus mRNA for fusion protein
7776	17628		1.94	6.0E-03	AA32961.1	EST_HUMAN	U2602.41 NCI CGAP K411 Homo sapiens cDNA clone IMAGE:2131202 3' similar to SW-R18A, HUMAN
7949	17760	26339	1.15	6.0E-03	X65068.1	NT	P-4942.005 RIBOSOMAL PROTEIN L34
8127	18015	26263	2.28	6.0E-03	AW92164.1	EST_HUMAN	M thermophilum complete plasmid pV1 DNA
8186	18072		2.21	6.0E-03	1154884.1	NT	EST374237 MAGC resequences, MAGC Homo sapiens cDNA
8220	18102	26346	1.86	6.0E-03	AA20766.1	EST_HUMAN	le91c12.x1 NCI CGAP P-28 Homo sapiens cDNA clone IMAGE:2964070 3' similar to TR-000519 O00519
8220	18102	26357	1.86	6.0E-03	AA20766.1	EST_HUMAN	le91c12.x1 NCI CGAP P-28 Homo sapiens cDNA clone IMAGE:2964070 3' similar to TR-000519 O00519
8360	18227		3.91	6.0E-03	UH4666.1	NT	FATTY ACID AMIDE HYDROLASE ;
8331	18228	26479	3.54	6.0E-03	BE373886.1	EST_HUMAN	FATTY ACID AMIDE HYDROLASE ;
							Mus musculus zinc-finger protein mRNA, complete cds
							6015724.F1 NH MGCL 57 Homo sapiens cDNA clone IMAGE:3839747 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
9185	19022		1.59	6.0E-03	AF010466.1	NT	Rhodococcus capsulatus strain SB1003, partial genome
9310	19519		3.6	6.0E-03	AE000833.1	NT	Methanobacterium thermoautotrophicum from basins 425192 to 450296 (section 39 of 148) of the complete genome
9372	19038		1.34	6.0E-03	AB023356.1	NT	Anguilla japonica mRNA for actinin B, complete cds
9392	19593		2.21	6.0E-03	U90790.1	NT	Pseudomonas carolin f. sp. neri guanine nucleotide binding protein alpha subunit (pcg1) gene, complete cds
9722	19262		1.67	6.0E-03	BE78019.1	EST_HUMAN	601482321F1 NIH_MGC_08 Homo sapiens cDNA clone IMAGE338538.5
9741	19274		1.34	6.0E-03	AJ245480.1	NT	Brassica napus 5g gene for S-luciferase glycoprotein, cullivar 72
953	10599	20406	1.9	5.0E-03	L29105.1	NT	Chlamydia trachomatis partial ORF8; aminooacyl-RNA synthase, complete cds; complete ORFA, and gprE-like protein, complete cds
953	10599	20407	1.9	5.0E-03	L29105.1	NT	Chlamydia trachomatis partial ORF8; aminooacyl-RNA synthase, complete cds; complete ORFA, and gprE-like protein, complete cds
954	10599	20406	2.82	5.0E-03	L29105.1	NT	Chlamydia trachomatis partial ORF8; aminooacyl-RNA synthase, complete cds; complete ORFA, and gprE-like protein, complete cds
1006	11012	20407	2.82	5.0E-03	AJ010467.1	NT	Chlamydia trachomatis partial ORF8; aminooacyl-RNA synthase, complete cds; complete ORFA, and gprE-like protein, complete cds
1552	11457	20854	1.36	5.0E-03	AJ010467.1	EST_HUMAN	ad79405.x1 Sarcos leidis, NIH Homo sapiens cDNA clone IMAGE-173595.3'
2846	12516	22405	0.91	5.0E-03	AB03907.1	NT	Homo sapiens mRNA for KIAA1180 protein, partial cds
2905	13832	22829	0.85	5.0E-03	BE26905.1	EST_HUMAN	601194762F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE335979.5'
3037	13024	22830	4.08	5.0E-03	T07623.1	EST_HUMAN	X68193.1 Sarcos leidis brain, NIH Homo sapiens cDNA clone IMAGE22355.3'
3116	13941		1.76	5.0E-03	AJ16140.2	NT	Arabidopsis thaliana DNA chromosome 4, coding fragment No. 3
3129	13054	22853	1.04	5.0E-03	AF17184.1	EST_HUMAN	X99922.1 Sarcos leidis brain, NIH Homo sapiens cDNA clone IMAGE-15898.3'
3240	13163		1.06	5.0E-03	AJ297357.1	NT	Homo sapiens partial UMD1 gene set LIM contains containing protein 1 and KIAA0851 gene
3641	13555	23341	4.16	5.0E-03	AF17448.2	NT	Pseudomonas aeruginosa strain PAO1 penicillin-binding protein 1B (pbpB) gene, complete cds
3698	13912	22396	0.93	5.0E-03	U38944.1	EST_HUMAN	Citrus sinensis seed storage protein cDNA, complete cds
3801	13901		1.38	5.0E-03	U1286675.1	EST_HUMAN	EST12218 Utricularia minor 1 Homo sapiens cDNA 3 and
4207	14106	22866	0.93	5.0E-03	U176355.1	EST_HUMAN	X07950.1 Utricularia minor 1 Homo sapiens cDNA 3 and
4209	13912	22396	0.91	5.0E-03	U38944.1	NT	Citrus sinensis seed storage protein cDNA, complete cds
4503	14386	21811	0.94	5.0E-03	AJ131015.1	NT	Homo sapiens SCL gene locus
4619	14607	24296	2.46	5.0E-03	AJ762967.1	EST_HUMAN	cm15602.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NIHBC_cm15602 random
5541	15458	24528	5.34	5.0E-03	P35500	SWISSPROT	SODIUM CHANNEL PROTEIN PARA (PARALYTIC PROTEIN)

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5985	15594	25695	2.43	5.0E-03	000407	SWISSPROT	PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE FA-FY (UBIQUITIN THIOLESTERASE FA-FY) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE FA-FY) (DEUBIQUITINATING ENZYME FA-FY) (FAT FACETS PROTEIN RELATED, Y-LINKED) (UBIQUITIN-SPECIFIC PROTEASE 9, Y CHROMOSOME)
5977	15581		6.17	5.0E-03	9520399.1	EST_HUMAN	009449549T1 NR1_MGC_17 Homo sapiens cDNA clone IMAGE:2980871 3'
6031	15101	24877	6.02	5.0E-03	AS22624.1	NT	Mus musculus MMT1 gene for S-adenosylmethionine decarboxylase, complete cds
5556	16424	26605	6.36	5.0E-03	AS201616.1	NT	Homo sapiens MSLT1 mRNA, complete cds
6764	10673	26885	1.97	5.0E-03	743682	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
7006	10883		6.92	5.0E-03	1061152.1	NT	Mouse complement receptor (CR2) mRNA, 3' and
8103	17988		7.44	5.0E-03	119466.1	EST_HUMAN	950F Heart Homo sapiens cDNA, clone 694
8310	18187	28495	3.17	5.0E-03	AW170384.1	EST_HUMAN	nt9505.1 Scores: NHOcC_cervical_tumor Homo sapiens cDNA clone IMAGE:298040 3' similar to contains 1.12 E11 repetitive element;
8310	18187	28495	3.17	5.0E-03	AW170384.1	EST_HUMAN	nt9505.1 Scores: NHOcC_cervical_tumor Homo sapiens cDNA clone IMAGE:298040 3' similar to contains 1.12 E11 repetitive element;
8309	18276	28527	1.95	5.0E-03	149183.1	EST_HUMAN	nt9505.1 Scores: NHOcC_cervical_tumor Homo sapiens cDNA clone IMAGE:298040 3' similar to contains 1.12 E11 repetitive element;
8433	18307	28563	1.77	5.0E-03	10046793	NT	M00904.1 Stratiogene placenta (R337223) Homo sapiens cDNA clone IMAGE:70866 5'
8624	18368		3.73	5.0E-03	BE049095.1	EST_HUMAN	Mus musculus myohypopharyngeal protein, MNOS-4760 (LOC353212), mRNA
9227	19709		5.04	5.0E-03	AF041874.1	NT	124604.1/NT1 CGAP_Bim32 Homo sapiens cDNA clone IMAGE:2291022 5'
9460	19091		6.85	5.0E-03	AF067253.1	NT	Gallus gallus glyceraldehyde-3-phosphate dehydrogenase mRNA, complete cds
9555	19153		1.55	5.0E-03	110347.1	NT	Buglia mally Y chromosome marker
9562	19174		1.28	5.0E-03	AA456997.1	EST_HUMAN	Human pro-alpha1 type II collagen (COL2A1) gene exon 1-34, complete cds
9516	19529		4.19	5.0E-03	BF472332.1	EST_HUMAN	275403.31 Scores: ovary tumor NHOT Homo sapiens cDNA clone IMAGE:609548 3' similar to SW_DVAG_MOUSE P14686 PROBABLE DIPHEOL OXIDASE A2 COMPONENT1;
9791	19301	25197	1.94	5.0E-03	AW449109.1	EST_HUMAN	002077774F NH1_MGC_82 Homo sapiens cDNA clone IMAGE:252007 5'
9808	19801		1.4	5.0E-03	Q02388	EST_HUMAN	UHF-B13-44F-408-CU1.1/NT1 CGAP_Sut6 Homo sapiens cDNA clone IMAGE:2734215 3'
9929	19400		1.41	5.0E-03	AA65709.1	EST_HUMAN	COLLAGEN ALPHA1(VIII) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN) [LC COLLAGEN]
232	10201	20015	2.97	4.0E-03	AW1501196.1	EST_HUMAN	267405.02 Scores: fetal brain NH1_MGC_187 Homo sapiens cDNA clone IMAGE:309068 3'
318	10280	20197	2.18	4.0E-03	RA462.1	EST_HUMAN	UHFH-290-36C-044-CU1.1/NT1_MGC_150 Homo sapiens cDNA clone IMAGE:3076831 5'
436	10380	20203	0.94	4.0E-03	PS4675	EST_HUMAN	Y6764.4.1 Scores: fetal brain NH1_Homo sapiens cDNA clone IMAGE:35988 3'
586	10526	20333	3	4.0E-03	AA395339.1	EST_HUMAN	PHOSPHATIDYLINOSITOL 3-KINASE 3 (PI3KINASE) (PI3K)
809	10785	20637	1.81	4.0E-03	RA4462.1	EST_HUMAN	nt7591.2.1 Scores: NHL_1_CBC_51 Homo sapiens cDNA clone IMAGE:162669 3'
803	10819		3.43	4.0E-03	RA474910.1	EST_HUMAN	Y6764.4.1 Scores: fetal brain NH1_Homo sapiens cDNA clone IMAGE:35988 3'
1133	11047	20859	32.55	4.0E-03	AA090777.1	EST_HUMAN	RC3-B1(333)-11(10/04/2102) BT0333 Homo sapiens cDNA
1153	11059	20910	1.56	4.0E-03	AW784740.1	EST_HUMAN	RC3-B1(333)-11(10/04/2102) BT0333 Homo sapiens cDNA clone IMAGE:510988 5'
							R5C-UN0014-170400-023-001 UN0014 Homo sapiens cDNA

Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon NO.	ORF SEQ ID NO.	Expression Signal	Mod Stimulr (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1261	11169	21040	1.33	4.0E-03	AA24374.1	EST_HUMAN	zsl9041.01 NCI CGAP_G031 Homo sapiens cDNA clone IMAGE:701736 5'
1508	11472		1.31	4.0E-03	AV708305.1	EST_HUMAN	AV708305 ADC Homo sapiens cDNA clone ADCAC605 5'
1709	11610	21480	2.2	4.0E-03	U33472.1	NT	Rattus norvegicus type 1 astrocyte and oligodendrocyte associated protein AT1-46 mRNA, complete cds
1971	11864	21757	20.87	4.0E-03	AA05977.1	EST_HUMAN	Z81406.11 Stragelene cten (8977204) Homo sapiens cDNA clone IMAGE:103968 5'
2200	12087		1.95	4.0E-03	BE410555.1	EST_HUMAN	901304161F1 NFH MG6_21 Homo sapiens cDNA clone IMAGE:3693510 5'
2232	12117	22019	1.48	4.0E-03	AV744740.1	EST_HUMAN	RG8-UM0014:70400-025-Q81 UM0014 Homo sapiens cDNA
2625	12400	22260	1.86	4.0E-03	UR2111.2	NT	Homo sapiens x2a region near ALD locus containing dual specificity phosphatase 9 (DUSP9), fibronectin protein L16a (FBL16a), Cdc2/Cdk5 cyclin-dependent protein kinase 1 (CDK5), creatine transporter (CRTTR), CDM protein (CDM), adenosine deaminase protein >
2628	12400	22261	1.80	4.0E-03	UR2111.2	NT	Homo sapiens x2a region near ALD locus containing dual specificity phosphatase 9 (DUSP9), fibronectin protein L16a (FBL16a), Cdc2/Cdk5 cyclin-dependent protein kinase 1 (CDK5), creatine transporter (CRTTR), CDM protein (CDM), adenosine deaminase protein >
2669	12526	22414	2.65	4.0E-03	AJ77385.1	NT	Homo sapiens polyubiquitin-containing C10orf4 gene
2686	12526	22415	2.66	4.0E-03	AJ77385.1	NT	Homo sapiens polyubiquitin-containing C10orf4 gene
2694	12530	22418	1.02	4.0E-03	AL163264.2	NT	Homo sapiens chromosome 21 segment HS21C084
3487	13403	22207	0.94	4.0E-03	AI108423.1	EST_HUMAN	X8904.X1 NCI CGAP_C018 Homo sapiens cDNA clone IMAGE:266276 3'
3487	13403	22208	0.94	4.0E-03	AI108423.1	EST_HUMAN	X8904.X1 NCI CGAP_C018 Homo sapiens cDNA clone IMAGE:266276 3'
3572	13469	22278	0.83	4.0E-03	Q13605	SWISSPROT	OLFACTORY RECEPTOR 81 (OLFACTORY RECEPTOR-LIKE PROTEIN OLF1)
3636	13469	22278	0.83	4.0E-03	Q13605	SWISSPROT	Mus musculus tumor susceptibility protein 101 (tag 101) gene, complete cds
3852	13763	23559	0.86	4.0E-03	AF060685.1	NT	Homo sapiens TNNI1 gene, exons 1-11 (and joined CDS)
3914	13923		1.79	4.0E-03	AJ011712.1	NT	ab116a08.x5 Stragelene lung (8977210) Homo sapiens cDNA clone IMAGE:341142 3' similar to contains ALU repetitive element;
4509	14402	21160	1.13	4.0E-03	AI732754.1	EST_HUMAN	
5194	15030	22795	13.17	4.0E-03	AJ07187.1	NT	Foot and mouth disease virus serotype A-12 118ab capsid protein VP3
5225	15149	24916	1.95	4.0E-03	AF005956.1	NT	Drosophila melanogaster morc207 (morc207) mRNA, complete cds
5315	15236	24939	19.53	4.0E-03	AF166625.1	NT	Rattus norvegicus beta-casein binding protein mRNA, complete cds
5540	15467	25527	4.23	4.0E-03	P04196	SWISSPROT	(HPRG)
5542	15469	25529	1.15	4.0E-03	P21849	SWISSPROT	MAJOR SURFACE LABELED TROPHOZOITE ANTIGEN PRECURSOR
5704	15812		3.23	4.0E-03	U22180.1	NT	Rattus norvegicus opsin gene, complete cds
5809	15914	24827	1.79	4.0E-03	BE464853.1	EST_HUMAN	901760161F1 NFH MG6_12 Homo sapiens cDNA clone IMAGE:3461954 5'
6032	15945	24910	1.52	4.0E-03	U75406.1	NT	Lycopodium obscurum knotted 3 protein (TKn3) mRNA, complete cds
6271	16136	26291	4.14	4.0E-03	Q02817	SWISSPROT	MUGIN 2 PRECURSOR (MUGIN 2)
6690	16570	26762	3.81	4.0E-03	AF119444.1	NT	Diclyctetium discoidum AXL development protein DG1122 (DG1122) gene, partial cds

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Table 4

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Probe SEQ ID NO.	Exon NO.	ORF/SEQ ID NO.	Expression Signal	Most Similar Protein BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6774	16653	26841	2.02	4.0E-03	7692067	NT	Homo sapiens KIA03346 gene product (KIA03346), mRNA hs-0171.x1 Source, NFI_L_GBC_S1 Homo sapiens cDNA clone IMAGE:206015 3' similar to contains Alu repetitive element;
7056	16653	27123	7.4	4.0E-03	AL553963.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C009
7151	17028	441	4.41	4.0E-03	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
7159	17036	27226	3.39	4.0E-03	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
8472	18345	28009	6.64	4.0E-03	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
9255	19725		3.95	4.0E-03	BE816173.1	EST_HUMAN	PM4-BN0138-19300-002-508 BN0138 Homo sapiens cDNA
9317	19009		2.25	4.0E-03	BE289280.1	EST_HUMAN	601119164FT NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3208056 5'
9628	19202		3	4.0E-03	BP22425.1	EST_HUMAN	7q7408.x1 NCI_CGAP_L424 Homo sapiens cDNA clone IMAGE:3' similar to contains Alu repetitive element/contains element MER31 repetitive element;
9696	19940		1.57	4.0E-03	AW161496.1	EST_HUMAN	h00207.x1 NCI_CGAP_K4111 Homo sapiens cDNA clone IMAGE:2653932 3' similar to contains element LTR5 repetitive element;
9679	19203		1.57	4.0E-03	AW161441.1	EST_HUMAN	RG3-ST0281-20400-015-03 ST0281 Homo sapiens cDNA
9650	19416	25136	1.52	4.0E-03	U1143655	NT	Homo sapiens chr22-associated linker 2 (KIA03671), mRNA
337	10323	20146	1.62	3.0E-03	AF011620.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
651	10767	20538	7.66	3.0E-03	AF011620.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
1638	11542	21401	1.84	3.0E-03	AA459110.1	EST_HUMAN	h07245.x1 NCI_CGAP_P2 Homo sapiens cDNA clone IMAGE:762884 similar to contains Alu repetitive element;
2211	12037		0.87	3.0E-03	AF955965.1	NT	Homo sapiens NFI-C class 1, region
2248	12182		3.9	3.0E-03	Z03921.1	NT	S. cerevisiae (cv. H10) mRNA for thiophosphate isomerase
2249	12193	20239	1.12	3.0E-03	U46856.1	NT	Mus musculus plectoral fold factor gene, partial cds
2249	12193	20300	1.32	3.0E-03	U46856.1	NT	Mus musculus plectoral fold factor gene, partial cds
2363	12890		0.84	3.0E-03	U69506.1	NT	Arabidopsis thaliana TGA3 gene
3044	12971	22705	4.53	3.0E-03	BE376295.1	EST_HUMAN	80123782FT NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3009933 5'
3112	13037	22833	2.62	3.0E-03	AF162367.1	EST_HUMAN	L23-UM0076-20300-006-003 UM0076 Homo sapiens cDNA
3371	13290	23096	1.95	3.0E-03	U46905.1	NT	Human muscle alpha-1(XIII) collagen (COL1A1) gene, exon 1 and 2
3379	13297		6.75	3.0E-03	Y12600.1	NT	C. elegans sem-5 gene
3655	13805	25691	7.43	3.0E-03	AF762892.1	EST_HUMAN	AY762892 MDS Homo sapiens cDNA clone MDS5501 5'
3655	13805	25692	7.43	3.0E-03	AF762892.1	EST_HUMAN	AY762892 MDS Homo sapiens cDNA clone MDS5501 5'
3950	13868	29052	1.58	3.0E-03	AF762278.1	EST_HUMAN	antitrypsin Caspase Wfms tumor Homo sapiens cDNA clone IMAGE:1155689 5'
4058	13960		1.34	3.0E-03	Z03521.1	NT	S. cerevisiae (cv. H10) mRNA for thiophosphate isomerase
4296	14194	23978	11.91	3.0E-03	AJ01432.1	NT	Rattus norvegicus gurl gene
4417	14311	24096	4.37	3.0E-03	AL559141.1	EST_HUMAN	h06P10.18 connexin Homo sapiens cDNA 3'
4430	14518	24309	0.88	3.0E-03	AL110097.1	EST_HUMAN	h06P10.18 connexin Homo sapiens cDNA 3'

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4727	14613	24399	1.54	3.0E-03	AF23754.1	EST_HUMAN	ab150436 Stragelung lung (H937210) Homo sapiens cDNA clone IMAGE:841142 3' similar to contains A1u repetitive element;
4745	14630	24416	7.09	3.0E-03	BE78945.1	EST_HUMAN	601482718FT NIH MGCC 88 Homo sapiens cDNA clone IMAGE:3865483 5'
5089	14668	24733	1.11	3.0E-03	4506414	NT	Homo sapiens RAP1, GTPase activating protein 1 (RAP1GA1) mRNA
5099	14666	24734	1.11	3.0E-03	4506414	NT	Homo sapiens RAP1, GTPase activating protein 1 (RAP1GA1) mRNA
5220	15143	24837	3.17	3.0E-03	8922466	NT	Homo sapiens hypochelated protein FLJ10539 (FLJ10539), mRNA
5410	15330	28380	1.41	3.0E-03	AJ246961.1	NT	Mus musculus mRNA for hypothetical protein (ORF2 ortholog)
5946	15851	25974	0.97	3.0E-03	AA456701.1	EST_HUMAN	ast1310.1 Scores, NHMMPU_S1 Homo sapiens cDNA clone IMAGE:313163 5'
6277	16141	26297	1.54	3.0E-03	AJ011419.1	NT	Kluyveromyces fragilis pcp3 gene for putative-cytoplasmic permease
6442	16303	26468	3.71	3.0E-03	A5021736.1	NT	Oryza sativa gene for b2p protein, complete cds
6741	16620	26809	2.01	3.0E-03	N62560.1	EST_HUMAN	2627604.1 Scores, parathyroid tumor, N6HPA Homo sapiens cDNA clone IMAGE:304763 3'
6826	16806	27001	1.29	3.0E-03	P51989	SWISSPROT	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A2 HOMOLOG 1 (HNRNP A2(A))
6940	16818	27011	1.57	3.0E-03	AL183265.2	NT	Homo sapiens chromosome 21 segment HS21C088
6991	16966		1.38	3.0E-03	Q6C081	SWISSPROT	NONSTRUCTURAL PROTEIN V
7199	17076		8.62	3.0E-03	AW613774.1	EST_HUMAN	h8910.1 NCI COAP_GU1 Homo sapiens cDNA clone IMAGE:2660131 3' similar to contains L1 L1 L1 repetitive element;
7230	17107	27297	4.1	3.0E-03	AL161692.2	NT	Arabidopsis thaliana DNA chromosome 4, coding fragment Nc 85
7244	17121	27317	8.9	3.0E-03	A1616734.1	EST_HUMAN	cc3413.2 NCI COAP_K43 Homo sapiens cDNA clone IMAGE:163247 3' similar to gb257138_rn41
7599	17446		3.43	3.0E-03	P08672	SWISSPROT	CIRCULINOSPOROZOOTIC PROTEIN PRECURSOR (CS)
7694	17544	27688	1.29	3.0E-03	P41389	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS REVERSE TRANSCRIPTASE];
7742	17682	27813	1.48	3.0E-03	P51989	SWISSPROT	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A2 HOMOLOG 1 (HNRNP A2(A))
7839	17866	27831	4.05	3.0E-03	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
8222	18104		2.89	3.0E-03	8603026	NT	Homo sapiens ATRXGTP-binding protein (HEB), mRNA
8655	18573	28669	2.11	3.0E-03	A100222.1	NT	Phaeocystis carolinensis heat-shock protein endoprotease mRNA, partial cds
8744	17803	28137	2.01	3.0E-03	A7260265.1	NT	Homo sapiens golin-hlike protein (GLP) gene, complete cds
8773	18590	28871	3.05	3.0E-03	A1094481.1	NT	Homo sapiens thymidine repeat DNA binding protein p28-CGGBP (CGGBP) gene, complete cds
8773	18590	28878	3.05	3.0E-03	A1094481.1	NT	Homo sapiens thymidine repeat DNA binding protein p28-CGGBP (CGGBP) gene, complete cds
8841	18654	28942	1.93	3.0E-03	P11389	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS REVERSE TRANSCRIPTASE];
9069	19542		2.02	3.0E-03	A125056.1	EST_HUMAN	promoter-5ED77 b1 tumor Homo sapiens cDNA 5'
9109	18870	28780	1.54	3.0E-03	AA693154.1	EST_HUMAN	cd77b10.1 Scores, total, N6HPA_2w Homo sapiens cDNA clone IMAGE:1622779 3' similar to contains L1 L8 MER26 repetitive element;

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9159	19498		1.35	3.0E-03	AB006603.1	NT	Homo sapiens gene for CMP-N-acetylneuraminic acid hydroxylase, partial cds
9339	18019	25290	2.33	3.0E-03	AJ26282.1	NT	9 alpha noncoding mRNA for coronavirus (c208 gene)
504	10461	20283	0.89	2.0E-03	Q04682	SWISSPROT	RING CANAL PROTEIN (KELCH PROTEIN)
504	10446	20289	0.89	2.0E-03	Q04682	SWISSPROT	RING CANAL PROTEIN (KELCH PROTEIN)
788	12677		7.01	2.0E-03	J70874.1	EST_HUMAN	h190307.1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:108341.5
1340	11246	21104	1.93	2.0E-03	M20789.1	NT	Human alpha-2-plasmin inhibitor gene, exons 6 and 7
1343	11249	21106	1.99	2.0E-03	A4661605.1	EST_HUMAN	musubi.at NCI CGAP AMT Homo sapiens cDNA clone IMAGE:1217593
1343	11259	21115	12.6	2.0E-03	AF284446.1	NT	Homo sapiens tumor-related protein DRG2 (DRG2) gene, complete cds
1474	11370	21243	1.11	2.0E-03	P48509	SWISSPROT	PLATELET ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN)
1500	11404	21263	1.91	2.0E-03	A457693	NT	Homo sapiens procollagen-lyase, 2-oxoglutarate 5-dioxygenase (lyase hydroxylase, Ehlers-Danlos syndrome type VI) (FLOD) mRNA
1500	11404	21263	1.91	2.0E-03	A457693	NT	Homo sapiens procollagen-lyase, 2-oxoglutarate 5-dioxygenase (lyase hydroxylase, Ehlers-Danlos syndrome type VI) (FLOD) mRNA
1573	11477	21264	1.91	2.0E-03	A457693	NT	Homo sapiens procollagen-lyase, 2-oxoglutarate 5-dioxygenase (lyase hydroxylase, Ehlers-Danlos syndrome type VI) (FLOD) mRNA
1733	11834	21602	1.38	2.0E-03	AA450138.1	EST_HUMAN	COLLAGEN ALPHA 1(VI) CHAIN PRECURSOR
1980	11845	21791	2.17	2.0E-03	AA450138.1	EST_HUMAN	COLLAGEN ALPHA 1(VI) CHAIN PRECURSOR
2203	12090	21982	1.04	2.0E-03	AF303691.1	NT	Mus musculus myelin expression factor-3-like protein gene, partial cds
2636	12408		4.82	2.0E-03	AF137982.1	EST_HUMAN	Homo sapiens chromosome 21 segment H521C102
3370	13289	23008	4.03	2.0E-03	AA450138.1	EST_HUMAN	U1H-BF1-actg-10-01.1 NCI CGAP S343 Homo sapiens cDNA clone IMAGE:271610.3
3372	13294	23083	1.02	2.0E-03	BF568955.1	EST_HUMAN	z42a10.1t Soares, fetal, fetus, N2ZHF8, 5w Homo sapiens cDNA clone IMAGE:789114.5
3615	13529	23315	4.87	2.0E-03	X87344.1	NT	6021839601T NIH MGCC 42 Homo sapiens cDNA clone IMAGE:500070.3
3659	13760	23572	0.92	2.0E-03	AB040802.1	NT	H sapiens D1A, D1B, HLA-21, 1P22, LMP2, TAP-1, LMP7, TAP2, DOB, DOB2 and H1N68, 9, 13 and 14 genes
4024	13827	23703	2.16	2.0E-03	P03374	SWISSPROT	Rattus norvegicus mRNA for GREB1, complete cds
4127	14027		9.77	2.0E-03	U08491.1	NT	ENH POLYPROTEIN CONTAINS: COAT PROTEIN GP42; COAT PROTEIN GP36
4448	14340	24130	1.89	2.0E-03	A2512.1	NT	Rattus norvegicus 5-hydroxytryptamin-2 receptor gene, partial cds
4446	14340	24131	1.89	2.0E-03	A2512.1	NT	Drosophila melanogaster shortlight class 2 (cs) mRNA, complete cds
4808	14496	24285	0.94	2.0E-03	AF223391.1	NT	Drosophila melanogaster shortlight class 2 (cs) mRNA, complete cds
4812	14500		1.7	2.0E-03	R87773.1	EST_HUMAN	Homo sapiens cdc20b channel alpha1E subunit (CAGNATE) gene, exons 7, 49, and partial cds, alternatively spliced
5077	14947		0.82	2.0E-03	AJ245167.1	NT	y45492.2.1 Soares adult brain N2441B557 Homo sapiens cDNA clone IMAGE:100890.3
5194	15057	24620	1.04	2.0E-03	A1005150.1	NT	Caninus domesticus c9h19 gene for immunoglobulin heavy chain variable region
5194	15057	24621	1.04	2.0E-03	A1005150.1	NT	Homo sapiens extracellular glycoprotein lamin precursor, gene, complete cds
5194	15057	24621	1.04	2.0E-03	A1005150.1	NT	Homo sapiens extracellular glycoprotein lamin precursor, gene, complete cds

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6372	15322	25128	1.37	2.0E-03 BF241410.1	EST_HUMAN	601879386F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4104892.5'	
6467	19445	25438	1.76	2.0E-03 AB014563.1	NT		Homo sapiens mRNA for KIA0063 protein, partial cds
6501	15420	25482	1.87	2.0E-03 U63711.1	NT		Xenopus laevis zebrin mRNA, complete cds
6716	16024	25725	3.25	2.0E-03 P22477	SWISSPROT		ATP-DEPENDENT NUCLEASE SUBUNIT B
6716	16024	25726	3.25	2.0E-03 P22477	SWISSPROT		ATP-DEPENDENT NUCLEASE SUBUNIT B
6829	15735	25849	1.82	2.0E-03 Q65203	SWISSPROT		CARBONIC ANHYDRASE-RELATED PROTEIN 2 PRECURSOR (CARP 2) (CARP II) (CA-X)
6829	15735	25847	1.82	2.0E-03 Q65203	SWISSPROT		CARBONIC ANHYDRASE-RELATED PROTEIN 2 PRECURSOR (CARP 2) (CARP II) (CA-X)
6931	15737	25849	7.14	2.0E-03 BF030187.1	EST_HUMAN		601887434F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4121406.5'
6960	15756	25874	2.2	2.0E-03 Q4UKP4	SWISSPROT		ADAMTS 7 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 7) (ADAMTS-7) (ADAM-TS7)
6961	15767	25898	1.96	2.0E-03 XG4451.1	NT		Leuculentum mRNA for fcyb-RNA synthase (LcyRS)
6979	15904		1.36	2.0E-03 AB91095.1	EST_HUMAN		W638906.v1 Soares, Diethylmale, cdon, NIHCD Homo sapiens cDNA clone IMAGE:2622177.3' similar to SW-10620 HUMAN P47914.60S RIBOSOMAL PROTEIN L29 contains element MSR1 3' repetitive element ;
6212	15904	26129	2.68	2.0E-03 BE007686.1	EST_HUMAN		CHLBT0360-061269-054-001 BT03689 Homo sapiens cDNA
6961	16571	26763	2.11	2.0E-03 AW562004.1	EST_HUMAN		H37D68.31 Soares_NFL_I_GBC_S31 Homo sapiens cDNA clone IMAGE:2634035.3' similar to TR-C060976
6794	16663	26653	5.19	2.0E-03 N20287.1	EST_HUMAN		X432068.v1 Soares melanocyte 2NHM Homo sapiens cDNA clone IMAGE:264442.3' similar to contains L4132 L1 ras2615 element ;
6794	16663	26654	5.19	2.0E-03 N20287.1	EST_HUMAN		X432068.v1 Soares melanocyte 2NHM Homo sapiens cDNA clone IMAGE:264442.3' similar to contains L4132 L1 ras2615 element ;
7513	17301	27668	3.12	2.0E-03 P24821	SWISSPROT		TEMASON PRECURSOR (TN) (HEXABRACHION) (CYTOTACTIN) (NEURONECTIN) (GMEI) (JI) (MITOGENIC ANTIGEN) (GLOMA-ASSOCIATED-EXTRACELLULAR MATRIX ANTIGEN) (GP 160-229) (TENASCIN-C) (TN-C)
7775	17625		5.41	2.0E-03 AA251376.1	EST_HUMAN		zat006.v1 NCI_OGAP_OG031 Homo sapiens cDNA clone IMAGE:364754.3'
8379	18296		2.78	2.0E-03 M66524.1	NT		Human dyoprotin gene
8779	16390	26620	1.78	2.0E-03 P07354	SWISSPROT		PROTEOGLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP)
8829	18642		1.77	2.0E-03 BF330609.1	EST_HUMAN		RC3-F703033-010600-115-g04 BT03533 Homo sapiens cDNA
8836	18649	26036	12.17	2.0E-03 Z11740.1	NT		H.sapiens variable number tandem repeat (VNTR) locus DNA
9062	18635		2.07	2.0E-03 AB25745.1	EST_HUMAN		I69H03.v1 NCI_OGAP_K04T1 Homo sapiens cDNA clone IMAGE:2263989.3' similar to SW-VATG_MANSE
9066	18647	25115	2.88	2.0E-03 AF157516.2	NT		Q25552 VACUOLAR ATP SYNTHASE SUBUNIT G ;
9113	14947		4.48	2.0E-03 AJ245167.1	NT		Homo sapiens SELL (SELL) gene, partial cds
9322	18703		2.76	2.0E-03 AV897696.1	EST_HUMAN		Carnelia dromedaria cckp19 gene for immunoglobulin heavy chain variable region

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9414	190660	28278	1.69	2.0E-03	Y05938.1	NT	H sapiens M1 gene for muscarinic acetylcholine receptor
9485	19097		9.02	2.0E-03	D42427.1	NT	Human DNA for CD38, exon 1
9525	19134		2.92	2.0E-03	AL463203.2	NT	Human sapiens chromosome 21 segment HS21C003
9532	19559		1.67	2.0E-03	A875037.1	EST HUMAN	96002.x1 Source, J Biol. Med. 105:2178, 96 Homo sapiens cDNA clone IMAGE:249057 3' similar to contains Alu repetitive element;
9593	19247		1.27	2.0E-03	AF120756.1	NT	Homo sapiens MSH56 gene, partial cds; and CLIC1, DDAH, G6b, G6c, G8d, G6a, G6f, BAT5, G6b, CS22B, BAT4, G4, Apo M1, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds
9856	19521		1.66	2.0E-03	A1907586.1	EST HUMAN	X1907586 GK Homo sapiens cDNA clone GKCX2005 5'
432	10377	20158	1.38	1.0E-03	H93471.1	EST HUMAN	Y68026.x1 Source, J Biol. Med. 105:2178, 96 Homo sapiens cDNA clone GKCX2005 5'
812	10740	20557	2.38	1.0E-03	A1720263.1	EST HUMAN	a670003.x1 Barhead cdon HPIRB7 Homo sapiens cDNA clone IMAGE:232334 5'
812	10740	20559	2.38	1.0E-03	A1720263.1	EST HUMAN	a670003.x1 Barhead cdon HPIRB7 Homo sapiens cDNA clone IMAGE:232334 5'
1079	10995	20836	2.14	1.0E-03	A1956783.1	EST HUMAN	C13825 AU-BINDING PROTEINOMYL-COA HYDRATASE ;
1089	11015	20857	1.44	1.0E-03	A1954572.1	EST HUMAN	W485005.x1 NC1 CGAP P491 Homo sapiens cDNA clone IMAGE:232225 3'
1150	11083	20903	1.45	1.0E-03	A1952916.1	EST HUMAN	W485005.x1 NC1 CGAP P491 Homo sapiens cDNA clone IMAGE:232225 3'
1832	11875	21768	3.61	1.0E-03	F47608	SWISSPROT	W485005.x1 NC1 CGAP P491 Homo sapiens cDNA clone IMAGE:232225 3'
2100	11957	21959	8.02	1.0E-03	AJ131016.1	NT	repetitive element;
2851	12878	22579	1.16	1.0E-03	AB033117.1	NT	Homo sapiens SCL gene locus
3154	13079	22879	2.26	1.0E-03	F18915	SWISSPROT	HIGH MOLECULAR WEIGHT FORM OF MYOSIN I (HMYIWI)
3154	13079	22880	2.26	1.0E-03	F18915	SWISSPROT	Homo sapiens mRNA for KIA1231 protein, partial cds
3262	13185	22984	1.16	1.0E-03	P08547	SWISSPROT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED)
3495	13413	23218	0.79	1.0E-03	P08547	SWISSPROT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONIC ANHYDRASE)
3498	13413	23219	0.79	1.0E-03	U68001.1	NT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONIC ANHYDRASE)
3614	13528		1.24	1.0E-03	AB044400.1	NT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
3865	13766	23559	1.02	1.0E-03	A694400.1	NT	Human MJC2 gene, promoter region
4334	14231	24013	3.54	1.0E-03	BE030162.1	EST HUMAN	Homo sapiens SVMT gene for synaptic vesicle monoamine transporter, exons 14, 15
4377	14273	24054	3.77	1.0E-03	BE246836.1	EST HUMAN	S. cerevisiae chromosome X, reading frame ORF YJ8149x
4564	14459	24244	0.87	1.0E-03	U23449.1	NT	RC1-TN0128-100500-021-001 TN0128 Homo sapiens cDNA
							TCBAP-D4909 Predicted pre-B cell acute lymphoblastic leukemia Bcr/ta-HGSC project-TGBA Homo sapiens cDNA clone TCBA009
							Casophthalid elegans 5' end leader RNA (SL3 alpha), (SL4), and (SL5) genes

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4717	14903	24388	1.76	1.0E-03	AB73485.1	EST_HUMAN	ov4504Lx1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:1640282.3'
4717	14903	24389	1.76	1.0E-03	AB73485.1	EST_HUMAN	ov4504Lx1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:1640282.3'
4718	14904	24390	6.23	1.0E-03	BE151067.1	EST_HUMAN	PMO-H10339-200400-010-D02 HT10339 Homo sapiens cDNA
5009	14883	24649	16.98	1.0E-03	O419409	SWISSPROT	APOLIPROTEIN A-IV PRECURSOR (APO-AIV)
5103	14971	24747	0.93	1.0E-03	AF095870.1	EST_HUMAN	AV689570 GKC Homo sapiens cDNA clone SK00M11.5'
5260	15173	24646	2.03	1.0E-03	AA280651.1	EST_HUMAN	zz4401.1 L1 NC1, GAP, GCB1 Homo sapiens cDNA clone IMAGE:700345.5'
5317	15238	25042	3.00	1.0E-03	AJ006945.1	NT	Homo sapiens KYL0311 gene
5349	15259	25056	2.01	1.0E-03	K03332.1	NT	Epstein-Barr virus (AG876 isolate) U2-R2 domain encoding nuclear protein EBNA2, complete cds
5349	15259	25057	2.01	1.0E-03	K03332.1	NT	Epstein-Barr virus (AG876 isolate) U2-R2 domain encoding nuclear protein EBNA2, complete cds
5423	15344	25307	1.66	1.0E-03	Q02389	SWISSPROT	COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN)
5666	15577	25307	4.08	1.0E-03	X07659.1	NT	Mouse nucleolin gene
5759	15608		8.56	1.0E-03	11529178	NT	Homo sapiens T cell lymphoma invasion and metastasis 1 (TIMM1), mRNA
5824	15730	25842	1.32	1.0E-03	BT7611.1	EST_HUMAN	Y83311.1 Soares fetal liver spleen (NFLS) Homo sapiens cDNA clone IMAGE:115772.5'
5857	15763	26259	1.4	1.0E-03	AW602585.1	EST_HUMAN	OVS-NH1024-250400-171-g05 NT1024 Homo sapiens cDNA
6243	16108	26259	2.4	1.0E-03	D19838.1	NT	Human gene for fourth semioctin receptor subype
6419	16281		1.37	1.0E-03	AJ22042.1	NT	Homo sapiens 699 to conf6 between AVL1 and GBT on chromosome 21q22, segment 23
							Homo sapiens X28 acsin (near ALD locus containing dual specificity phosphatase 9 (DUSP9), fibronectin protein 15a (FBN15a), C24-Calmodulin-dependent protein kinase 1 (CAMK1), creatine transporter (CRT1), CD4 protein (CD4), adenocysticobiprotein >
6603	16362	26537	1.63	1.0E-03	U52111.2	NT	Human TRPA2 protein gene, exons 1, 2 and 3
6638	16364	26573	3.13	1.0E-03	M53376.1	NT	Homo sapiens peritaxin-1 gene
6638	16516	26707	5.35	1.0E-03	AJ21973.1	NT	Homo sapiens endostatin-like protein 1 (EXTL1) gene, exons 2 through 11, and complete cds
6768	16877	26857	2.39	1.0E-03	AF135953.1	NT	Y-carboxy gene encoding vaxoprotein
7175	17052		1.4	1.0E-03	117264.1	NT	Human class III alcohol dehydrogenase (ADH5) cDNA, complete cds
7273	17190	27445	4.27	1.0E-03	K03947.1	NT	Human class III alcohol dehydrogenase (ADH5) cDNA, complete cds
7273	17190	27446	4.27	1.0E-03	K03947.1	NT	Human class III alcohol dehydrogenase (ADH5) cDNA, complete cds
7273	17190	27446	4.27	1.0E-03	K03947.1	NT	Human class III alcohol dehydrogenase (ADH5) cDNA, complete cds
7541	17352	27602	1.85	1.0E-03	AF011400.1	NT	Thermoga naspallina alpha-1,6-galactosidase (alpha-1,6-galactosidase) gene, complete cds
7541	17352	27603	1.85	1.0E-03	AF011400.1	NT	Thermoga naspallina alpha-1,6-galactosidase (alpha-1,6-galactosidase) gene, complete cds
8055	17947	28196	22.37	1.0E-03	AW302533.1	EST_HUMAN	RG1-CT0276-181099-011-409 CT0279 Homo sapiens cDNA
8055	17947	28197	22.37	1.0E-03	AW302533.1	EST_HUMAN	RG1-CT0276-181099-011-409 CT0279 Homo sapiens cDNA
8133	18021	28268	2.44	1.0E-03	BE170659.1	EST_HUMAN	QV3-HT0543-230300-130-403 HT0543 Homo sapiens cDNA
							UP3412.1 NC1, GAP, HSC3 Homo sapiens cDNA clone IMAGE:2246446.3' similar to TR028165 Q28165 PVA1, cDNA
8196	18083		2.69	1.0E-03	A553947.1	EST_HUMAN	0V195949 MD5 Homo sapiens cDNA clone MDS0DF11.5'
8467	18370		3.4	1.0E-03	AV1750946.1	EST_HUMAN	0V195949 MD5 Homo sapiens cDNA clone IMAGE:3318524.5'
9046	18931	26113	2.82	1.0E-03	BE594488.1	EST_HUMAN	0V195949 MD5 Homo sapiens cDNA clone IMAGE:3318524.5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9497	19108	25287	1.95	1.0E-03	9507208	NT	Rattus norvegicus transformation related protein 83 (Trp83), mRNA
9917	19837		2.15	1.0E-02	AB47355.1	EST_HUMAN	ICDH3L1, NCI_GCAP Cor16 Homo sapiens cDNA clone IMAGE:20850133 similar to contains AU repetitive element
9926	19707	24004	4.2	1.0E-03	BE73072.1	EST_HUMAN	
5131	14968	24769	0.81	9.0E-04	U11970.1	NT	Human retinol-binding protein 2, mRNA
5485	15412		1.56	9.0E-04	U20727	SWISSPROT	Human retinol-binding protein 2, mRNA
7591	17404		1.42	9.0E-04	U20727	NT	Human retinol-binding protein 2, mRNA
1472	11377		1.39	8.0E-04	AB037203.1	NT	Xenopus laevis galactose-4-epimerase mRNA, for beta-amylase synthesis, complete cds
3843	13754	25548	1.37	8.0E-04	AB037203.1	EST_HUMAN	Xenopus laevis galactose-4-epimerase mRNA, for beta-amylase synthesis, complete cds
4059	13989		4.2	8.0E-04	R07008.1	EST_HUMAN	
4656	14842	24332	4.2	8.0E-04	U20727	SWISSPROT	
8465	18468		2.39	8.0E-04	U20727	NT	
8476	18463		2.16	8.0E-04	U20727	EST_HUMAN	
1765	11584	21582	1.61	8.0E-04	AA77084.1	EST_HUMAN	
2350	12200	21271	1.13	7.0E-04	U20727	NT	
2032	12547	22437	3.28	7.0E-04	U20727	NT	
3245	13103	22855	1.03	7.0E-04	AL10320.2	NT	
5923	18823		2.24	7.0E-04	AF165331.1	EST_HUMAN	
8851	18838		3.2	7.0E-04	U78027.1	NT	
8871	18863	28973	2.61	7.0E-04	Z40961.1	EST_HUMAN	
5558	18165		3.29	7.0E-04	BE07841.1	EST_HUMAN	
9790	16500		2.72	7.0E-04	R17336.1	EST_HUMAN	
9813	16521		3.28	7.0E-04	9005655	NT	
3877	13788	28576	1.34	6.0E-04	AB82525.1	EST_HUMAN	
3999	13905	28650	0.85	6.0E-04	K01315.1	NT	
3999	13905	28681	0.85	6.0E-04	K01315.1	NT	
4002	13962	27956	3.28	6.0E-04	U45693.1	NT	
6550	16470		4.35	6.0E-04	P49408	SWISSPROT	
7733	17693		3.13	6.0E-04	AL048007.2	EST_HUMAN	
7800	17693	27887	2.24	6.0E-04	BE06860.1	EST_HUMAN	
9776	18503	28881	2.07	6.0E-04	AJ223942.1	NT	
8852	18844	28950	6.32	6.0E-04	AW013847.1	EST_HUMAN	
8906	18714		2.46	6.0E-04	Q01788	SWISSPROT	

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6225	19598		2.25	6.0E-04	AW302519.1	EST_HUMAN	RC3-H17038-201189-012-408 HT269 Homo sapiens cDNA
6603	19421	25170	1.49	6.0E-04	11418157	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1I subunit (CAGNA1I), mRNA
635	10572	20395	5.82	6.0E-04	O10441	SWISSPROT	HYPOPHOSPHATASE 2 (HPP2) Homo sapiens cDNA
1485	11390		1.83	6.0E-04	AW165184.1	EST_HUMAN	QV0-CT0225-021689-305-407 CT0225 Homo sapiens cDNA
3357	13286	23085	1.42	6.0E-04	AA546331.1	EST_HUMAN	IKZF1-111111 NCL CGAP C011 Homo sapiens cDNA clone IMAGE:1014794 3' similar to contains ALU repetitive element
5391	15281	25113	2.19	6.0E-04	AF248954.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
5995	15801	20026	5.72	6.0E-04	AA186303.1	EST_HUMAN	Z0333068.1 Stratiotype colon (6637264) Homo sapiens cDNA clone IMAGE:586863 5'
6384	15227	20387	13.6	6.0E-04	U22054.1	NT	Gonella gorilla involucrin gene medium alpha, complete cds
6636	16519	25710	5.57	6.0E-04	A1863392.1	EST_HUMAN	q01306.x1 Soares, placenta, stromal, 2NAP3929V Homo sapiens cDNA clone IMAGE:172819 3' similar to gk-XF1602, x1 NCL CGAP K511 Homo sapiens cDNA clone IMAGE:2680273 3'
7345	17213	27412	1.45	6.0E-04	AA046561.1	EST_HUMAN	q16603.x1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:1594587 3'
7543	17394	27603	4.69	6.0E-04	AW170935.1	EST_HUMAN	q16602.x1 NCL CGAP K011 Homo sapiens cDNA clone IMAGE:2786683 3'
8343	18220		4.17	6.0E-04	AL046807.2	EST_HUMAN	DK-F2569/2024_11 583 (synonym: huc5) Homo sapiens cDNA clone DKF-Z569H/2024
8950	15281	25113	17.6	6.0E-04	AF248954.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
9164	15830		2.27	6.0E-04	AA566113.1	EST_HUMAN	nt5192.x1 NCL CGAP P11 Homo sapiens cDNA clone IMAGE:513375
9944	16413		1.45	6.0E-04	AW141665.1	EST_HUMAN	nt7105.x1 NCL CGAP K511 Homo sapiens cDNA clone IMAGE:2680273 3'
336	10333		1.13	4.0E-04	BF241482.1	EST_HUMAN	80176534F1 NH1.MGC.55 Homo sapiens cDNA clone IMAGE:4104897 5'
657	10392	20410	1.42	4.0E-04	U32748.1	NT	Hemophilus influenzae Rd genome, CS of 153 of the complete genome
829	10755	20066	1.57	4.0E-04	A172268.1	EST_HUMAN	as17003.x1 Barbedash colony HPI.R17 Homo sapiens cDNA clone IMAGE:2344039 3' similar to TR.Q13825
826	10755	20037	1.57	4.0E-04	A172268.1	EST_HUMAN	as17003.x1 Barbedash colony HPI.R17 Homo sapiens cDNA clone IMAGE:2344039 3' similar to TR.Q13825
14469	11354	21218	3.92	4.0E-04	AW753356.1	EST_HUMAN	Q13825 ALU-BINDING PROTEIN, HENOTL-1 COA HYDROLASE.1
2036	11926	21823	1.88	4.0E-04	AL163278.2	NT	RC3-CT0264-100100-025-61 CT0264 Homo sapiens cDNA
2037	11926		1.19	4.0E-04	AL048704.1	EST_HUMAN	Homo sapiens chromosome 21 segment H531078
2936	12457	22348	2.73	4.0E-04	O96615	EST_HUMAN	DKF-Z64005.1 t1 431 (synonym: huc5) Homo sapiens cDNA clone DKF-Z6434D059 5'
3127	13002	22830	1.89	4.0E-04	AF281074.1	SWISSPROT	SERPIN-2 (S1) (G1U1 PROTEIN 2)
3316	13257	23041	0.84	4.0E-04	AW169824.1	EST_HUMAN	Homo sapiens nucleolin 2 (NRP2) gene, complete cds, alternatively spliced
4226	14126	23800	2.75	4.0E-04	AA576331.1	EST_HUMAN	AV66624.GG Homo sapiens cDNA clone GIC0FH07 5'
							NT10413 NCL CGAP C011 Homo sapiens cDNA clone IMAGE:991930 3' similar to gk-M21121 T-CELL SPECIFIC RANTES PROTEIN PRECURSOR (HUMAN)

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
4228	14126	23801	2.76	4.0E-04	AA676331.1	EST_HUMAN	NT010151 NC1 CGAP_Cot1 Homo sapiens cDNA clone IMAGE:5951930 3' similar to gb:M21121 T-CELL
4437	14332	24121	1.29	4.0E-04	AA08324.1	EST_HUMAN	SPNFC10 RANTES PROTEIN PRECURSOR (HUMAN);
5020	14893	24691	3.72	4.0E-04	BE590690.1	EST_HUMAN	001345585Ft NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3578010 5'
5132	14956	24770	0.9	4.0E-04	NA48313.1	EST_HUMAN	Y17850.11 Soares, multiple, sclerotic 2NUHNSP Homo sapiens cDNA clone IMAGE:270643 5' similar to contains Alu repetitive element;
5972	16546	27040	1.62	4.0E-04	NA25007.1	EST_HUMAN	X33912.71 Soares melanocyte 2NHHM1 Homo sapiens cDNA clone IMAGE:284142 5'
7598	17439	27655	2.79	4.0E-04	AD25699.1	EST_HUMAN	0067603.1 Soares testis, NHT Homo sapiens cDNA clone IMAGE:164341 3'
7623	17512		1.44	4.0E-04	A102865.1	EST_HUMAN	Man musculi neuropilin-3 (nt17) mRNA, alternatively spliced, complete cds
8520	19505		1.62	4.0E-04	A1254622.1	NT	Homo sapiens SMARCA4 isoform (SMARCA4) gene, complete cds, alternatively spliced
8677	19479		1.84	4.0E-04	Q05860	SWISSPROT	FORMIN (LIMB DEFORMITY PROTEIN)
1591	10124	19442	3.04	3.0E-04	AL119436.1	EST_HUMAN	DKEZ761121.11761 (synonym: hem2) Homo sapiens cDNA clone DKFZ761121.6'
1581	10160	19977	2.22	3.0E-04	P46259	SWISSPROT	180 KD SECRETORY PHOSPHOLIPASE A2 RECEPTOR PRECURSOR (PLA2-R)
862	10768	20539	1.27	3.0E-04	U83991.1	NT	Human short chain acyl CoA dehydrogenase gene, exons 1 and 2
1510	11707		1.16	3.0E-04	U839974.1	EST_HUMAN	0239402.1 NC1 CGAP_Fc28 Homo sapiens cDNA clone IMAGE:2119062 3'
3339	13190	23689	3.37	3.0E-04	P35147	SWISSPROT	GLUTAMATE DEHYDROGENASE 2 PRECURSOR (GDH)
3823	13793	23581	3.63	3.0E-04	P40449	SWISSPROT	Homo sapiens X0 pseudotuberculari zoon, segment 172
3395	13873		1.18	3.0E-04	A1271755.1	NT	0064-H10335-193200-007-012 HT03339 Homo sapiens cDNA
4711	14597		4.8	3.0E-04	BE153778.1	EST_HUMAN	Q194-D10045-231290-006-008 D10048 Homo sapiens cDNA
4784	14693	24456	0.85	3.0E-04	AT183772.1	EST_HUMAN	Y10411.11 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:763471 5' similar to gb:M62762
5522	14824		1.34	3.0E-04	A111204.1	NT	V-actin gene encoding vWickapin
5735	15543		4.82	3.0E-04	AL162571.2	NT	Homo sapiens chromosome 21 segment 115210391
6001	15925	26198	8.88	3.0E-04	AL163278.2	NT	HOMOBLAST GROWTH FACTOR RECEPTOR 3 PRECURSOR (FGFR-3)
6835	16585	28975	3.49	3.0E-04	P22507	SWISSPROT	160SLAST ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT (HUMAN);
7706	17656	27780	1.42	3.0E-04	AA544055.1	EST_HUMAN	206550.11 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:763471 5' similar to gb:M62762
7677	17827	28008	3.86	3.0E-04	AA761201.1	EST_HUMAN	VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT (HUMAN);
9118	19726	24908	2.33	3.0E-04	AA23901.1	EST_HUMAN	ADONISOMAL PROTEIN L7A (HUMAN);
9463	19576	25008	4.32	3.0E-04	AB016252.1	NT	0038004.1 NC1 CGAP_172 Homo sapiens cDNA clone IMAGE:1010430 similar to contains L1 L2 L1
9874	19991		2.01	3.0E-04	AL134483.1	EST_HUMAN	Homo sapiens mRNA for KIA04749 protein, partial cds
1091	10141	19987	1.18	2.0E-04	AF217796.1	NT	DKEZ76547L185.117647 (synonym: fibrin) Homo sapiens cDNA clone DKEZ76547L185.5' similar to gb:M69072 60S RIBOSOMAL PROTEIN L7A (HUMAN);
							protein 1 (AFRFP1) genes, complete cds

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Probe SEQ ID NO.	Em SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
470	10413	20232	2.15	2.0E-04	AIJ46707.1	EST_HUMAN	AU146707 HEMER1 Homo sapiens cDNA clone HEUB1001283.3'
889	10375	20053	4.48	2.0E-04	U63682.1	NT	Human dyx19ap1 gene
889	10375	20054	4.48	2.0E-04	U63682.1	NT	Human dyx19ap1 gene
1162	11075		4	2.0E-04	AJ26629.1	EST_HUMAN	qf6891.X1 Soares_INT_1_GBC_S1 Homo sapiens cDNA clone IMAGE:195362.3' similar to contains MERS32. MERS32 negative element
1169	11031		1.89	2.0E-04	AI163203.2	EST_HUMAN	Homo sapiens chromosome 21 segment HS210003
1171	11099		1.44	2.0E-04	AF224393.1	NT	Nude musculosa 5' flanking region of Pknox gene
2193	12024		1.28	2.0E-04	AA478990.1	EST_HUMAN	200605.01 Soares overy tumor/ N4H0T Homo sapiens cDNA clone IMAGE:740337.3' similar to contains A1u repetitive element
2628	12293	22393	4.15	2.0E-04	U60606.1	EST_HUMAN	Human germline T-cell receptor beta chain TCRBV/175/1A1T1, TCRBV/2531, TCRBV/105/1P, TCRBV/295/1P, TCRBV/185/1P, TCRBV/45/1A1T, HVB relic, TCRBV285/P, TCRBV345/1, TCRBV/145/1, am65039.1T, TCRBV/45/1A1T, TRV4, TRV3, TRV6, TRV7, TRV8, TCRB61, TCRBV/151, TCRBV/152> am65039.1T, Johnston frontal cortex Homo sapiens cDNA clone IMAGE:153760.3'
3399	13307	23105	2.83	2.0E-04	BE502317.1	EST_HUMAN	QV25101035-070600-104-307 BT1068 Homo sapiens cDNA
3417	13334	23130	0.88	2.0E-04	U54374.1	NT	Human tyrosine kinase TXK (b6) gene, exons 9 and 10
3937	13749	23541	0.78	2.0E-04	AF987844.1	EST_HUMAN	EST336050 IMAGE resequences, IMAGE Homo sapiens cDNA
4051	13983		4.81	2.0E-04	U61029.1	NT	Phascolarctid adipic acid reductase (FVNR2) gene, complete cds
4569	14461	24248	1.27	2.0E-04	HE8055.1	EST_HUMAN	yc61611.1 Soares, phae1_gland_N3HPG Homo sapiens cDNA clone IMAGE:232566.5'
4569	14461	24250	1.27	2.0E-04	HE8055.1	EST_HUMAN	yc61611.1 Soares, phae1_gland_N3HPG Homo sapiens cDNA clone IMAGE:232566.5'
4689	14575		1.31	2.0E-04	U60526.1	NT	Danio rerio proteasome 28 kDa subunit homolog mRNA, complete cds
4991	14860	24630	1.7	2.0E-04	AB307997.1	NT	Gallus gallus proteasome 28 kDa subunit homolog gene, exons 1 to 6, partial cds
5403	15322	26571	1.83	2.0E-04	AF684392.1	EST_HUMAN	AF684392.1 NC1 Homo sapiens cDNA clone GDCU010.3'
8411	15331	26581	1.98	2.0E-04	AB060882.1	EST_HUMAN	qf6891.X1 RCI CGAP U3a Homo sapiens cDNA clone IMAGE:2207769.3'
6291	16155		2.15	2.0E-04	AJ17112.1	EST_HUMAN	AJ17112.1 MAMMA1 Homo sapiens cDNA clone MAMMA1000769.5'
6493	16352		11.07	2.0E-04	P68548	SWISSPROT	LINE1 REVERSE TRANSCRIPTASE HOMOLOG
						SWISSPROT	MYOESIN 2 (M-PROTEIN) (65 KD TITIN-ASSOCIATED PROTEIN) (168 KD CONNECTIN- ASSOCIATED PROTEIN)
6497	16356	26827	1.6	2.0E-04	P54298	SWISSPROT	Solanum lycopersicum phytochrome F (PHYF) gene, partial cds
6035	16518	20708	1.33	2.0E-04	U32444.2	NT	Solanum lycopersicum phytochrome F (PHYF) gene, partial cds
6035	16518	20709	1.33	2.0E-04	U32444.2	NT	Homo sapiens DNA, DLEC1 to ORCLT4 gene region, section 12 (DLEC1, ORCLT3, ORCLT4 genes, complete cds)
6919	16989	26990	1.19	2.0E-04	AB308988.1	NT	Homo sapiens DNA, DLEC1 to ORCLT4 gene region, section 12 (DLEC1, ORCLT3, ORCLT4 genes, complete cds)
6919	16989	26991	1.19	2.0E-04	AB308988.1	NT	Homo sapiens DNA, DLEC1 to ORCLT4 gene region, section 12 (DLEC1, ORCLT3, ORCLT4 genes, complete cds)

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Mod Similar (Top) HI BLAST E Value	Top HI Accession No.	Top HI Database Source	Top HI Descriptor
6982	16559	27054	2.29	2.0E-04	AF050593.1	NT	Human sapiens FRK38 common fragile region, diadenosine triphosphate hydrolase (FHD) gene, exon 5
7729	17579	27801	1.46	2.0E-04	BE162303.1	EST_HUMAN	RC3-H10234-151095-011365 HT0254 Homo sapiens cDNA
7754	17924	27828	1.71	2.0E-04	AA050777.1	EST_HUMAN	zfp631.11 Scores, tests, JMT Homo sapiens cDNA IMAGE:742894.5
8225	18107	28360	6.14	2.0E-04	AF173073.1	EST_HUMAN	AV790373 HTF Homo sapiens cDNA clone HTFAA01.5
8515	18387		1.88	2.0E-04	AA253133.1	NT	Homo sapiens partial E-Hf4 receptor gene, exons 2 to 5
8525	18490	28762	5.67	2.0E-04	AF140282.1	EST_HUMAN	[0171] x1 NCI CGAP_Gsc4 Homo sapiens cDNA clone IMAGE:2140289.3 similar to contains Alu repetitive element;
8726	18582	28866	2.84	2.0E-04	AW138740.1	EST_HUMAN	UHH-B1-adm-c-04-UJ151 NCI CGAP_Sut3 Homo sapiens cDNA clone IMAGE:2717180.3
776	10580	20516	0.98	1.0E-04	HE9646.1	EST_HUMAN	y26c00.81 Scores melanocyte 2NHHM Homo sapiens cDNA clone IMAGE:262864.3 similar to contains L1/L11 repetitive element;
1059	10076	20810	2.43	1.0E-04	PT1369	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN (CONTAINS: REVERSE TRANSCRIPTASE);
1098	11014	28355	3.87	1.0E-04	AW013347.1	EST_HUMAN	UHH-B10-sab-e-09-UJ151 NCI CGAP_Sut3 Homo sapiens cDNA clone IMAGE:2708828.3
1098	11014	28356	3.87	1.0E-04	AW013347.1	EST_HUMAN	UHH-B10-sab-e-09-UJ151 NCI CGAP_Sut3 Homo sapiens cDNA clone IMAGE:2708828.3
1310	11216		2.97	1.0E-04	U02918.1	NT	Angiogenesis dopaminergic D1A1 receptor (D1A1) gene, complete cds
1610	11515	21374	3.24	1.0E-04	AF148806.1	NT	Kap60's sarcomere-associated heparinase ORF 68 gene, partial cds; and ORF 69, kap60in, vFLIP, v-cyelin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphotyrosyl-tyrosine kinase synthase, and LAMP (LAMP) genes, complete cds
1610	11515					NT	Kap60's sarcomere-associated heparinase ORF 68 gene, partial cds; and ORF 69, kap60in, vFLIP, v-cyelin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphotyrosyl-tyrosine kinase synthase, and LAMP (LAMP) genes, complete cds
1817	11714	21376	3.24	1.0E-04	AF148806.1	NT	Kap60's sarcomere-associated heparinase ORF 68 gene, partial cds; and ORF 69, kap60in, vFLIP, v-cyelin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphotyrosyl-tyrosine kinase synthase, and LAMP (LAMP) genes, complete cds
2600	12469	22383	1.29	1.0E-04	AB048342.1	NT	Equus caballus DNA, chromosome 2n(14), microsatellite TK98
2600	12469	22384	1.29	1.0E-04	AF169593.1	NT	Homo sapiens membrane-bound aminopeptidase P (AMPEP-2) gene, complete cds
2655	12522	22341	1.15	1.0E-04	BE218833.1	EST_HUMAN	h45608.1 NCI CGAP_L024 Homo sapiens cDNA clone IMAGE:3176366.3
2655	12522	22412	1.15	1.0E-04	BE218833.1	EST_HUMAN	h45608.1 NCI CGAP_L024 Homo sapiens cDNA clone IMAGE:3176366.3
3247	13170	22649	1.04	1.0E-04	QB2203	SWISSPROT	SPUDCORME ASSOCIATED PROTEIN 62 (SP 62) (SPlicing FACTOR 3A SUBUNIT 2) (SF3A65)
3675	13589	23376	1.1	1.0E-04	AF140282.1	EST_HUMAN	[0171] x1 NCI CGAP_Gsc4 Homo sapiens cDNA clone IMAGE:2140289.3 similar to contains Alu repetitive element;
3971	13878	28654	1.78	1.0E-04	MT140.21	NT	Mouse alpha 1 type-V collagen mRNA
3997	13988	28676	1.08	1.0E-04	AV947727.1	EST_HUMAN	AV947727 GLI3 Homo sapiens cDNA clone GLOBID04.3
4352	14258	24043	0.85	1.0E-04	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
5028	14901	24671	1.56	1.0E-04	7662015	NT	Homo sapiens KNA0237 gene product (KNA0237), mRNA

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Single Exon Probes Expressed in Heart

Probe SEQ ID NC	Exon SEQ ID NC	ORF SEQ ID NC	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9028	14801	24672	1.98	1.0E-04	7692015	NT	Homo sapiens KIAA0237 gene product (KIAA0237), mRNA
9033	14905	24676	0.99	1.0E-04	A1357156.1	EST_HUMAN	g52944.x1 NC1 CGAP GC4 Homo sapiens cDNA clone IMAGE:2005975 3'
9148	15015		0.99	1.0E-04	Z72550.1	NT	Saccharomyces cerevisiae chromosome VII resulting frame ORF YGL038c
9572	15497	25503	1.35	1.0E-04	P08547	EST_HUMAN	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
9204	16126	26293	12.77	1.0E-04	A1251980.1	EST_HUMAN	g557410.x1 NC1 CGAP C632 Homo sapiens cDNA clone IMAGE:1865633 3'
9498	16126	26293	14.47	1.0E-04	A1251980.1	EST_HUMAN	g557410.x1 NC1 CGAP C632 Homo sapiens cDNA clone IMAGE:1865633 3'
7380	17249	27455	2.53	1.0E-04	A1800230.1	EST_HUMAN	w29408.x1 Sources NF1_T GBC S1 Homo sapiens cDNA clone IMAGE:2356742 3'
7384	17263	27458	1.46	1.0E-04	O88909	SWISSPROT	CYSTATIN-RELATED EPIDIDYMAL SPERMATOGENIC PROTEIN PRECURSOR (CYSTATIN B)
7452	17413	27628	1.75	1.0E-04	10653076	NT	Homo sapiens phospholipid scramblase 1 (PLSCR1), mRNA
7448	17698		3	1.0E-04	P08547	EST_HUMAN	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
8649	18513		2.17	1.0E-04	M25537.1	NT	Mouse alpha leukocyte interferon gene, complete cds
8913	18721	28012	1.99	1.0E-04	A1002098.1	NT	Homo sapiens mRNA for KIAA1142 protein, partial cds
9035	18824		1.84	1.0E-04	BE692795.1	EST_HUMAN	CMB-OT0042-130700-475-H3 CTS404 Homo sapiens cDNA
9568	19188		1.65	1.0E-04	AW683326.1	EST_HUMAN	CABAN0010-230300-124-ab9 NIN010 Homo sapiens cDNA
883	10316	20439	1.7	9.0E-05	A4719333.1	EST_HUMAN	g55451.1 x1 Sources testis NHT Homo sapiens cDNA clone 1202489 3'
3995	13902	23678	0.8	9.0E-05	A1762209.1	EST_HUMAN	w55451.1 x1 NC1 CGAP C618 Homo sapiens cDNA clone IMAGE:2304008 3' similar to contains MER6.11
9028	15543	25542	1.47	9.0E-05	O30718	SWISSPROT	PROLYL-4-HYDROXYLASE ALPHA-2 SUBUNIT PRECURSOR
7455	17294		2.9	9.0E-05	D85538.1	NT	Homo sapiens gene for cholesteryl ester transfer protein (CETP), complete cds
7457	17298	27470	2.93	9.0E-05	AF123982.1	NT	Homo sapiens myo-GD binding protein 1 (MBD1) gene, exon 15b
						NT	probable element; NCL CGAP B18 Homo sapiens cDNA clone IMAGE:2569728 3' similar to contains L1 (2 L1)
9479	18392	28917	2.9	9.0E-05	AW076078.1	EST_HUMAN	g52940.x1 NCL CGAP Lymph3 Homo sapiens cDNA clone IMAGE:1962495 3' similar to contains element
9598	19498	28705	1.85	9.0E-05	A187378.1	EST_HUMAN	MLR repetitive element;
8890	15543	25542	4.4	9.0E-05	O30718	SWISSPROT	PROLYL-4-HYDROXYLASE ALPHA-2 SUBUNIT PRECURSOR
						NT	Homo sapiens MSH45 gene, partial cds; and CLUC1, DDH4, G8b, G9c, G9d, G9e, G9f, BAT3, G9b, CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LIT-1, LTB, TNF, and L7A genes, complete cds
804	10733	20576	1.46	8.0E-05	AJ251046.1	NT	Pisum sativum mRNA for beta-1,3 glucanase (ga2 gene)
846	10773		3.53	8.0E-05	AJ251046.1	NT	Pisum sativum mRNA for beta-1,3 glucanase (ga2 gene)
2920	12847		0.78	8.0E-05	M83575.1	NT	Human placenta derived growth factor A chain (PDGFA) gene, exon only
4852	10080		1.15	8.0E-05	F28172.1	EST_HUMAN	HSPD16794 HMO3 Homo sapiens cDNA clone s200000304
9191	18394	28930	1.87	8.0E-05	M89197.1	NT	Human haaptoglobin and haaptoglobin-related protein (HP and HPR) genes, complete cds

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Probe SEQ ID NO.	Exon ID NO.	ORF SEQ ID NO.	Expression Signal	Mean Similarity (BLAST E- Value)	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
9911	19589		3.45	8.0E-06	AA27833.1	EST HUMAN	258901.1 NOL CGAP CG81 Homo sapiens cDNA clone IMAGE:704503 3' similar to contains Adu
344	10303	20118	2.9	7.0E-06	AIW84746.1	EST HUMAN	negative element/contains element MSR1 repetitive element
344	10303	20119	2.9	7.0E-06	AIW84746.1	EST HUMAN	RCS-C10208-220950-011-E04 C10208 Homo sapiens cDNA
595	10496	20302	1.05	7.0E-06	AIW84746.1	EST HUMAN	RCS-C10208-220950-011-E04 C10208 Homo sapiens cDNA
595	10496	20303	1.05	7.0E-06	AIW84746.1	EST HUMAN	HUM072014F Human fowes cDNA Homo sapiens cDNA clone EST HFD072014
1039	10957	20800	2.32	7.0E-06	Q22949	SWISSPROT	HUM072014F Human fowes cDNA Homo sapiens cDNA clone EST HFD072014
2696	12551	22440	6.24	7.0E-06	AL163278.2	NT	PROBABLE GLYCEROL 3-PHOSPHATE ACYLTRANSFERASE, MITOCHONDRIAL PRECURSOR (GPAT)
3121	13046	22843	5.78	7.0E-06	AB000080.1	NT	Homo sapiens chromosome 21 segment HS21C078
4276	14175	23953	1.27	7.0E-06	AL163201.2	NT	Dysostetium discoidum gene for TRFA, complete cds
4344	14241	24023	0.82	7.0E-06	U06080.1	NT	Homo sapiens chromosome 21 segment HS21C001
4842	14723	24506	0.84	7.0E-06	9845300	NT	Caenorhabditis elegans Slp1p homolog mRNA, complete cds
5202	15055		1.12	7.0E-06	AA387612.1	EST HUMAN	Rat embryonalovirus Masiuichi, complete genome
7598	17295	27505	3.04	7.0E-06	U07095.1	EST HUMAN	EST178713 Placenta1 Homo sapiens cDNA
8501	18374		2.89	7.0E-06	10835046	EST HUMAN	EST109624 Fetal brain, Striatum (cat638205) Homo sapiens cDNA clone HBED60
1991	11874	21768	1.57	6.0E-06	4885170	NT	Homo sapiens sarcophag, spition (SCPC) mRNA
1991	11874	21767	1.57	6.0E-06	4885170	NT	Homo sapiens chromosome X cont reading frame 6 (CXORF6) mRNA
2644	12418	22305	1.42	6.0E-06	AIW55241.1	EST HUMAN	h644005.1 NOL CGAP CG8 Homo sapiens cDNA clone IMAGE:2209531 3' similar to gh.03350 DNA
2652	12519	22405	0.86	6.0E-06	264509.1	NT	TOPISOMERASE (HUMAN)
2652	12519	22406	0.86	6.0E-06	264509.1	NT	H sapiens four-armed chromosome 6 Hicull1 fragment, SC69238510
2783	10698	20416	2.45	6.0E-06	284503.1	NT	H sapiens four-armed chromosome 6 Hicull1 fragment, SC69238510
5605	15510	25560	3.33	6.0E-06	Q172850	SWISSPROT	Homo sapiens chromosome 10p11.23 region, complete cds
5605	15510	25560	3.33	6.0E-06	Q172850	SWISSPROT	CONTACTIN PRECURSOR (GLYCOPROTEIN GP135)
5655	15761	26679	1.49	6.0E-06	NT2623.1	EST HUMAN	CONTACTIN PRECURSOR (GLYCOPROTEIN GP135)
5918	10793	26689	2.61	6.0E-06	AIW80653.1	EST HUMAN	Y94971.11 Sources fetal liver spiken TNF15 Homo sapiens cDNA clone IMAGE:246212 5'
7330	17254	27457	1.37	6.0E-06	U06607	SWISSPROT	P46-HN0503-310300-001-HU HN0503 Homo sapiens cDNA
7330	17254	27458	1.37	6.0E-06	U06607	SWISSPROT	CAB-BINDING PROTEIN PRECURSOR (CABP)
7454	17354		1.28	6.0E-06	T04149.1	EST HUMAN	Y94971.11 Striatum (cat638205) Homo sapiens cDNA clone IMAGE:116062 5'
8131	18019	28287	3.98	6.0E-06	RT6639.1	EST HUMAN	Y94971.11 Sources placenta H624P Homo sapiens cDNA clone IMAGE:116062 5'
8907	18621	28911	3.59	6.0E-06	AA040415.1	EST HUMAN	repetitive element/contains L1-RT1 repetitive element
9534	19587	25073	8.44	6.0E-06	AIW880110.1	EST HUMAN	258902.1 Sources, pregnant, uterus, NHGPU Homo sapiens cDNA clone IMAGE:497035 5'

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar Cloned BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6905	18427		1.54	6.0E-05	BE58403.1	EST_HUMAN	7p8a4c48.1 NCI COAP Homo sapiens cDNA clone IMAGE:3307769.3
1332	11237	21141	14.37	5.0E-05	AW320096.1	EST_HUMAN	QVAT10234-241199-040-RT11 S10234 Homo sapiens cDNA
1819	11716		1.63	5.0E-05	8923891	NT	Homo sapiens 22k1a peroxisomal membrane protein-like (LOC55695), mRNA
3831	12760	22550	0.99	5.0E-05	AJ251058.1	NT	Homo sapiens MEPA1A gene, promoter region and exon 1
2807	13607	22563	2.99	5.0E-05	AJ251884.1	NT	Homo sapiens parafil SLC22A33 gene for extracellular monomeric transporter (EMT), exon 1
5302	13311	25165	9.01	5.0E-05	X59855.1	NT	Human MLC1 embryonic gene for embryonic myosin alkaline light chain, 3'UTR
5648	15559	25642	3.46	5.0E-05	AF655544.1	EST_HUMAN	AV653544 QLG Homo sapiens cDNA clone GLQDA03.3
9238	19173		2.96	5.0E-05	P49193	SWISSPROT	RETINAL BINDING PROTEIN (RALBP)
9590	18173		3.47	5.0E-05	P49193	SWISSPROT	RETINAL BINDING PROTEIN (RALBP)
2776	10193		4.58	4.0E-05	U12821.1	NT	Human renin (REN) gene, 5' flanking region
7486	17356		7.17	4.0E-05	AF20635.1	NT	Homo sapiens FPI-1300 mRNA, complete cds
8150	18038	28236	4.6	4.0E-05	AW627046.1	EST_HUMAN	hisc07.x1 Scavenger, NFL, T, GRC, S1 Homo sapiens cDNA clone IMAGE:2074380.3 similar to contains element MIR repetitive element.
9237	16889		2.17	4.0E-05	AW117580.1	EST_HUMAN	xib64c0.1 Scores, NFL, T, GRC, S1 Homo sapiens cDNA clone IMAGE:265102.3
665	10599	20417	0.84	3.0E-05	AI245051.1	EST_HUMAN	q6f4c0.1 Scores, fold, jwz, spleen, INFLS, S1 Homo sapiens cDNA clone IMAGE:1849458.3 similar to contains ALU repetitive element; contains element KER repetitive element.
7043	10391	20624	1.38	3.0E-05	AV273851.1	EST_HUMAN	x24g93.1 Scores, NFL, T, GRC, S1 Homo sapiens cDNA clone IMAGE:2614100.3
1115	11030	20870	1.28	3.0E-05	BE037988.1	EST_HUMAN	601461468FT NIH_MGC_66 Homo sapiens cDNA clone IMAGE:385142.5
1115	11030	20871	1.28	3.0E-05	BE037988.1	EST_HUMAN	601461468FT NIH_MGC_66 Homo sapiens cDNA clone IMAGE:385142.5
2038	12653	22442	0.91	3.0E-05	CE2228	SWISSPROT	3'UTR EMIN
4285	14184	23644	6.89	3.0E-05	BE163211.1	EST_HUMAN	RNA-IT00821-120200-001-570 IT00821 Homo sapiens cDNA
4285	14184	23665	6.89	3.0E-05	BE163211.1	EST_HUMAN	RNA-IT00821-120200-001-570 IT00821 Homo sapiens cDNA
4395	14291	24045	1.19	3.0E-05	AA369579.1	EST_HUMAN	EST176958 Placenta 1 Homo sapiens cDNA similar to similar to p53-associated protein
4395	14291	24046	1.19	3.0E-05	AA369579.1	EST_HUMAN	EST176958 Placenta 1 Homo sapiens cDNA similar to similar to p53-associated protein
4519	14412	24197	0.85	3.0E-05	AF148773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1,2, and 3
4731	10599	20417	0.84	3.0E-05	AI245051.1	EST_HUMAN	q6f4c0.1 Scores, fold, jwz, spleen, INFLS, S1 Homo sapiens cDNA clone IMAGE:1849458.3 similar to contains ALU repetitive element; contains element KER repetitive element.
6151	15018	24786	0.97	3.0E-05	AV726030.1	EST_HUMAN	AV726030 HTC Homo sapiens cDNA clone HTCCGA01.5
5412	15332	25362	1.54	3.0E-05	BE73197.1	NT	Mus musculus myosin light chain 2, precursor (myosin-light-chain-2), mRNA
6011	16491	26077	2.23	3.0E-05	BE73197.1	EST_HUMAN	601461468FT NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842293.5
8983	16742	26935	1.62	3.0E-05	AA284049.1	EST_HUMAN	266006.01 Striatum scabrous brain S11 Homo sapiens cDNA clone IMAGE:707841.3
7154	17031	27225	1.95	3.0E-05	AF770949.1	EST_HUMAN	h4646c0.1 NCI COAP Lux1 Homo sapiens cDNA clone IMAGE:3009393.3
7156	17035	27228	1.5	3.0E-05	6012431	NT	Homo sapiens Interleukin-1 receptor antagonist homolog 1 (IL1H1), mRNA
7373	17242	27447	1.33	3.0E-05	AA372562.1	EST_HUMAN	EST84475 Cdon adenocarcinoma IV Homo sapiens cDNA, 5' end

Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
7570	17421		3.16	3.0E-05 A179331.1	EST_HUMAN	EST_HUMAN	wg04603.x1 Soares, NSF, RA, GW, OT, PA, P, S1 Homo sapiens cDNA clone IMAGE:2387283 3'
2276	12180	22068	1.76	2.0E-05 A256021.1	EST_HUMAN	EST_HUMAN	q98811.x1 Soares, NF, T, GGC, S1 Homo sapiens cDNA clone IMAGE:1965062 3' similar to contains
2838	12412	22302	3.02	2.0E-05 H11762.1	NT	NT	MERS132 MERS3, myosin heavy chain 11
2891	12846		7.21	2.0E-05 A140092.1	EST_HUMAN	EST_HUMAN	Homo skin fibroblast culture (AGE) genes, complete cds
3098	13025	22921	1.5	2.0E-05 AG090395.1	EST_HUMAN	EST_HUMAN	ZNF492.12 Striatum, IN1, neuron (K067203) Homo sapiens cDNA clone IMAGE:532734 5' similar to contains At repetitive element; contains element L1 repetitive element;
3304	13225	23027	0.94	2.0E-05 AF184941.1	EST_HUMAN	EST_HUMAN	RCS1.B1033.1c-12320.01-A408 B1033.Homo sapiens cDNA
3323	13243	23060	1.14	2.0E-05 AG2921.1	NT	NT	Homo sapiens pAT-prox (NCR1) gene, complete cds
3449	13366		1.1	2.0E-05 AG3565.1	NT	NT	H4 sapiens INT for endogenous retroviral like element
3737	13549		0.85	2.0E-05 AL039107.1	EST_HUMAN	EST_HUMAN	S. cerevisiae 12.8 kb fragment of the left arm of chromosome XV
4810	14403	24191	0.50	2.0E-05 A1263348.1	EST_HUMAN	EST_HUMAN	DKF256024GJ11.569 (synonym: Hnf42) Homo sapiens cDNA clone D1FZP559B1004 5'
4992	14460		1.06	2.0E-05 BE37471.1	EST_HUMAN	EST_HUMAN	MER18.b3 MER18 repetitive element;
4763	14666	24453	0.91	2.0E-05 AJ191018.1	NT	NT	Homo sapiens SCL gene locus
5520	15538	25802	1.42	2.0E-05 AD011732.1	NT	NT	Homo sapiens TNNT1 genes, exons 1-11 (and joined CDS)
5993	15968	26022	2.19	2.0E-05 AF017430.1	EST_HUMAN	EST_HUMAN	w004012.1 NC1 CGAP SS1 Homo sapiens cDNA clone IMAGE:1236419 3'
6126	15972	26108	2.19	2.0E-05 Y06926.1	NT	NT	P.fakaputun mRNA for AARPT protein, partial
6135	15983		8.04	2.0E-05 AB91026.1	EST_HUMAN	EST_HUMAN	w035007.x1 Soares, Desclafraffe, colon NHGD Homo sapiens cDNA clone IMAGE:282277 3'
6243	16100	26280	2.21	2.0E-05 AF224282.1	NT	NT	Heterodontus francisci HoxA40 (HoxA40), HoxA7 (HoxA7), HoxA6 (HoxA6), HoxA5 (HoxA5), HoxA4 (HoxA4), HoxA3 (HoxA3), Hox2 (HoxA2), and HoxA1 (HoxA1) genes, complete cds
6243	16100	26281	2.21	2.0E-05 AF224282.1	NT	NT	Heterodontus francisci HoxA40 (HoxA40), HoxA7 (HoxA7), HoxA6 (HoxA6), HoxA5 (HoxA5), HoxA4 (HoxA4), HoxA3 (HoxA3), Hox2 (HoxA2), and HoxA1 (HoxA1) genes, complete cds
6903	16493	26571	2.3	2.0E-05 A3381040.1	EST_HUMAN	EST_HUMAN	G23H035.x1 NC1 CGAP CLL1 Homo sapiens cDNA clone IMAGE:2109389 3'
8024	17874	28116	2.45	2.0E-06 N41751.1	EST_HUMAN	EST_HUMAN	y091a06.1 Soares, placenta, 98days, 2NbHF-86dW Homo sapiens cDNA clone IMAGE:285570 5'
8024	17874	28117	2.45	2.0E-06 N41751.1	EST_HUMAN	EST_HUMAN	yw01a06.1 Soares, placenta, 98days, 2NbHF-86dW Homo sapiens cDNA clone IMAGE:259570 5'
8030	15693		2.42	2.0E-06 AL091026.1	EST_HUMAN	EST_HUMAN	yw030707.x1 Soares, Diaphragm, colon, NHGD Homo sapiens cDNA clone IMAGE:259570 5'
8748	17697	28141	2.93	2.0E-05 BE179801.1	EST_HUMAN	EST_HUMAN	KC3H.B1062.200300.012-E12 TH0502 Homo sapiens cDNA
9335	19514		2.98	2.0E-05 BC546228.1	EST_HUMAN	EST_HUMAN	hw21612.x1 NC1 CGAP XG11 Homo sapiens cDNA clone IMAGE:3149382 3' similar to TR-O.2832 Q12892.01 VGLYOPHRIN PEPT?

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Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (14p) Htt BLASTE Value	Top Htt Accession No.	Top Htt Database Source	Top Htt Descriptor
9442	19677		3.73	2.0E-05	AW074694.1	EST_HUMAN	x56940.x1 NCI_CGAP_C07 Homo sapiens cDNA clone IMAGE:2873932 3' similar to contains L1 L33 L1 repetitive element;
9496	19503		2.25	2.0E-05	AF275948.1	NT	Homo sapiens ASCA1 (ASCA1) gene, complete cds
9637	16208	28237	1.81	2.0E-05	AU131513.1	EST_HUMAN	AU131513.1 NT2RP3 Homo sapiens cDNA clone NT2RP3002707 5'
2693	12729	22417	1.67	1.0E-05	AF63282.2	NT	Homo sapiens chromosome 21 segment HS21C082
3699	13513	23301	1.67	1.0E-05	AF088273.1	NT	Drosophila melanogaster arm Lamin 120 Suppressor of Hairless (Su(H)) gene, partial cds
3950	13797	23503	6.24	1.0E-05	P81274	SWISSPROT	MOSAIC PROTEIN LCN
4932	13584	23701	1.09	1.0E-05	AF16203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4190	14090	23853	2.01	1.0E-05	AA43119.1	EST_HUMAN	x59494.1 Soares, testis, NIH Homo sapiens cDNA clone IMAGE:781494 5'
4732	14627	24413	2.15	1.0E-05	AW411934.1	EST_HUMAN	X49491.1 NCI_CGAP_L384.1 Homo sapiens cDNA clone IMAGE:2859519 3'
4892	14793	24539	4.46	1.0E-05	AF163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
6049	15632	25032	1.42	1.0E-05	AF124903.1	NT	Homo sapiens Srsf gene for splicing protein
6211	15993	26128	3.54	1.0E-05	AA641849.1	EST_HUMAN	h519612.x1 NCI_CGAP_G051 Homo sapiens cDNA clone IMAGE:1184114 3' similar to contains L1 L1 L1 L1 repetitive element;
6213	16079	26228	0.45	1.0E-05	AA641849.1	NT	Homo sapiens phosphatase A2, group X (PLA2G10) mRNA and translated products
6572	16430		1.3	1.0E-05	P19174	SWISSPROT	S210 PROTEIN (SIOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (R055A-X)
7168	17045		2.16	1.0E-05	AF16227.2	NT	Homo sapiens chromosome 21 segment HS21C027
7240	17117	27312	2.46	1.0E-05	AA452378.1	EST_HUMAN	x63813.1 Soares, testis, NIH Homo sapiens cDNA clone IMAGE:788510 3' similar to
7352	17220	27420	11.6	1.0E-05	AA239110.1	EST_HUMAN	3012032 PEROSOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN),
7704	17554	27778	1.2	1.0E-05	AF251521.1	EST_HUMAN	positive element contains element TAA repetitive element;
7704	17554	27779	1.2	1.0E-05	AF251521.1	EST_HUMAN	UPI-B2-89k-a3-08-BU1.1 NCI_CGAP_S044 Homo sapiens cDNA clone IMAGE:272458 3'
							UPI-B2-89k-a3-08-BU1.1 NCI_CGAP_S044 Homo sapiens cDNA clone IMAGE:272458 3'
7851	17701		1.78	1.0E-05	AW469995.1	EST_HUMAN	h607610.x1 NCI_CGAP_H012 Homo sapiens cDNA clone IMAGE:2673010 3' similar to contains L1 L2 L1 repetitive element;
8291	18170	28414	2.2	1.0E-05	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RefSeq gene, and sodium phosphate transporter (NPT3) gene, complete cds
8291	18170	28415	2.2	1.0E-05	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RefSeq gene, and sodium phosphate transporter (NPT3) gene, complete cds
2637	12504	22398	5.59	6.0E-06	AF183911.1	EST_HUMAN	372605.x1 NCI_CGAP_H5C3 Homo sapiens cDNA clone IMAGE:324636 3'
3057	12584	22775	3.06	9.0E-06	AF18993.1	EST_HUMAN	q5111608.x1 Soares, placenta, B291reflts, 2NbpP8u6W Homo sapiens cDNA clone IMAGE:17891 91 3'

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Table 4
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Probe SEQ ID NO	Exon ID NO	ORF SEQ ID NO	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3559	13473		2.64	9.0E-06	M81755.1	NT	Human alanine:glyoxylate aminotransferase (AGXT) gene, exons 1 and 2
5509	15513	25591	2.58	9.0E-06	L22416.1	NT	Homo sapiens differentiation antigen CD29 gene, exons 5, 6
6570	16428	26611	10.24	9.0E-06	AI034370.1	EST_HUMAN	cc20p01.11 Sources, fetal liver, spleen, INFL3_31 Homo sapiens cDNA, clone IMAGE:1656012 3' similar to contains Alu repetitive element;
6531	16809	27004	1.16	9.0E-06	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
7192	17059	27257	2.81	9.0E-06	Q63759	SWISSPROT	SUSH1 REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) [DOWN-REGULATED BY V-SRC]
7192	17059	27258	2.81	9.0E-06	Q63759	SWISSPROT	SUSH1 REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) [DOWN-REGULATED BY V-SRC]
8305	18186	28434	4.58	9.0E-06	U05114.1	NT	Human apolipoprotein E (APOE) gene, hepatic control region HCR-2
2493	12722	22251	3.35	9.0E-06	Q10364	SWISSPROT	POTATIVE SERINE/THREONINE PROTEIN KINASE C22E12.14C
8632	18765	26037	1.95	8.0E-06	AW362539.1	EST_HUMAN	RG3-CT0283-201199-011-H11 CT0283 Homo sapiens cDNA
8632	18765	26037	2.24	8.0E-06	Q02357	SWISSPROT	ANKYRN1 (ERYTHROCYTE ANKYRN)
8632	18765	26038	2.24	8.0E-06	Q02357	SWISSPROT	ANKYRN1 (ERYTHROCYTE ANKYRN)
938	10956		1.7	7.0E-06	AA669729.1	EST_HUMAN	cd0910.11 Strikature lung (#697210) Homo sapiens cDNA, clone IMAGE:854251 3' similar to contains MER20 H1 MER20 repetitive element;
1420	11326	21191	3.19	7.0E-06	7862177	NT	Homo sapiens KIA0055 gene product (KIA0055), mRNA
2844	12772		6.66	7.0E-06	AI936234.1	EST_HUMAN	ov16970-11 NC_CGAP_103 Homo sapiens cDNA, clone IMAGE:1911268 3' similar to contains Alu repetitive element;
3516	13432		0.85	7.0E-06	AI335542.1	EST_HUMAN	EST169335 Thyroid Homo sapiens cDNA, 5' and similar to EST containing L1 repeat
4495	15472		8.73	7.0E-06	AW830141.1	EST_HUMAN	OV2-OT0625-250400-175-091 OT0625 Homo sapiens cDNA
5072	19936	24600	8.39	7.0E-06	BE215972.1	EST_HUMAN	981841329F1 NH_MGC_57 Homo sapiens cDNA, clone IMAGE:403872 5'
2857	12814	22607	1.03	8.0E-06	BE009165.1	EST_HUMAN	OV2-OT0519-010300-105-411 OT0378 Homo sapiens cDNA
3535	13349	23359	1.02	8.0E-06	BE009165.1	EST_HUMAN	OV2-OT0519-010300-105-411 OT0378 Homo sapiens cDNA
4547	12838	22637	1.77	8.0E-06	Q01465	SWISSPROT	OVARIAN ABUNDANT MESSAGE PROTEIN (OAM PROTEIN)
4653	14539	24328	2.01	8.0E-06	AI040098.1	EST_HUMAN	cd06242.41 Sources, fetal liver, spleen, INFL3_31 Homo sapiens cDNA, clone IMAGE:1656738 3' similar to contains MER20 H1 MER20 repetitive element;
5281	15203	24579	1.46	8.0E-06	AF167441.1	NT	Must musculus E-cadherin binding protein E7 mRNA, complete cds
7670	17520		1.88	8.0E-06	AI180192.1	EST_HUMAN	IL5-JM0070-11040-003-492 JM0070 Homo sapiens cDNA
6900	19377	25195	1.8	8.0E-06	11181517	NT	Homo sapiens calcium channel, voltage-dependent, alpha 11 subunit (CACNA11), mRNA
5985	19504	25708	3.58	5.0E-06	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
5825	15731	25843	1.98	5.0E-06	U07591.1	NT	Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met)
7637	17687	27507	6.9	5.0E-06	AA13920.1	EST_HUMAN	EST186466 Colon carcinoma (HCC) cell line Homo sapiens cDNA, 5' and

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9795	19311	20204	4.74	5.0E-06	A056045.1	EST_HUMAN	HA0877 Human fetal liver cDNA library Homo sapiens cDNA
651	10569	20380	4.41	4.0E-06	F16287.1	EST_HUMAN	yca6d03.1 Soares infant brain N1B Homo sapiens cDNA clone IMAGE:58254 5' similar to contains Alu repetitive element/contains L1 repetitive element;
828	10755	20605	9.3	4.0E-06	AW103354.1	EST_HUMAN	x05912.2 NC1 CGAP Exo2 Homo sapiens cDNA clone IMAGE:235574 5' similar to contains Alu repetitive element/contains element MER21 repetitive element;
1312	11218	21074	5.18	4.0E-06	A034628.1	EST_HUMAN	B33409.X1 NC1 CGAP FHS2 Homo sapiens cDNA clone IMAGE:2036108 3'
1312	11218	21074	5.18	4.0E-06	A034628.1	EST_HUMAN	B33409.X1 NC1 CGAP FHS2 Homo sapiens cDNA clone IMAGE:2036108 3'
1488	11983	21227	2.23	4.0E-06	BF065612.1	EST_HUMAN	QV2-NT0046-205060-250-607 NT0046 Homo sapiens cDNA
2218	12104	22008	1.22	4.0E-06	AW015401.1	EST_HUMAN	UH-H80-sait-045-01.1 NC1 CGAP Sub1 Homo sapiens cDNA clone IMAGE:2710425 3'
3025	12953	22746	1.39	4.0E-06	AF148346.1	NT	Gallus gallus Dactyl protein (Dact3) mRNA, complete cds
3819	13731	23520	1.78	4.0E-06	AW848255.1	EST_HUMAN	U3-G10244-150200-074-063 C10244 Homo sapiens cDNA
4702	14588	24378	1.58	4.0E-06	A1885289.1	EST_HUMAN	W4610.X1 NC1 CGAP Brn25 Homo sapiens cDNA clone IMAGE:2432562 3' similar to contains element MER22 repetitive element;
4840	14721	24504	1.02	4.0E-06	A183278.2	NT	Homo sapiens chromosome 21 segment HS21C079
7105	16950	27177	3.31	4.0E-06	AF009590.1	NT	Homo sapiens 1 cell receptor beta locus, TGRB7/TSX2 to TGRB7/TSX2 region
8745	17895	28159	3.74	4.0E-06	AB007565.1	NT	Homo sapiens mRNA, chromosome 1 specific transcripts K1A0488
2117	12008	21604	1.27	3.0E-06	AA706502.1	EST_HUMAN	B34008.X1 Soares fetal liver sapiens INFLS_51 Homo sapiens cDNA clone IMAGE:432663 3' similar to contains L1.H1.L1 repetitive element;
2117	12008	21605	1.27	3.0E-06	AA706502.1	EST_HUMAN	B34008.X1 Soares fetal liver sapiens INFLS_51 Homo sapiens cDNA clone IMAGE:432663 3' similar to contains L1.H1.L1 repetitive element;
2220	12105		1.37	3.0E-06	AF202353.1	NT	Homo sapiens PF1208 mRNA, complete cds
2891	12818	22810	0.95	3.0E-06	AJ682218.1	EST_HUMAN	aa0917.1 Soares testis INFLS_51 Homo sapiens cDNA clone IMAGE:1409252 3' similar to contains LTR1.8 LTR1 repetitive element;
3228	13152		2.14	3.0E-06	AJ682218.1	EST_HUMAN	W22063.X1 NC1 CGAP UH1 Homo sapiens cDNA clone IMAGE:2425916 5' similar to TR-080/34 Oa0734
3716	13928	22412	1.26	3.0E-06	AB047004.1	EST_HUMAN	INP4612.X1 NC1 CGAP JNTS Homo sapiens cDNA clone IMAGE:3124151 3'
3716	13928	22413	1.26	3.0E-06	AB047004.1	EST_HUMAN	INP4612.X1 NC1 CGAP JNTS Homo sapiens cDNA clone IMAGE:3124151 3'
4376	14272	24053	0.9	3.0E-06	U36266.1	EST_HUMAN	X67850.1 Stragapine ovary (#607217) Homo sapiens cDNA clone IMAGE:72725 5' similar to contains L1 repetitive element
4401	14355	24146	4.31	3.0E-06	X54816.1	NT	Homo sapiens gene for alpha-1 microglobulin, bikunin, exon 1-3 (encoding alpha-1-microglobulin, N-terminus.)
6290	16154		1.92	3.0E-06	P00848	SWISSPROT	LINE1 REVERSE TRANSCRIPTASE HOMOLOG
9494	19110		4.17	3.0E-06	AW385252.1	EST_HUMAN	RG01-T0001-261199-01-A03 L10007 Homo sapiens cDNA
195	10167		3.28	2.0E-06	P54366	SWISSPROT	HOMEOBOX PROTEIN G005E01D

Single Exon Probes Expressed in Heart

Probe ID	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
1930	11465		6.27	2.0E-06	P21414	SWISSPROT	POLY(POLY(AMINO ACIDS)) POLYMERASE SUBUNIT 1 (HUMAN)
2326	12207	22106	2.85	2.0E-06	A6767138.1	EST_HUMAN	MERS20 repeat element; 1
2418	12295	22192	2.14	2.0E-06	P04929	SWISSPROT	HISTONINE-RICH GLYCOPROTEIN PRECURSOR
2519	12393	22295	2.89	2.0E-06	P08719	SWISSPROT	KNOX-ASSOCIATED HISTIDINE-RICH PROTEIN PRECURSOR (KARP)
3475	13391	23190	1.11	2.0E-06	A6767595.1	EST_HUMAN	ABP67595 GLO Homo sapiens cDNA clone GLOP0805 3'
3700	13514	23349	1.5	2.0E-06	AA1735118.1	EST_HUMAN	p20205.1 Staphylococcus aureus (S23721) Homo sapiens cDNA clone IMAGE 586232 5'
3710	13623	23360	1.5	2.0E-06	A3003096.1	NT	Mus musculus gene for odorant receptor A16, complete cds
5878	15784	25804	5.08	2.0E-06	A181194.1	EST_HUMAN	y57004.1 NC1 CGAP Lym12 Homo sapiens cDNA clone IMAGE 2410085 3'
7136	17013	27206	1.95	2.0E-06	H2051.1	EST_HUMAN	NHKT Homo sapiens cDNA clone IMAGE 233974 3' similar to gb.Y4829
9403	16988	24801	1.35	2.0E-06	P22031	SWISSPROT	KERATIN, TYPE II CYTOSKELETAL 8 (HUMAN)
9548	19018		2.46	2.0E-06	BE328232.1	EST_HUMAN	PROTEIN MOV-10
91	19813	19813	1.9	1.0E-06	O76982	SWISSPROT	nsf2002.1 NC1 CGAP_KR13 Homo sapiens cDNA clone IMAGE 3144890 3' similar to contains L112.L1
841	10378	20364	1.81	1.0E-06	AQ341384.1	NT	ORGANIC CATION/CARBONATE TRANSPORTER 2 (SOLUTE CARRIER FAMILY 22, MEMBER 6) (HIGH AFFINITY SODIUM-DEPENDENT CARBONATE COTRANSPORTER)
1435	11340	21260	2.21	1.0E-06	F009125	SWISSPROT	MUS MUSCULUS DPMGME protein (DPMGME) mRNA, complete cds
1507	11412	21271	1.98	1.0E-06	AI193278.2	NT	MEROZOITE SURFACE PROTEIN CNZ-3
1554	11450	21317	0.93	1.0E-06	AQ034441.1	EST_HUMAN	Human sapiens chromosome 21 segment HSFL210078
1584	11459	21318	0.93	1.0E-06	AQ034441.1	EST_HUMAN	nfsls2.1 Scores: fvec_upper_upper_nfls2_1 NFSLs_51 Homo sapiens cDNA clone IMAGE 425982 3' similar to contains Alu repetitive element;
1955	11470		1.2	1.0E-06	P27265	SWISSPROT	DNA-DIRECTED RNA POLYMERASE III LARGEST SUBUNIT
1969	11844	21729	4.74	1.0E-06	AF196474.1	NT	Human sapiens p47-phox (NCF1) gene, complete cds
1949	11844	21730	4.74	1.0E-06	AF196474.1	NT	Human sapiens p47-phox (NCF1) gene, complete cds
4273	14172	23649	11.11	1.0E-06	U07061.1	NT	Human ABL genes, exon 1b and intron 1b, and defining MDSO4 Met protein (M9604 Met) gene, complete cds
5043	14915	24988	1.38	1.0E-06	AL163955.2	NT	Human sapiens chromosome 21 segment HS210395
5043	14915	24989	1.38	1.0E-06	AL163955.2	NT	Human sapiens chromosome 21 segment HS210395
5233	15157	24925	4.89	1.0E-06	BF133015.1	EST_HUMAN	NR1-ET1080-030700-002-63 B T0300 Homo sapiens cDNA
6107	19007	26739	6.11	1.0E-06	P02871	SWISSPROT	FIBRINOGEN ALPHAPHASE CHAIN PRECURSOR
6513	15922	26881	1.16	1.0E-06	A1347010.1	EST_HUMAN	gq44042.1 NC1 CGAP_Cot8 Homo sapiens cDNA clone IMAGE 102842 3'

Probes Exposed

[illegible]

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) HT BLAST E Value	Top HT Accession No.	Top HT Database Source	Top HT Descriptor
4547	14440	24223	1.44	5.0E-07	AF149774.1	NT	Homo sapiens NOTO1 protein (NOTO1) gene, exons 4 through 14 and complete cds
6203	15603	26506	1.71	5.0E-07	A360981.1	EST_HUMAN	IGFBP5.x1 NCL CGAP QLL1 Homo sapiens cDNA clone IMAGE:2107953 3' similar to contains Au repetitive element;contains element ASR repetitive element.
6203	15993	26907	1.71	5.0E-07	A360981.1	EST_HUMAN	IGFBP5.x1 NCL CGAP QLL1 Homo sapiens cDNA clone IMAGE:2107953 3' similar to contains Au repetitive element;contains element ASR repetitive element.
6548	16211	26373	15.93	5.0E-07	AW070985.1	EST_HUMAN	rs11602.x1 NCL CGAP B18 Homo sapiens cDNA clone IMAGE:2698982 3' similar to gpX18341
7832	17763	26521	4.11	5.0E-07	A006587.1	EST_HUMAN	CYTROCHROME C OXIDASE POLYPEPTIDE VARIANT (HUMAN)
8805	18519	26609	4.31	5.0E-07	PJ11087	SWISSPROT	COLLAGEN ALPHA 1(I) CHAIN PRECURSOR
8893	16576		2.06	5.0E-07	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
9712	18556		2.02	5.0E-07	AW62357.1	EST_HUMAN	QY0-070385-210400-2044312 C103881 Homo sapiens cDNA
9718	13527	26308	1.89	4.0E-07	AW006002.1	EST_HUMAN	rs24705.x1 NCL CGAP C03 Homo sapiens cDNA clone IMAGE:2504467 3'
7295	17112	27305	5.29	4.0E-07	AW19134.1	EST_HUMAN	rs9911.x1 NCL CGAP L034.1 Homo sapiens cDNA clone IMAGE:2654648 3'
8508	19186	28432	3.84	4.0E-07	A765528.1	EST_HUMAN	rs11608.x1 NCL CGAP K412 Homo sapiens cDNA clone IMAGE:2369703 3'
8839	19185	28433	3.84	4.0E-07	A765528.1	EST_HUMAN	rs11608.x1 NCL CGAP K412 Homo sapiens cDNA clone IMAGE:2369703 3'
8552	18422		2.05	4.0E-07	BE071828.1	EST_HUMAN	PW1-5N0085-03000-003-412 BN0083 Homo sapiens cDNA
434	10379	20200	5.01	3.0E-07	U19718.1	NT	Human microfilament-associated glycoprotein (MFAP2) gene, putative promoter region and alternatively spliced untranslated exons
598	10507	20314	2.38	3.0E-07	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
1332	17258	21114	2.19	3.0E-07	M09140.1	NT	Human polymorphic microsatellite DNA
1508	11513		2.23	3.0E-07	M64857.1	NT	Human EGF cluster
2000	11683					EST_HUMAN	rs24029.x1 NCL CGAP O02 Homo sapiens cDNA clone IMAGE:5808325 similar to contains Au repetitive element;contains L1.8 L1 repetitive element.
2242	12126	22026	1.01	3.0E-07	AA529763.1	EST_HUMAN	Human synaptic microsatellite DNA
2420	12297	22194	1.15	3.0E-07	M09149.1	NT	Human polymorphic microsatellite DNA
2420	12297	22194	17.25	3.0E-07	BE008077.1	EST_HUMAN	rs24029.x1 NCL CGAP O02 Homo sapiens cDNA clone IMAGE:5808325 similar to contains Au repetitive element;contains L1.8 L1 repetitive element.
2420	12297	22195	17.25	3.0E-07	BE008077.1	EST_HUMAN	rs24029.x1 NCL CGAP O02 Homo sapiens cDNA clone IMAGE:5808325 similar to contains Au repetitive element;contains L1.8 L1 repetitive element.
2698	13926	22718	0.85	3.0E-07	184704.1	EST_HUMAN	rs24029.x1 NCL CGAP O02 Homo sapiens cDNA clone IMAGE:5808325 similar to contains Au repetitive element;contains L1.8 L1 repetitive element.
3122	13047	23944	1.82	3.0E-07	P30139	SWISSPROT	HYPODERMAL GLYCOPROTEIN IN GUT-TRIM INTERGENIC REGION PRECURSOR
4324	14512	24302	7.05	3.0E-07	AV65020.1	EST_HUMAN	rs24029.x1 NCL CGAP O02 Homo sapiens cDNA clone IMAGE:5808325 similar to contains Au repetitive element;contains L1.8 L1 repetitive element.
4654	14540	24329	0.89	3.0E-07	A197296.1	EST_HUMAN	rs24029.x1 NCL CGAP O02 Homo sapiens cDNA clone IMAGE:5808325 similar to contains Au repetitive element;contains L1.8 L1 repetitive element.
4696	14871	24634	1.47	3.0E-07	T57950.1	EST_HUMAN	rs24029.x1 NCL CGAP O02 Homo sapiens cDNA clone IMAGE:5808325 similar to contains Au repetitive element;contains L1.8 L1 repetitive element.
4696	14871	24635	1.47	3.0E-07	T57950.1	EST_HUMAN	rs24029.x1 NCL CGAP O02 Homo sapiens cDNA clone IMAGE:5808325 similar to contains Au repetitive element;contains L1.8 L1 repetitive element.

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar EST/HT BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6476	15366	25442	10.26	3.0E-07	088607	SWISSPROT	PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4)
8026	15603		5.32	3.0E-07	AA815175.1	EST_HUMAN	(PEPTIDYLARGININE DEIMINASE TYPE ALPHA)
6433	16294	26436	3	3.0E-07	AW797193.1	EST_HUMAN	QV7-UM0036-200300-115-g02 UM0036 Homo sapiens cDNA
8918	18726		3	3.0E-07	AF029308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and tyrosinogen gene families
9559	19408		2.76	3.0E-07	AJ132621	NT	Rattus norvegicus mRNA for 45 kDa secretory protein, partial
26	10013	19807	2.62	2.0E-07	AF262688.1	NT	Homo sapiens TRF2-interacting telomeric RAP1 protein (RAP1) mRNA, complete cds
148	10122	19940	4.76	2.0E-07	L77599.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric end
148	10122	19941	4.76	2.0E-07	L77599.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric end
175	10146	19922	118.1	2.0E-07	U38849.1	NT	Fugu rubripes beta-cytoplasmic (vascular) actin gene, complete cds
731	10693	20495	1.71	2.0E-07	AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
731	10693	20496	1.71	2.0E-07	AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
828	10853	20701	3.11	2.0E-07	AA222260.1	EST_HUMAN	z08b07.41 Stragelene NT2 neuronal precursor 897230 Homo sapiens cDNA clone IMAGE:460069 3' similar to g06131850 GLYOPHORN A PRECURSOR (HUMAN) contains Alu repetitive element
828	10854	20703	3.38	2.0E-07	BS04042.1	EST_HUMAN	z01504.41 Stragelene lung (8972710) Homo sapiens cDNA clone IMAGE:60790 3' similar to contains L1 repetitive element
1147	11090	20693	1.28	2.0E-07	C23768	SWISSPROT	UB150ANTIGEN
1302	11493	21347	1.34	2.0E-07	Q39701	SWISSPROT	HYPOTHETICAL 72.6 KD PROTEIN C27.10 IN CHROMOSOME I
3033	13547	23334	14.74	2.0E-07	AF125348.1	NT	Homo sapiens cDNA, 1 (GVA) gene, exon 3 and partial cds
5078	14648	24723	0.97	2.0E-07	AW070995.1	EST_HUMAN	z060107.21 Soares, NFL, T, GBC, S1 Homo sapiens cDNA clone IMAGE:2687485 3' similar to NP-C0842.1
5078	14648	24724	0.97	2.0E-07	AW070995.1	EST_HUMAN	z060107.21 Soares, NFL, T, GBC, S1 Homo sapiens cDNA clone IMAGE:2687485 3' similar to NP-C0842.1
5198	15051	24825	0.95	2.0E-07	AL163012	NT	CE00023 PROBABLE PABP/GAP DOMAINS
5198	15051	24826	0.95	2.0E-07	AL163012	NT	CE00023 PROBABLE PABP/GAP DOMAINS
5009	15199	24975	1.73	2.0E-07	AW88905.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C-01
5009	15914	25041	1.96	2.0E-07	AG08716.1	EST_HUMAN	RCS-NM0056-204400-021-g11 NN0056 Homo sapiens cDNA
6934	16812		3.91	2.0E-07	AV729303.1	EST_HUMAN	g060605.21 Soares, Jellis, NHT Homo sapiens cDNA clone IMAGE:1639177 3'
7627	17478		1.61	2.0E-07	AL163003.2	NT	AV729303 HIC Homo sapiens cDNA clone HT CAGE02 5'
7627	17478		1.61	2.0E-07	AL163003.2	NT	Homo sapiens chromosome 21 segment HS21C103
7891	17741	27894	6.48	2.0E-07	AW825007.1	EST_HUMAN	GM-NM0003-280300-124-405 NN0003 Homo sapiens cDNA
9094	19567		1.46	2.0E-07	AIF23462.1	EST_HUMAN	z08b11.16 Stragelene lung carcinoma 097218 Homo sapiens cDNA clone IMAGE:566029 3' similar to contains THR b2 THR repetitive element
1096	11002		1.21	1.0E-07	AL162822.2	NT	Homo sapiens chromosome 21 segment HS21C082

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ. ID NO.	Exon SEQ. ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (10) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2331	12212	22110	0.94	1.0E-07	P10233	SWISSPROT	RETROVIRUS-RELATED GAG POLYPROTEIN (VERSION 1)
2403	12290	22177	0.94	1.0E-07	7540818	NT	Homo sapiens RAB, member of RAS oncogene family-like 2A (RABL2A), transcript variant 2, mRNA
2707	11410	21269	1.75	1.0E-07	P09256	SWISSPROT	GLYCOPROTEIN GPV
3694	11002	21269	1.33	1.0E-07	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
4105	14095	23874	2.37	1.0E-07	AV1718962.1	EST_HUMAN	AV1718962 GLC Homo sapiens cDNA clone GLCPRF04 5'
4105	14095	23875	2.37	1.0E-07	AV1718962.1	EST_HUMAN	AV1718962 GLC Homo sapiens cDNA clone GLCPRF04 5'
8103	15097	28132	5.2	1.0E-07	BE047871.1	EST_HUMAN	1245008.Y1 NC1 CGAP_Bms2 Homo sapiens cDNA clone IMAGE2281339 5'
8103	15097	28133	5.2	1.0E-07	BE047871.1	EST_HUMAN	1245008.Y1 NC1 CGAP_Bms2 Homo sapiens cDNA clone IMAGE2281339 5'
8424	10265	28447	9.94	1.0E-07	NS5081.1	EST_HUMAN	X15307.1 Scores (eal liver spleen INFLS Homo sapiens cDNA clone IMAGE245484 3'
8732	10691	26850	2.81	1.0E-07	P07135	SWISSPROT	ENTEROPEPTIDASE (ENTEROKINASE)
8732	10691	26851	2.81	1.0E-07	P07135	SWISSPROT	ENTEROPEPTIDASE (ENTEROKINASE)
7130	17057	27246	3.24	1.0E-07	AL1603576.1	EST_HUMAN	251010.1 Scores (fetal liver spleen INFLS S1 Homo sapiens cDNA clone IMAGE434346 3'
7114	17554	27790	2.37	1.0E-07	BF974324.1	EST_HUMAN	6023371.1F1 NH_MGC_83 Homo sapiens cDNA clone IMAGE427428 5'
7718	17598	27792	1.29	1.0E-07	AA398311.1	EST_HUMAN	EST185954 Brain IV Homo sapiens cDNA
7930	17830	27792	1.98	1.0E-07	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
8384	18533	28090	3.88	1.0E-07	BE043770.1	EST_HUMAN	116391.1X1 NC1 CGAP_X6111 Homo sapiens cDNA clone IMAGE3132212 3' similar to TR088722 088722
8407	18113	28090	3.37	1.0E-07	AS4647.1	NT	Human ALD gene for porphobilan synthase
8501	19222	27705	4.61	1.0E-07	X01703.1	NT	Human tandem immunoglobulin constant region complex (germline)
7680	17638	27705	1.57	9.0E-08	AV734819.1	EST_HUMAN	AV734819 cDNA Homo sapiens cDNA clone cCAP1506 5'
8520	18302	28856	2.91	9.0E-08	AI091052.1	EST_HUMAN	ind0407.1X1 NC1 CGAP_Casf Homo sapiens cDNA clone IMAGE244832 3' similar to contains OFR.2
8022	18730	28025	3.91	9.0E-08	AL163301.2	NT	OFR repetitive element;
9316	19008	28025	3.91	9.0E-08	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
591	12871	28025	2.85	9.0E-08	AI011352.1	EST_HUMAN	Homo sapiens partial stein-1 gene
1034	10962	28025	3.88	8.0E-08	BE795493.1	EST_HUMAN	verf6005.1 Scores (NFL T GBC S1 Homo sapiens cDNA clone IMAGE2328273 3'
1034	10962	28025	3.88	8.0E-08	BE795493.1	EST_HUMAN	verf6005.1 Scores (NFL T GBC S1 Homo sapiens cDNA clone IMAGE3943976 3'
13415	13415	28025	1.43	8.0E-08	BE795493.1	EST_HUMAN	901590133F1 NH_MGC_7 Homo sapiens cDNA clone IMAGE3943976 5'
7074	10951	27144	3.38	8.0E-08	AI732057.1	EST_HUMAN	cn15602.1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cnf15602 random
7074	10951	27145	3.38	8.0E-08	AI732057.1	EST_HUMAN	cn15602.1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cnf15602 random
7551	17402	27616	2.89	8.0E-08	AI970083.1	EST_HUMAN	EST382776 GAG16G16 resequencer, MAGK Homo sapiens cDNA
8570	18438	27616	2.39	8.0E-08	AI723417.1	NT	Homo sapiens microsomal epoxide hydrolase (EPHX1) gene, complete cds

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
73	10057	18674	3.27	7.0E-08	Q02357	SWISSPROT	ANKYRIN 1 (ERYTHROCYTE ANKYRIN)
3338	11244	21102	12.71	7.0E-08	X04809.1	NT	Rat mRNA for ribosomal protein L31
3528	13444	23240	1.09	7.0E-08	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
3528	13444	23241	1.09	7.0E-08	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
8169	18075		4.83	7.0E-08	A193743.1	EST_HUMAN	cong3.P11A6 conorm Homo sapiens cDNA 3'
8526	18724	20027	5.6	7.0E-08	U2470.1	NT	Rattus norvegicus Munc13-1 mRNA, complete cds
8770	13444	23240	4.84	7.0E-08	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
8770	13444	23241	4.84	7.0E-08	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
8634	19334		1.89	7.0E-08	A1131016.1	NT	Homo sapiens SCL gene locus
800	10729	20669	2.84	6.0E-08	A148348.2	NT	Homo sapiens chromosome 21 segment HS21C048
800	10729	20670	2.84	6.0E-08	A148348.2	NT	Homo sapiens chromosome 21 segment HS21C048
2312	12163	22092	1.73	6.0E-08	B214398.1	EST_HUMAN	MRCH10166-1B1194-004-09 H10168 Homo sapiens cDNA
4155	14055	23829	0.99	6.0E-08	A148348.2	NT	Homo sapiens chromosome 21 segment HS21C048
8717	14834	28818	2.26	6.0E-08	P14399	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS REVERSE TRANSCRIPTASE ; ENONUCLEASE]
8819	18823		1.74	6.0E-08	A1483209.2	NT	Homo sapiens chromosome 21 segment HS21C039
79	10063	18880	3.08	5.0E-08	A148303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2189	12076	21381	1.97	5.0E-08	A4403881.1	EST_HUMAN	HQ38899.1 NC1_OGAP_Thy1 Homo sapiens cDNA clone IMAGE:643193 similar to contains Alu repetitive element
9178	18042	24808	1.12	5.0E-08	Q06278	SWISSPROT	ALDEHYDE OXIDASE
9037	18830		4.36	5.0E-08	P06861	SWISSPROT	COMPLEMENT C3 PRECURSOR (C3C3 CONVERTASE)
8245	18888	23517	1.94	5.0E-08	A1616178.1	EST_HUMAN	CYCLOTRIN-19-100-04-12 C10228 Homo sapiens cDNA
1724	11625	21493	1.1	4.0E-08	P25723	SWISSPROT	DORSAL-VENTRAL PATTERNING TOLLOID PROTEIN PRECURSOR
1724	11625	21494	1.1	4.0E-08	P25723	SWISSPROT	DORSAL-VENTRAL PATTERNING TOLLOID PROTEIN PRECURSOR
7278	17155	27360	1.41	4.0E-08	L2571.1	NT	Chondral greases tumoral transcription factor (UBF2) mRNA, complete cds
7608	17768	28030	4.17	4.0E-08	A050027.1	EST_HUMAN	ar22d10.1l Gieseler Wtms Homo sapiens cDNA clone IMAGE:1669411 3' similar to contains Alu repetitive element/contains element MER22 repetitive element
8274	18154		1.79	4.0E-08	A1238717.1	NT	Homo sapiens mRNA for UCA suppressor TRNA-associated antigenic protein (RNA448 gene)
9439	18313	28570	3.88	4.0E-08	B1462493.1	EST_HUMAN	302248024F1 NH1 MGC: 627 Homo sapiens cDNA clone IMAGE:4333300 5'
8439	18313	28571	3.88	4.0E-08	B1462493.1	EST_HUMAN	302248024F1 NH1 MGC: 627 Homo sapiens cDNA clone IMAGE:4333300 5'
5061	10680		1.54	4.0E-08	W17619.1	EST_HUMAN	2655603.1 Scores: field1_hsd1_NH1H19W Homo sapiens cDNA clone IMAGE:344558 5' similar to contains L1 H1 L1 repetitive element
9703	19252		1.46	4.0E-08	A1843353.1	EST_HUMAN	8954f11.x1 NC1_OGAP_Cor10 Homo sapiens cDNA clone IMAGE:2062076 3' similar to contains MER18.b3

Table 4

Single Exon Probes Expressed in Heart

Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exam NO.	ORF SEQ ID	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5164	15048	24812	7.24	3.0E-08	AA101195.1	EST_HUMAN	2445603.1 Striatopaleo INT neuron (4837233) Homo sapiens cDNA clone IMAGE:63248 5'
5164	15048	24813	7.24	3.0E-08	AA101196.1	EST_HUMAN	2445603.1 Striatopaleo INT neuron (4837233) Homo sapiens cDNA clone IMAGE:63249 5'
5446	15307	25423	1.99	3.0E-08	BEB18348.1	EST_HUMAN	1670410.7 N1L_MGC_10 Homo sapiens cDNA clone IMAGE:3044850 5' similar to cointatins A1U SYNTAXIN 17.
5163	15120	24854	3.58	3.0E-08	AL192737.1	EST_HUMAN	9075811.6 NCI_GCAP_F128 Homo sapiens cDNA clone IMAGE:1944045 5'
5451	16512	25478	1.41	3.0E-08	AL162462.2	NT	Homo sapiens chromosome 21 segment HS210348
5558	16415		2.97	3.0E-08	AA49532.1	EST_HUMAN	1636000.1 Score1_MSF_F8_SW_OT_PA_S1 Homo sapiens cDNA clone IMAGE:2787138 3'
9027	18819		11.6	3.0E-08	R184320.1	EST_HUMAN	TRC13837 C13837 MER57 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE ; repetitive element
199	10171		15.76	3.0E-08	AW302986.1	EST_HUMAN	1622003.1 Score1 Infant brain 1N1B Homo sapiens cDNA clone IMAGE:30048 5' similar to cointatins A1U repetitive element
223	10194	20245	7.97	2.0E-08	AA425566.1	EST_HUMAN	2044907.1 Score1_L1288_F08a_L0288a Homo sapiens cDNA clone IMAGE:2787138 3'
844	10351	20366	1.49	2.0E-08	AF198349.1	NT	Alu repetitive element contains element MER15 repetitive element
844	10351	20366	10.93	2.0E-08	AW094338.1	EST_HUMAN	Cellular gamma Dact2 protein (Dact2) mRNA, complete cds
844	10351	20367	10.93	2.0E-08	AW186438.1	EST_HUMAN	NIH-01 00860-240200-001-p08 OT0080 Homo sapiens cDNA
974	10858		37.42	2.0E-08	BE590771.2	EST_HUMAN	NIH-01 00860-240200-001-p08 OT0080 Homo sapiens cDNA
1319	11228	21082	1.98	2.0E-08	BL183247.2	NT	NIH-01 68321F1 N1L_MGC_21 Homo sapiens cDNA clone IMAGE:3138963 5'
1707	11608		1.03	2.0E-08	BE749471.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS210347
1811	11708		3.68	2.0E-08	AN270271.1	EST_HUMAN	9041570.06951 N1L_MGC_21 Homo sapiens cDNA clone IMAGE:2845109 5'
2368	12248	22140	1.42	2.0E-08	AA751948.1	EST_HUMAN	9041570.06951 N1L_MGC_21 Homo sapiens cDNA clone IMAGE:2845109 5'
2466	12371		2.16	2.0E-08	K002716.1	NT	mus40401.1 NCI_GCAP_111 Homo sapiens cDNA clone IMAGE:2731418 3'
3171	13095	22501	6.02	2.0E-08	Q42280	SWISSPROT	Sheep Hs-PRNA-GUG
3171	13095	22502	6.02	2.0E-08	Q42280	SWISSPROT	WNT14 PROTEIN PRECURSOR
3183	13855		2.02	2.0E-08	Q42280	SWISSPROT	WNT14 PROTEIN PRECURSOR
3368	13952	23686	1.98	2.0E-08	AW181820.1	EST_HUMAN	RC3-37 0167-161059-012-063 STD197 Homo sapiens cDNA
3368	13952		0.78	2.0E-08	U62868.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds
4305	14203		3.35	2.0E-08	AA449040.1	EST_HUMAN	sa126037.1 NCI_GCAP_GCB1 Homo sapiens cDNA clone IMAGE:314390 5' similar to cointatins L112 L1
4876	14756		2.89	2.0E-08	AA572881.1	EST_HUMAN	hwt1768.02 NCI_GCAP_GCB1 Homo sapiens cDNA clone IMAGE:314390 5' similar to cointatins L112 L1
8722	16502	26791	1.31	2.0E-08	AA450121.1	EST_HUMAN	capo126161.1 Striatopaleo fetal telom 937202 Homo sapiens cDNA clone IMAGE:896274 3'
8895	17199	26002	11.82	2.0E-08	BF589004.1	EST_HUMAN	ncs2309.1 NCI_GCAP_K611 Homo sapiens cDNA clone IMAGE:3057968 5'

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon SEQ ID NO.	OPF SEQ ID NO.	Expression Signal	Max Similar (Top) BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1493	12096	21267	1.13	1.0E-08	P31792	SWISSPROT	POLYPROTEIN CONTAINS: REVERSE TRANSCRIPTASE; ENDONUCLEASE
2005	11897		2.92	1.0E-08	BE141959.1	EST_HUMAN	PMA-HT0130-180989-001-F12 HT0130 Homo sapiens cDNA
3155	13090	22891	1.24	1.0E-08	BE248844.1	EST_HUMAN	TCBAP-1D5232 Pediatric pre-B cell acute lymphoblastic leukemia Bayle-HGSC project/ CSEA Homo sapiens cDNA clone TCBAP5232
3155	13090	22892	1.24	1.0E-08	BE248844.1	EST_HUMAN	TCBAP-1D5232 Pediatric pre-B cell acute lymphoblastic leukemia Bayle-HGSC project/ CSEA Homo sapiens cDNA clone TCBAP5232
5191	15054	24818	1.49	1.0E-09	AL165280.2	NT	Homo sapiens chromosome 21 segment HS21C080
5438	13358	25414	4.05	1.0E-09	AJ010770.1	NT	Homo sapiens hyponatremia gene, exon 1-50
6975	16832	27045	1.84	1.0E-08	AJ015304.1	EST_HUMAN	033405.s1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE181878.3
8633	18408	28773	3.68	1.0E-08	AF047408.1	NT	Homo sapiens major histocompatibility locus class III region
9434	18074		2.01	1.0E-08	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
9604	18316		6.3	1.0E-08	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
9884	18518		1.78	1.0E-08	BR75988.1	EST_HUMAN	MR4-ST0240-240700-015-g04 ST0240 Homo sapiens cDNA
4149	14049	23823	2.98	9.0E-09	AL165279.2	NT	Homo sapiens chromosome 21 segment HS21C079
4149	14049	23824	2.98	9.0E-09	AL165279.2	NT	Homo sapiens chromosome 21 segment HS21C079
3444	13381		1.07	8.0E-09	BE120763.1	EST_HUMAN	RCS-BH1058-270400-031-C08 BH1058 Homo sapiens cDNA
6307	18171	26528	8.12	8.0E-09	AH183500.1	EST_HUMAN	g45247.1 Soares, fetal heart NHT1819V Homo sapiens cDNA clone IMAGE1752164.3 similar to
8858	18548	28743	2.71	8.0E-09	AI1200159.1	EST_HUMAN	containing MSK1.1 MSK1.1 putative kinase
7196	17673		3.08	8.0E-09	AJ458802.1	EST_HUMAN	C306-NH1003-010300-273-268 NH1003 Homo sapiens cDNA
3555	13499		1.68	7.0E-09	D68642.1	NT	077408.1 Soares, NFL_T_05C.S1 Homo sapiens cDNA clone IMAGE155275.3
4558	14450	24236	0.99	7.0E-09	D06948.1	NT	Homo sapiens DNA for 3-kilobase/CS4 thidase beta-subunit of mitochondrial ribosomal protein, exon 2, 3
7335	17203	27403	3.27	7.0E-09	D07068.1	NT	Homo sapiens gene for epsilon smooth muscle gamma-actin, exon 2, 3
7850	17700	27945	1.84	7.0E-09	BE257480.1	EST_HUMAN	Human lysosomal membrane glycoprotein-2 (LAMP-2) gene, 3' end and flanking region
2107	11998		1.09	6.0E-09	AL040499.1	EST_HUMAN	DN11H17371 NH1003, 16 Homo sapiens cDNA clone IMAGE3351834.5
3941	13949	28925	1.06	6.0E-09	A4557940.1	EST_HUMAN	DKFZ340340817.1 r24 (synonym: hnc3) Homo sapiens cDNA clone DKFZ340340814.5
4908	14788	24562	4.44	6.0E-09	BE189421.1	EST_HUMAN	m1741.1:1 NCL CGAP_HST01 Homo sapiens cDNA clone IMAGE1040924 similar to contains L112 L1
5305	18228	28500	8.19	6.0E-09	AW195784.1	EST_HUMAN	PMT-HT0327-160200-001-L05 HT0327 Homo sapiens cDNA
7384	17170	27370	2.28	6.0E-09		NT	380508.1 Soares, NFL_T_05C.S1 Homo sapiens cDNA clone IMAGE2701311.3
7896	17746		4.08	6.0E-09	AF200929.2	NT	Homo sapiens fibroblast growth factor receptor 3 (achondroplasia, rhizomelic dwarfism) (FGFR3) mRNA
1394	11299	21157	3.09	5.0E-09	BE149284.1	EST_HUMAN	Homo sapiens testis-specific kinase substrate1 (TSKS) gene, complete cds
						NT	RC3-HT0292-120200-014-H10 HT0292 Homo sapiens cDNA

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID/NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6639	15764	25681	1.92	5.0E-09 AA394454.1	EST_HUMAN	EST_HUMAN	EST168746 fad lung H homo sapiens cDNA 5' end
7811	17681	27801	2.89	5.0E-09 AW796957.1	EST_HUMAN	EST_HUMAN	PU21UM0653 240300-005-03b UN06153 Homo sapiens cDNA
510	10462		1.88	4.0E-09 AL163282.2	NT	NT	Homo sapiens chromosome 21 segment HS21C082
949	10873		2.31	4.0E-09 AL163285.2	NT	NT	Homo sapiens chromosome 21 segment HS21C085
1453	11359	21222	0.86	4.0E-09 G958718	EST_HUMAN	EST_HUMAN	Homo sapiens hypothetical protein (AF038109), mRNA
2379	12359	22151	6.36	4.0E-09 AA3303878.1	EST_HUMAN	EST_HUMAN	EST156385 Infant brain Homo sapiens cDNA 5' end similar to similar to heat shock protein, 90 kDa
2379	12359	22151	6.36	4.0E-09 AA3303878.1	EST_HUMAN	EST_HUMAN	MER18 repeat element
2303	12184	22082	3.82	3.0E-09 BE222239.1	EST_HUMAN	EST_HUMAN	HO0909.x1 NQ1 CGAP L1244 Homo sapiens cDNA clone IMAGE31186120 3' similar to contains MER18.13
2506	12380	22270	1.26	3.0E-09 BE222239.1	EST_HUMAN	EST_HUMAN	MER18 repeat element
2014	12482	22371	1.1	3.0E-09 F23249	SWISSPROT	SWISSPROT	PROTEIN MOV10
3287	13208	23008	1.1	3.0E-09 BE222239.1	EST_HUMAN	EST_HUMAN	HO0909.x1 NQ1 CGAP L1244 Homo sapiens cDNA clone IMAGE31186120 3' similar to contains MER18.13
3428	14228	24008	3.22	3.0E-09 AJ779325.1	NT	NT	HER18 repeat element
7614	14085	24068	1.54	3.0E-09 OR07965	SWISSPROT	SWISSPROT	Homo sapiens eukaryotic initiation factor 4A (EIF4A1) gene, partial cds
7894	17734	24088	1.73	3.0E-09 AL163247.2	NT	NT	263.1 KDa PROTEIN C20R05 (K1AA0333)
8384	18281	28510	3.8	3.0E-09 BF103943.1	EST_HUMAN	EST_HUMAN	TF208a.1 Scores NSF FB 9W OT PA P S11 Homo sapiens cDNA clone IMAGE357050 3'
8384	18281	28511	3.8	3.0E-09 BF103943.1	EST_HUMAN	EST_HUMAN	TF208a.1 Scores NSF FB 9W OT PA P S11 Homo sapiens cDNA clone IMAGE357050 3'
7951	10724		0.93	2.0E-09 X16074.1	NT	NT	H sapiens PADPR-1 gene for NAD(P) ADP-ribosyltransferase
12271	11144	20965	5.23	2.0E-09 AL163244.2	NT	NT	Homo sapiens chromosome 21 segment HS21C084
1687	11541		10.52	2.0E-09 AL118573.1	EST_HUMAN	EST_HUMAN	DNF220.0161770.1 701 (anonymous) human2 Homo sapiens cDNA clone DKF276181770.5'
2278	12762	22059	3.26	2.0E-09 OR07935	SWISSPROT	SWISSPROT	263.1 KDa PROTEIN C20R05 (K1AA0333)
3769	13769	23861	2.95	2.0E-09 E060241	SWISSPROT	SWISSPROT	BRAIN SPECIFIC ANGIOGENESIS INHIBITOR 2 PRECURSOR
6405	16266	26128	8.0	2.0E-09 AA481430.1	EST_HUMAN	EST_HUMAN	z60369.01 Scores, total, felus, NUDHf8 9w Homo sapiens cDNA clone IMAGE:798187 5' similar to contains AU repeat element
7055	18032	27122	1.37	2.0E-09 AJ271735.1	NT	NT	Homo sapiens Xq pseudotribosomal region; segment 1/2
8569	18457	28726	2.11	2.0E-09 AL163248.2	NT	NT	Homo sapiens chromosome 21 segment HS21C046
9576	10724		11.53	2.0E-09 X16074.1	NT	NT	H sapiens PADPR-1 gene for NAD(P) ADP-ribosyltransferase
9640	10749		1.32	2.0E-09 AA226070.1	EST_HUMAN	EST_HUMAN	nc11002.1 NQ1 CGAP P11 Homo sapiens cDNA clone IMAGE:1007810 similar to contains AU repeat element
1033	11009	20850	2.48	1.0E-09 503162A	NT	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
1063	11009	20851	2.48	1.0E-09 503162A	NT	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
1616	11520		0.96	1.0E-09 A123041.1	NT	NT	Homo sapiens 559 kb contig between AML1 and CBRT on chromosome 21q22; segment 1/3

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (19) HT BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2483	12330		0.94	1.0E-09	A155906.1	EST_HUMAN	g44et1.x1 NQI CGAP_Bm25 Homo sapiens cDNA clone IMAGE:20189123 similar to contains MER12.12 MER12 repetitive element;
2890	12788	22580	1.51	1.0E-09	U90017.1	NT	Homo sapiens basic transcription factor 2 p41 (ht2p4) gene, partial cds, neuronal apoptosis inhibitory protein (nrip) and survival motor neuron protein (smn) genes, complete cds
2895	12822	22614	3.25	1.0E-09	M28099.1	NT	Homo sapiens nuclear phosphoprotein B23 (NPM1) mRNA, complete cds
2895	12822	22615	3.25	1.0E-09	M28099.1	NT	Homo sapiens nuclear phosphoprotein B23 (NPM1) mRNA, complete cds
2949	12976	22674	1.23	1.0E-09	P11789	SWISSPROT	MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES (MLCK) [CONTAINS: TELOKIN]
3302	12600	22722	0.78	1.0E-09	BE135440.1	EST_HUMAN	6X105802F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3416177.5
4692	14678		4.26	1.0E-09	A4719297.1	EST_HUMAN	2158903.x1 Soares, Jaisal, gland_N3:PCO Homo sapiens cDNA clone IMAGE:414039.3 similar to contains Alu repetitive element; contains element MER22 repetitive element;
6590	15476	25549	1.37	1.0E-09	U07000.1	NT	Human breakpoint cluster region (BCR) gene, complete cds
6736	15644	25749	3.21	1.0E-09	P26684	SWISSPROT	GRG15P26684/20ITE PROTEIN PRECURSOR (CS)
7911	17781		3.1	1.0E-09	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
9478	19099	24908	2.14	1.0E-09	11418127	NT	Homo sapiens GTP binding protein 1 (GTPBP1), mRNA
1297	11195	27048	1.9	9.0E-10	AW987740.1	EST_HUMAN	MRS-SN0046-090500-202-c07 SN0040 Homo sapiens cDNA
2903	12793	22532	6.03	9.0E-10	A1870071.1	EST_HUMAN	w879823.v1 Soares, Diego,grafic, color_NHCD Homo sapiens cDNA clone IMAGE:2847253.3 similar to SW9923.2 HUMAN P29314.6S RIBOSOMAL PROTEIN L29 contains element PTR5 repetitive element;
6937	18023	26172	4.63	8.0E-10	AU459393.1	EST_HUMAN	TR-004372 004372 PUTATIVE P160
141	10115	19355	0.43	8.0E-10	U93503.5	NT	Homo sapiens MYC (MYC) and DNA-PKcs (PRKDC) genes, partial cds
3300	13222	23022	0.97	8.0E-10	BE080746.1	EST_HUMAN	QY1-EB70561-16230-071.61 BT0831 Homo sapiens cDNA
4108	14009	23752	2.62	8.0E-10	A370832.1	EST_HUMAN	EST-82654 Small intestine Homo sapiens cDNA 5' end
7725	17675		2.32	8.0E-10	U30393.2	NT	Homo sapiens lens major fibrillar protein (MF) gene, complete cds
9005	19809	29100	2.31	8.0E-10	AL162860.2	NT	Homo sapiens chromosome 21 segment HS21C083
985	10019	20444	12.45	7.0E-10	7706226	NT	Homo sapiens TPA inducible protein (LOC51559), mRNA
985	10019	20445	12.45	7.0E-10	7706226	NT	Homo sapiens TPA inducible protein (LOC51559), mRNA
1605	11610	21371	1.97	7.0E-10	Q13342	SWISSPROT	L13P100 PROTEIN (L13P100) HOMOLOG OF SP100
1974	11867		1.97	7.0E-10	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
2512	12386	22708	10.98	7.0E-10	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
3049	12976		2.65	7.0E-10	X00806.1	NT	H sapiens DHFR gene, exon 3
6764	15662	25769	3.98	7.0E-10	AJ343220.1	EST_HUMAN	EST161247 Gall bladder II Homo sapiens cDNA 5' end
6514	16373		1.39	7.0E-10	P35904	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
885	10821	20686	2.81	6.0E-10	AJ40877.1	NT	Human sapiens ASC3 gene, CEGP1 gene, C11orf14 gene, C11orf16 gene and C11orf17 gene
2644	12511	22402	1.47	6.0E-10	AJ42406.1	EST_HUMAN	LOC2007.X1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2065021 3'
4634	14322		2.51	6.0E-10	AW635719.1	EST_HUMAN	RCS-CT0254-051069-0172 CT0254 Homo sapiens cDNA
9052	18865		1.79	6.0E-10	AW971623.1	EST_HUMAN	EST-354012 IMAGE-ressequencing, MAGL Homo sapiens cDNA
5647	19557		3.54	6.0E-10	BE596410.1	EST_HUMAN	RCS-AN0070-10800-014-N07 NN0070 Homo sapiens cDNA
744	10347		4.5	6.0E-10	AL046304.1	EST_HUMAN	DKF-ZK344N219.1T 434 (synonym: Nss3) Homo sapiens cDNA D1FZ2-14N216 5'
3430	13347	23152	1.48	5.0E-10	Q10163	SWISSPROT	HYPOTHETICAL GENE 48 PROTEIN
6334	15157		1.82	5.0E-10	BF105159.1	EST_HUMAN	20182218FT NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4042413 5'
7486	17366	27570	1.79	5.0E-10	P34678	SWISSPROT	HYPOTHETICAL 67.9 KD PROTEIN ZK683.8 IN CHROMOSOME III
7486	17366	27571	1.79	5.0E-10	P34678	SWISSPROT	HYPOTHETICAL 67.9 KD PROTEIN ZK683.8 IN CHROMOSOME III
106	10087		0.86	4.0E-10	AJ221083.1	EST_HUMAN	gamma9.41 Soares, placenta, 829weeks, 2N6HP89N Homo sapiens cDNA clone IMAGE:294844 3' similar to contains A1u
1951	11846	21732	1.4	4.0E-10	AW594709.1	EST_HUMAN	gamma9.41 Soares, placenta, 829weeks, 2N6HP89N Homo sapiens cDNA clone IMAGE:294844 3' similar to contains A1u
2627	12401	22362	6.09	4.0E-10	AL163303.2	NT	gamma9.41 Soares, placenta, 829weeks, 2N6HP89N Homo sapiens cDNA clone IMAGE:294844 3' similar to contains A1u
6259	16125	28278	19.23	4.0E-10	AF224669.1	NT	gamma9.41 Soares, placenta, 829weeks, 2N6HP89N Homo sapiens cDNA clone IMAGE:294844 3' similar to contains A1u
8436	18310		7.7	4.0E-10	AF00528.1	NT	gamma9.41 Soares, placenta, 829weeks, 2N6HP89N Homo sapiens cDNA clone IMAGE:294844 3' similar to contains A1u
807	10822	20688	1.72	3.0E-10	N36113.1	EST_HUMAN	gamma9.41 Soares, placenta, 829weeks, 2N6HP89N Homo sapiens cDNA clone IMAGE:294844 3' similar to contains A1u
1326	11236		6.63	3.0E-10	AY085153.1	NT	gamma9.41 Soares, placenta, 829weeks, 2N6HP89N Homo sapiens cDNA clone IMAGE:294844 3' similar to contains A1u
4435	14330	24117	1.1	3.0E-10	AL163263.2	NT	gamma9.41 Soares, placenta, 829weeks, 2N6HP89N Homo sapiens cDNA clone IMAGE:294844 3' similar to contains A1u
4435	14330	24118	1.1	3.0E-10	AL163263.2	NT	gamma9.41 Soares, placenta, 829weeks, 2N6HP89N Homo sapiens cDNA clone IMAGE:294844 3' similar to contains A1u
5785	15572	25779	2.83	3.0E-10	P20330	SWISSPROT	gamma9.41 Soares, placenta, 829weeks, 2N6HP89N Homo sapiens cDNA clone IMAGE:294844 3' similar to contains A1u
8533	15739	23651	3.27	3.0E-10	BE305676.1	EST_HUMAN	gamma9.41 Soares, placenta, 829weeks, 2N6HP89N Homo sapiens cDNA clone IMAGE:294844 3' similar to contains A1u
6582	16420	26598	1.31	3.0E-10	AY745302.1	EST_HUMAN	gamma9.41 Soares, placenta, 829weeks, 2N6HP89N Homo sapiens cDNA clone IMAGE:294844 3' similar to contains A1u
6552	16420	26599	1.31	3.0E-10	AY745302.1	EST_HUMAN	gamma9.41 Soares, placenta, 829weeks, 2N6HP89N Homo sapiens cDNA clone IMAGE:294844 3' similar to contains A1u
7067	16844	27136	1.98	3.0E-10	H67208.1	EST_HUMAN	gamma9.41 Soares, placenta, 829weeks, 2N6HP89N Homo sapiens cDNA clone IMAGE:294844 3' similar to contains A1u
7233	17110	27302	1.47	3.0E-10	AW1860731.1	EST_HUMAN	gamma9.41 Soares, placenta, 829weeks, 2N6HP89N Homo sapiens cDNA clone IMAGE:294844 3' similar to contains A1u
7233	17110	27303	1.47	3.0E-10	AW1860731.1	EST_HUMAN	gamma9.41 Soares, placenta, 829weeks, 2N6HP89N Homo sapiens cDNA clone IMAGE:294844 3' similar to contains A1u
7979	17826		2.86	3.0E-10	T68891.1	EST_HUMAN	gamma9.41 Soares, placenta, 829weeks, 2N6HP89N Homo sapiens cDNA clone IMAGE:294844 3' similar to contains A1u

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8026	17879		1.64	3.0E-10/A178294.1	EST_HUMAN	EST_HUMAN	rs26903.1 NC1 CGAP GCBT Homo sapiens cDNA clone IMAGE:1269608 3'
9737	19271	25227	2.03	3.0E-10/BE17637.1	EST_HUMAN	EST_HUMAN	ILCH170618.110600-135-E07 HT0618 Homo sapiens cDNA
32	10018	18814	1.43	2.0E-10/P-43693	SWISSPROT	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
32	10018	18815	1.43	2.0E-10/P-43698	SWISSPROT	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
1850	11781		5.91	2.0E-10/U08017.1	NT	NT	Homo sapiens basic transcription factor 2 P44 (btf2-p44) gene, partial cds, neuronal apoptosis inhibitor protein (nrip) and survival motor neuron protein (smn) genes, complete cds
5547	15443		2.41	2.0E-10/Q26540	SWISSPROT	SWISSPROT	(HPRC)
8787	15683	29501	1.71	2.0E-10/AF260107.1	NT	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds, and cytochrome P450 polypeptide 6 (CYP3A5) gene, partial cds
8387	16230	28360	5.79	2.0E-10/BE17082.1	EST_HUMAN	EST_HUMAN	801585238.F1 NIH MGSC_7 Homo sapiens cDNA clone IMAGE:3940284 5'
1492	11397		3.95	1.0E-10/AJ067787.1	EST_HUMAN	EST_HUMAN	MR0-520039-290300-001-61 SN0038 Homo sapiens cDNA
1569	11493		3.14	1.0E-10/AJ06723.1	EST_HUMAN	EST_HUMAN	AV055123 GLC Homo sapiens cDNA clone GLC03A11 3'
2637	12471		2.4	1.0E-10/AJ065001.1	EST_HUMAN	EST_HUMAN	QY0-C10225-191169-055-e08 C10225 Homo sapiens cDNA
3458	13372	23178	0.89	1.0E-10/AJ083912.1	EST_HUMAN	EST_HUMAN	QY2-T10003-161169-015-g10 T10003 Homo sapiens cDNA
3770	13411		0.91	1.0E-10/AL041656.1	EST_HUMAN	EST_HUMAN	DKF-Zk45N1317.11.434 (synonym: hncs) Homo sapiens cDNA clone DKFZP454N1317 5'
3833	13842		5.44	1.0E-10/AF210854.1	NT	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
4036	13609	23718	4.51	1.0E-10/U62111.2	NT	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), fibronectin protein L18a (RPL18a), C22orf43, alpha-actinin-dependent protein kinase 1 (CAMKK1), creatine transporter (CRTX), CDM protein (CDM), adenosine deaminase protein >
4036	13609	23717	4.51	1.0E-10/U62111.2	NT	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), fibronectin protein L18a (RPL18a), C22orf43, alpha-actinin-dependent protein kinase 1 (CAMKK1), creatine transporter (CRTX), CDM protein (CDM), adenosine deaminase protein >
4042	13946	23724	2.25	1.0E-10/A031065.1	NT	NT	Homo sapiens PCGS1 mRNA for protein containing CXXC domain 1, complete cds
4079	13951		2.06	1.0E-10/M30029.1	NT	NT	Human progesterone-specific glycoprotein beta-1 (SP1) mRNA, test exon
5145	15012		0.93	1.0E-10/X87344.1	NT	NT	H sapiens DNA, DMB, HLA-Z1, IP22, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes
7889	17709		4.59	1.0E-10/AA031668.1	EST_HUMAN	EST_HUMAN	zr22908.r1 Stripedops nebulosus (pseudomorph) NT2RAJ1 9537234 Homo sapiens cDNA clone IMAGE:548314 5'
8286	19105	25408	3.4	1.0E-10/A035280.1	EST_HUMAN	EST_HUMAN	cyf6105.v3 Homo sapiens, fetal liver, spleen, INFL3.51 Homo sapiens cDNA clone IMAGE:1672661 3'
9037	15012		1.43	1.0E-10/X87344.1	NT	NT	H sapiens DNA, DMB, HLA-Z1, IP22, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes
9084	18855		1.3	1.0E-10/AA397885.1	EST_HUMAN	EST_HUMAN	z58510.t1 Sources_beta_HNT Homo sapiens cDNA clone IMAGE:729217 5'

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar Top Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
281	10226	20042	1.2	9.0E-11	BE145600.1	EST_HUMAN	IL2-H10203-025060-016-c8b H10203 Homo sapiens cDNA
2037	11947	21843	5.43	9.0E-11	AL134396.1	EST_HUMAN	DKF-Z6547D226_r1 647 (synonym: hfr1) Homo sapiens cDNA clone DKF-Z6547D226 5'
2037	11947	21844	5.43	9.0E-11	AL134396.1	EST_HUMAN	DKF-Z6547D226_r1 647 (synonym: hfr1) Homo sapiens cDNA clone DKF-Z6547D226 5'
3337	13257	23004	2.25	9.0E-11	AL134396.1	EST_HUMAN	DKF-Z6547D226_r1 647 (synonym: hfr1) Homo sapiens cDNA clone DKF-Z6547D226 5'
3337	13257	23005	2.25	9.0E-11	AA775686.1	EST_HUMAN	DKF-Z6547D226_r1 647 (synonym: hfr1) Homo sapiens cDNA clone DKF-Z6547D226 5'
4400	14295	24078	1.09	9.0E-11	AF070780.1	EST_HUMAN	af07801.at Stralagene schizo brain 311 Homo sapiens cDNA clone IMAGE 370287 3'
5421	15342		4	9.0E-11	BC079780.1	EST_HUMAN	RC6-BT0327-140200-011-E06 B10627 Homo sapiens cDNA
6410	18062	26312	2.59	9.0E-11	C16935.1	EST_HUMAN	C16935 Olfactin human scrotal pad mRNA (66572) Homo sapiens cDNA clone GEN-506808 5'
3078	13005		9.97	8.0E-11	H16971.1	EST_HUMAN	Y15911.at Scortis adult brain N2648557 Homo sapiens cDNA clone IMAGE-172173 3' similar to containe L1 repetitive element
3931	13702	23590	0.83	8.0E-11	AF176617.1	EST_HUMAN	trns4269.at NCI CGAP T4rt1 Homo sapiens cDNA clone IMAGE 2161938 3'
3937	13865	23641	4.03	8.0E-11	N53712.1	EST_HUMAN	Yw4946c.1 Walzmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE 265268 3'
1431	11336	21202	2.11	7.0E-11	AA339542.1	EST_HUMAN	EST34362 Embryo, 6 week 1 Homo sapiens cDNA, 5' and
6949	18827	27020	2.55	7.0E-11	AF163894.1	NT	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
7973	17723		1.22	7.0E-11	P14369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN (CONTAINS REVERSE TRANSCRIPTASE ; ENDONUCLEASE)
8545	19145		1.31	7.0E-11	AV701686.1	EST_HUMAN	A1701685 ADE Homo sapiens cDNA clone ADEA5C06 5'
4058	10352	20186	5.18	8.0E-11	ME2270.1	NT	Human matrix gla protein (MGF) gene, complete cds
4058	10352	20181	5.18	8.0E-11	ME2270.1	NT	Human matrix gla protein (MGF) gene, complete cds
6529	16393	25593	3.35	8.0E-11	P06547	SWISSPROT	LINE 1 REVERSE TRANSCRIPTASE HOMOLOG
6571	16790	25645	6.46	8.0E-11	AV727539.1	EST_HUMAN	A1727539 H1C Homo sapiens cDNA clone H1C3AC06 5'
111	9597	19788	0.92	9.0E-11	AL162383.2	NT	Homo sapiens chromosome 21 segment HS21C038
3320	8997	19788	1.45	9.0E-11	AL162383.2	NT	Homo sapiens chromosome 21 segment HS21C038
4135	14036	23911	1.45	9.0E-11	P49034	SWISSPROT	ALDEHYDE OXIDASE
5926	19531	25964	1.65	9.0E-11	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
5445	16307	25472	14.95	6.0E-11	111416799	NT	Homo sapiens procollagen beta 3 (PCDH3), mRNA
9875	18790	25072	1.75	5.0E-11	AA326890.1	NT	Homo sapiens K4X00851 gene (partia), XTS gene and LZTFL1 gene
1350	11285	1350	1.4	4.0E-11	AA330421.1	EST_HUMAN	Za01b121.t Soares, beta1, NHT Homo sapiens cDNA clone IMAGE730559 5'
2780	12622	22514	8.45	4.0E-11	BE989000.1	EST_HUMAN	00150763.H1 NH, MGC 71 Homo sapiens cDNA clone IMAGE730559 5'
4513	14411	24186	1.37	4.0E-11	D44666.1	EST_HUMAN	HUMS17Y008 Human brain cDNA Homo sapiens cDNA clone IMAGE730559 5'
5597	15803	25927	2.64	4.0E-11	P20036	SWISSPROT	PRE-MRNA SPLICING FACTOR RNA HELICASE PRP2
6362	16225		3.65	4.0E-11	AF224699.1	NT	Homo sapiens intronadense, beta A, lysosomal (MANEA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D) genes, complete cds
7405	17722		1.59	4.0E-11	BE149425.1	EST_HUMAN	RC1-HT10256-210100-013-008 H10256 Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Htt BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
9611	19190	25252	1.33	4.0E-11	11545725	NT	Homo sapiens SH2 domain binding protein 1 (SH2BP1), mRNA
1475	11331	21245	2.16	3.0E-11	6672077	NT	Male nucleate expressed in non-metastatic cells 2, protein (IMAGE33) (Nm2), mRNA
4179	4079		1.46	3.0E-11	AJ309248.1	EST_HUMAN	hsp70L120 Liver, Hepatocellular carcinoma Homo sapiens cDNA clone IMAGE3
944	10959	20716	1.98	2.0E-11	AJ155902.1	EST_HUMAN	g95004.1 Soares, beta2, NHT Homo sapiens cDNA clone IMAGE3
1168	11080	20926	3.64	2.0E-11	R24807.1	EST_HUMAN	W45912.1 Soares infant brain N1B Homo sapiens cDNA clone IMAGE35144.5
1168	11080	20927	3.34	2.0E-11	R24807.1	EST_HUMAN	W45912.1 Soares infant brain N1B Homo sapiens cDNA clone IMAGE35144.5
1596	11600	21359	3.91	2.0E-11	L17432.1	NT	Gallus gallus rib-binding, beta-A globin, beta-A globin, epsilon-globin, and epsilon receptor-like protein
1596	11600	21360	3.91	2.0E-11	L17432.1	NT	Gallus gallus rib-binding, beta-A globin, beta-A globin, epsilon-globin, and epsilon receptor-like protein
1808	11600	21360	3.91	2.0E-11	L17432.1	NT	Gallus gallus rib-binding, beta-A globin, beta-A globin, epsilon-globin, and epsilon receptor-like protein
1900	11605	21365	1.04	2.0E-11	AJ128371.1	EST_HUMAN	g93160.1 Soares, pregnant uterus, NHPU Homo sapiens cDNA clone IMAGE171313.3 similar to g1-02935 PEROMYXOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN)(contigs L1,11 L1 repetitive element)
2737	12589	22403	1.11	2.0E-11	AF087913.1	NT	Human endogenous retrovirus HERV-P-1470
3190	13083	22880	4.23	2.0E-11	AF10263	SWISSPROT	RETROVIRUS-RELATED GAG POLYPROTEIN (VERSION 1)
3284	13205	23005	0.87	2.0E-11	AJ147867.1	EST_HUMAN	hm34006.1 NOT CGAP XH11 Homo sapiens cDNA clone IMAGE215169.3
3452	13368		0.95	2.0E-11	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FH1) gene, exon 5
4501	14359		0.87	2.0E-11	AF163227.2	NT	Homo sapiens chromosome 21 segment HSD17C10027
4851	14732		5.46	2.0E-11	BE092558.1	EST_HUMAN	CY2-B10258-2591099-01-401 B10258 Homo sapiens cDNA
4991	14836	24604	1.32	2.0E-11	AJ307331.1	EST_HUMAN	nc83905.11 NQI CGAP GC1 Homo sapiens cDNA clone IMAGE379433.5 similar to SW PR18_YEAST
5810	15715	258228	1.83	2.0E-11	AA581026.1	EST_HUMAN	P15838 PRE-mRNA SPLICING FACTOR RNA HELICASE PRP16.1
7318	17194		1.49	2.0E-11	AF026308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and tyrosinogen gene families
7900	17960	27360	4.81	2.0E-11	Q13909	SWISSPROT	OLFACTORY RECEPTOR 91 (OLFACTORY RECEPTOR-LIKE PROTEIN OLF1)
8457	18330	28591	2.07	2.0E-11	AJ303693.1	EST_HUMAN	2627902.1 Soares, pregnant uterus, NHPU Homo sapiens cDNA clone IMAGE471794.3
8457	18330	28592	2.07	2.0E-11	AA030350.1	EST_HUMAN	2627902.1 Soares, pregnant uterus, NHPU Homo sapiens cDNA clone IMAGE471794.3
9190	19579		1.26	2.0E-11	AA704195.1	EST_HUMAN	377663.1 Soares, fetal liver, spleen, NFLS, S11 Homo sapiens cDNA clone IMAGE460924.3
9192	18027		2.26	2.0E-11	AA584243.1	EST_HUMAN	CR2-CH0027-210100-011-c01 CH0027 Homo sapiens cDNA
9216	18043	25355	1.98	2.0E-11	BF377859.1	EST_HUMAN	CH2-1N0140-076900-372-901 TN0140 Homo sapiens cDNA
9477	19103		1.86	2.0E-11	D06742.2	NT	Homo sapiens mRNA for KIAA0027 protein, ventral cells

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Table 4
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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9027	19201		2.38	2.0E-11	P08647	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
9930	19401		2.38	2.0E-11	J131016.1	NT	Homo sapiens SEC14 (S. cerevisiae-like 2 (SEC14.2), mRna
690	10504	20412	1.24	1.0E-11	AL163279.2	NT	Homo sapiens SCL gene locus
1199	11109	20054	2.66	1.0E-11	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
1493	11390		1.94	1.0E-11	AF119914.1	NT	Homo sapiens PRO3078 mRNA, complete cds
2079	11909	18832	3.12	1.0E-11	AF000573.1	NT	Homo sapiens homopolysialic 1,2-dioxygenase gene, complete cds
3454	13370	23174	1.32	1.0E-11	BE004316.1	EST_HUMAN	C10P-BN0105-170300-232-212 BN0105 Homo sapiens cDNA
5299	15191	24968	14.34	1.0E-11	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
6773	18632	28940	3.25	1.0E-11	AL163247.2	NT	Homo sapiens PHD finger protein 2 (PHF2) mRNA
6959	18906	27000	6.41	1.0E-11	R13174.1	EST_HUMAN	X73008.1 Source: Human brain; t1NB: Homo sapiens cDNA clone IMAGE:281068.5
7232	17109	27300	1.32	1.0E-11	BF395119.1	EST_HUMAN	OV4-NN1148-256000-423-403 NN1149 Homo sapiens cDNA
7232	17109	27301	1.32	1.0E-11	BF395119.1	EST_HUMAN	OV4-NN1148-256000-423-403 NN1149 Homo sapiens cDNA
8607	18474	28747	1.19	1.0E-11	BF650078.1	EST_HUMAN	93215407.F1 NIH MG6. 83 Homo sapiens cDNA clone IMAGE:426877.5
9702	19493		1.29	1.0E-11	Z63377.1	EST_HUMAN	HSAAACDHP, Human fetal brain, Vicia leucae Homo sapiens cDNA
9922	18493		0.82	9.0E-12	P26742	SWISSPROT	PREGNANCY ZONE PROTEIN PRECURSOR
2922	12849	22649	0.82	9.0E-12	AL163000.2	NT	Homo sapiens chromosome 21 segment HS21G100
7641	17491	27712	1.22	9.0E-12	AL163000.2	NT	Homo sapiens chromosome 21 segment HS21G100
7641	17491	27713	1.22	9.0E-12	AL163000.2	NT	Homo sapiens Xq pseudautosomal region segment 22
9270	18974		3.57	8.0E-12	AJ271738.1	NT	341D SPICULE MATRIX PROTEIN PRECURSOR (LSM84)
4652	14454	24241	2.75	7.0E-12	Q08694	SWISSPROT	323901.1 Sarcos, full [liver, spleen, intestine, S], Homo sapiens cDNA clone IMAGE:2291217.5
8596	18545	28528	11.23	7.0E-12	AL104735.1	EST_HUMAN	A1730354.HTF Homo sapiens cDNA clone=HITAF1703.9
3500	13471		0.92	6.0E-12	AV730354.1	EST_HUMAN	026911.1 NCL CGAP_00031 Homo sapiens cDNA clone IMAGE:1302273.3 similar to contains Alu repetitive element
4252	14151	28925	7.85	6.0E-12	AA782516.1	EST_HUMAN	Marone scalditis myoviral heavy chain FR34 (FR34) mRNA, complete cds
7201	17078	27263	1.19	6.0E-12	AF003249.1	NT	0410g11.1 NCL CGAP_00031 Homo sapiens cDNA clone IMAGE:1367688 similar to contains MER23a.12 (MER23a) repetitive element
7493	17262		1.86	6.0E-12	AA847898.1	EST_HUMAN	EST104462 Fetal brain, Striatum (callosop2008) Homo sapiens cDNA clone HFBD033
1027	10948	20790	2.88	5.0E-12	T06573.1	EST_HUMAN	242505.Y1 NCL CGAP_Bridged Homo sapiens cDNA clone IMAGE:2291217.5
3344	13254	23070	1.18	5.0E-12	BE047779.1	EST_HUMAN	242505.Y1 NCL CGAP_Bridged Homo sapiens cDNA clone IMAGE:2291217.5
3906	19380	25397	5.93	5.0E-12	AJ277381.1	NT	242505.Y1 NCL CGAP_Bridged Homo sapiens cDNA clone IMAGE:2291217.5
5171	19037		0.84	5.0E-12	AJ270661.1	EST_HUMAN	242505.Y1 NCL CGAP_00031 Homo sapiens cDNA clone IMAGE:1241373.3
5667	19578	26676	4.75	5.0E-12	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
5667	19578	26677	4.75	5.0E-12	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
9009	18915	28940	9.12	5.0E-12	AV1674780.1	EST_HUMAN	EST1389890 IMAGE resequences, MAGN Homo sapiens cDNA
7268	17145	27339	2.15	5.0E-12	AL104735.1	NT	Homo sapiens Xq pseudautosomal region segment 12

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7605	17745		4.67	5.0E-12	AL163303.2	NT	Human sapiens chromosome 21 segment HS21C103
244	10211	20027	3.42	4.0E-12	AA700383.1	EST_HUMAN	274911.1 Soares, fetal liver, spleen, INFLS_S1 Homo sapiens cDNA clone IMAGE:460676 3'
245	10211	20027	3.55	4.0E-12	AA700383.1	EST_HUMAN	274911.1 Soares, fetal liver, spleen, INFLS_S1 Homo sapiens cDNA clone IMAGE:460676 3'
4620	14413	24198	0.85	4.0E-12	AB98994.1	EST_HUMAN	524984.1 NCI, CGAP, Lutz Homo sapiens cDNA clone IMAGE:220746 3' similar to TRQ13330 Q13539
6737	16676		2.89	4.0E-12	AF109007.1	NT	Human sapiens S164 genes, partial cds; PST1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
9431	18305	28561	3.51	4.0E-12	AL220043.1	NT	Human sapiens Brachyotus tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like fibronectin protein (L44), and ITPA4 (FIP3) genes, complete cds
9520	19131		1.9	4.0E-12	U73027.1	NT	MT5493.1 Soares, NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2005377 3' similar to TRC14617
600	10598	20345	3.81	3.0E-12	AW341683.1	EST_HUMAN	014617.SMPR.1
600	10598	20346	3.81	3.0E-12	AW341683.1	EST_HUMAN	014617.SMPR.1
6047	17038	28167	3.08	3.0E-12	U37672.1	NT	Human prostate specific antigen gene, 5' flanking region
6047	17038	28168	3.08	3.0E-12	U37672.1	NT	Human prostate specific antigen gene, 5' flanking region
3421	13398	23143	1.03	2.0E-12	6754405	NT	Mouse myosin heavy chain-associated protein 2.2 (Myh2-2), mRNA
4025	13928	23704	1.04	2.0E-12	J01864.1	NT	Rat U3A small nuclear RNA
4025	13928	23705	1.04	2.0E-12	J01864.1	NT	Rat U3A small nuclear RNA
4324	14221		1.8	2.0E-12	BE063059.1	EST_HUMAN	CMA-BT0281-031199-087-a03 BT0281 Homo sapiens cDNA
4804	14688	24473	0.78	2.0E-12	OT3906	SWISSPROT	TBK13 PROTEIN (T-BOX PROTEIN 15)
4804	14688	24474	0.78	2.0E-12	OT3906	SWISSPROT	EST383946 IMAGE Resequences, MAGI Homo sapiens cDNA
5898	18604		2.22	2.0E-12	AW671857.1	EST_HUMAN	EST009009 Infant Brain, Bentic Soares Homo sapiens cDNA clone HIBB413 5' end
6258	18124	28277	3.34	2.0E-12	T06199.1	EST_HUMAN	Human sapiens A-like transposable element (ALTE), mRNA
6516	18376	29552	2.07	2.0E-12	11422229	NT	Human sapiens A-like transposable element (ALTE), mRNA
7397	17346		1.08	2.0E-12	AF16984.1	NT	Human sapiens putative BPEF syndrome breakpoint region protein gene, complete cds
7737	17587		8.13	2.0E-12	9516590.1	EST_HUMAN	MR3-H10487-150200-115-g01 HT0487 Homo sapiens cDNA
9175	18916		1.71	2.0E-12	AL103283.2	NT	Human sapiens chromosome 21 segment HS21C083
9377	19041		1.52	2.0E-12	11418248	NT	Human sapiens sulfatransferase-related protein (SLITX), mRNA
117	10095	10914	1.82	1.0E-12	AW627974.1	EST_HUMAN	h99069.1 NCI, CGAP, GU1 Homo sapiens cDNA clone IMAGE:2070040 3' similar to coriaria MER18.11
1944	11839		2.03	1.0E-12	AB87726.1	EST_HUMAN	MEM18 repetitive element;
3032	12950	22752	1.19	1.0E-12	AF000691.1	EST_HUMAN	hm1607.x1 NCI, CGAP, U2 Homo sapiens cDNA clone IMAGE:2439469 3' similar to contains L1, L3 L1 repetitive element;
						NT	Human sapiens testis-specific Testis Transcript Y2 (TTY2) mRNA, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8200	13201		1.05	5.0E-13	R78338.1	EST_HUMAN	Y620H.r1 Soares: placenta N26P Homo sapiens cDNA clone IMAGE:28559.5'
3351	13271		1.45	5.0E-19	AA35773.1	EST_HUMAN	Z77412.51 Soares: testis, NHT Homo sapiens cDNA clone IMAGE:74650.3' similar to contains AU
8234	18115	25867	2.75	3.0E-13	P07313	SWISSPROT	repulsive element/contains element MER22 repulsive element:
1824	11721		2.96	3.0E-13	AY378514.1	EST_HUMAN	MYOIN LIGHT CHAIN KINASE SKELETAL MUSCLE (MCK)
2411	12288		1.50	4.0E-13	AF005292.1	NT	P0210224-221069-001-411 H10224 Homo sapiens cDNA
5430	15360	25404	4.86	4.0E-13	BE169181.1	EST_HUMAN	Homo sapiens glicpican 3 (GPC3) gene, partial cds and flanking repeat regions
6278	15142	26266	1.92	4.0E-13	U066750.1	NT	PM3-HT0520-230200-002-Q8 H10520 Homo sapiens cDNA
6542	18400		1.52	4.0E-19	AA4261.1	EST_HUMAN	Homo sapiens mRNA for KIAA1339 protein, partial cds
7757	17807	27831	4.57	4.0E-19	AJ266831.1	EST_HUMAN	Y93305.r1 Soares: midbrain 2N04M Homo sapiens cDNA clone IMAGE:27060.5' similar to PIRUA32995
8507	18375	28445	1.63	4.0E-19	AA35819.1	EST_HUMAN	A32995.1 complex sterility protein - mouse,
8507	18375	28445	1.63	4.0E-19	AA35819.1	EST_HUMAN	repulsive element
173	10144		3.8	3.0E-19	AF005326.1	NT	z77810.51 Soares: testis, NHT Homo sapiens cDNA clone IMAGE:73851.4.3'
847	10774		1.37	3.0E-19	AA300310.1	EST_HUMAN	z77810.51 Soares: testis, NHT Homo sapiens cDNA clone IMAGE:73851.4.3'
2319	12203	22689	1.25	3.0E-13	AY271736.1	NT	Homo sapiens X-linked arylidic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat
2420	12065		2.83	3.0E-13	AF1163210.2	NT	z77810.51 Soares: testis, NHT Homo sapiens cDNA clone IMAGE:73851.4.3'
2620	12497	22387	4.23	3.0E-13	BF372992.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C010
3160	13075		2.86	3.0E-13	AA745644.1	EST_HUMAN	QMS-F10100-140700-242-H08 F10100 Homo sapiens cDNA
							db18402.21 NC1 CGAP K45 Homo sapiens cDNA clone IMAGE:124409.3'
6801	16461	26668	5.82	3.0E-13	U02111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal
8024	17255		4.03	3.0E-13	AF04768.1	EST_HUMAN	protein L16a (RPL16a), Ccp-Cadherin, -dependent protein kinase 1 (CAAMK), creatine transporter (CRTTR),
8403	19279	26831	3.86	3.0E-13	BE005609.1	EST_HUMAN	CDM protein (CDM), adenosine diphosphate protein >
8676	19668	26860	2.9	3.0E-13	AF16246.2	NT	CMA-BT0281-031199-007-463 BT0281 Homo sapiens cDNA
							Homo sapiens chromosome 21 segment HS21C040
144	10118	16038	2.77	2.0E-13	U02111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal
258	10207	20024	1.31	2.0E-13	U29839.1	NT	protein L16a (RPL16a), Ccp-Cadherin, -dependent protein kinase 1 (CAAMK), creatine transporter (CRTTR),
1249	11167	21005	4.71	2.0E-13	AF239710.1	NT	CDM protein (CDM), adenosine diphosphate protein >
3244	13167	22396	1.06	2.0E-13	BF43600.1	EST_HUMAN	Dar1a retro fibroblast growth factor receptor 4 mRNA, complete cds
							Homo sapiens DNA polymerase with small subunit (POLD2) gene, exons 1 through 11 and complete cds
							hnb7665.1 Soares: NSF_F9_9W_OT_PA_P_31 Homo sapiens cDNA clone IMAGE_3'

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF-SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
4019	13023		1.72	2.0E-13	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
5722	15929	25732	3.87	2.0E-13	Q06892	SWISSPROT	CELL SURFACE GLYCOPROTEIN 1 PRECURSOR (OUTER LAYER PROTEIN B) (S-LAYER PROTEIN 1)
5078	16061	26209	6.32	2.0E-13	X16012.1	NT	Human FRK gene for liver-type 6-phosphofructokinase [EC 2.7.1.11] exon 2
7676	17626	28067	3.37	2.0E-13	503186.1	EST_HUMAN	Homo sapiens mal-21 (C. elegans)-like 1 (MAD2L1) mRNA
9251	18061		7.42	2.0E-13	AV1692155.1	EST_HUMAN	CAC3-NN0001-100300-274-11 NN0001 Homo sapiens cDNA
288	10262	20072	1.37	1.0E-13	S71429.1	NT	FGF-1-fibroblast growth factor 1 [human, kidney, Genomic, 342 nt, segment 2 of 2]
870	10766	20546	4.39	1.0E-13	AAJ007673.1	NT	Homo sapiens LGI/O2B gene
1314	11220	21077	1.27	1.0E-13	X87344.1	NT	H. sapiens DMA, DM18, HLA-Z1, IIP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RINGB, 9, 13 and 14 genes.
1976	11969	21761	2.16	1.0E-13	AA720574.1	EST_HUMAN	nc1102.51 NCI CGAP GC50 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR 13
4488	11382	21689	1.48	1.0E-13	BF30087.1	EST_HUMAN	THR repetitive element.
8694	19872	23865	13.83	1.0E-13	BF108765.1	EST_HUMAN	60203006H1 NCI CGAP Bim44 Homo sapiens cDNA clone IMAGE:418566 5'
9076	18683		1.82	1.0E-13	AV1716377.1	EST_HUMAN	745610.41 Soares NSF FB, GW, DT, PA, P, S1 Homo sapiens cDNA clone IMAGE:3524443 3' similar to contains MER29.b/2 MER29 repetitive element.
9714	12656		1.16	1.0E-13	AA271795.1	NT	AV175377 DGB Homo sapiens cDNA clone DGBALE03 F
330	10289	20105	2.92	9.0E-14	AA781150.1	EST_HUMAN	Homo sapiens Xa head-to-tail repeat region; segment 1/2
331	10290	20106	2.95	9.0E-14	AA781150.1	EST_HUMAN	934011.41 Soares, testis, NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER18.11 MER19
2461	12228		4.04	9.0E-14	AV1691677.1	EST_HUMAN	934011.41 Soares, testis, NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER18.11 MER19
2126	12587	22462	4.62	9.0E-14	BA603162.1	NT	RO4-CT0222-080100-013-005 CT0222 Homo sapiens cDNA
3073	13000	22790	3.74	9.0E-14	AV1913295.1	EST_HUMAN	Homo sapiens 1FF gene cluster for tracheal factor, complete cds
3300	10289	20105	0.98	9.0E-14	AA781150.1	EST_HUMAN	934011.41 NCI CGAP JHT Homo sapiens cDNA clone IMAGE:2707853 3'
3728	13940	23426	5.22	9.0E-14	DI14647.1	NT	934011.41 Soares, testis, NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER18.11 MER19
4660	14636	24328	1.93	9.0E-14	AAJ002163.1	NT	Human DNA, SNTL repetitive element
3463	13069		1.87	8.0E-14	BE460093.1	EST_HUMAN	Sequans outp gene for seminal vesicle secreted protein, semenogelin 1
3872	13763		2.77	8.0E-14	RT76069.1	EST_HUMAN	1271605X1 NCI CGAP JHT Homo sapiens cDNA clone IMAGE:3201424 3'
7454	16447	20537	60.99	8.0E-14	X89291.1	NT	1271605X1 NCI CGAP JHT Homo sapiens cDNA clone IMAGE:141796 3'
7616	17303	27610	3.49	8.0E-14	AA216916.1	EST_HUMAN	H. sapiens DNA for endogenous retroviral like element
8732	19888		4.39	8.0E-14	BE026568.1	EST_HUMAN	217610.51 Stargenes fetal retina 937202 Homo sapiens cDNA clone IMAGE:626970 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Mean Similarity (Top Hit BLAST Value)	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1611	12699		3.07	7.0E-14	AW151673.1	EST_HUMAN	X67670.1 NCI CGAP_Cas4 Homo sapiens cDNA clone IMAGE:2823146.3 similar to contains MER10.12 MER10 repetitive element;
353	10319	20140	10.2	6.0E-14	AF026503.1	NT	Homo sapiens FRAS3 common fragile region, diadenosine triphosphatase hydrolase (FHT) gene, exon 5
5114	14982	24705	1.02	6.0E-14	8622549	NT	Homo sapiens hypothetical protein FLJ20585 (FLJ20585), mRNA
5114	14982	24757	1.02	6.0E-14	8623548	NT	Homo sapiens hypothetical protein FLJ20585 (FLJ20585), mRNA
7552	17502	27725	2.56	6.0E-14	AF026503.1	NT	Homo sapiens FRAS3 common fragile region, diadenosine triphosphatase hydrolase (FHT) gene, exon 5
7552	17502	27726	2.56	6.0E-14	AF026503.1	NT	Homo sapiens FRAS3 common fragile region, diadenosine triphosphatase hydrolase (FHT) gene, exon 5
502	10538	20348	3.92	5.0E-14	Q38120	SWISSPROT	CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER 1 (MULTIORUG RESISTANCE-ASSOCIATED PROTEIN 2) (CANALICULAR MULTIDRUG RESISTANCE PROTEIN)
4985	14860	24526	1.09	5.0E-14	AW073791.1	EST_HUMAN	X603805.1 NCI CGAP_GU1 Homo sapiens cDNA clone IMAGE:2575185.3 similar to contains L1.12 L1 repetitive element;
5397	15316	25393	5.12	5.0E-14	P08647	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOWLOG
1107	12685	171	1.71	4.0E-14	P04628	SWISSPROT	S-ANTIGEN PROTEIN PRECURSOR
1851	11732	21908	6.5	4.0E-14	AJ007973.1	NT	Homo sapiens LGMD2B gene
3593	13607		0.94	4.0E-14	AJ046502.1	EST_HUMAN	2467766.1 Soares pregnant uterus_NbHPU Homo sapiens cDNA clone IMAGE:487658.5 W73672.1 Soares multiple colorectal_2NbHMSF Homo sapiens cDNA clone IMAGE:271910.3 similar to contains L1.8 L1.1 repetitive element;
4194	14604	23673	1	4.0E-14	N48328.1	EST_HUMAN	W705003.1 NCI CGAP_LUH Homo sapiens cDNA clone IMAGE:2435332.3 similar to contains Alu repetitive element;
9771	10760		2.31	4.0E-14	A1868234.1	EST_HUMAN	R primatec mRNA for CRP-2 protein
954	10589	20705	2.13	3.0E-14	X05466.1	NT	Ap016724.1 NCI CGAP_HN11 Homo sapiens cDNA clone IMAGE:2743343.3 similar to contains Alu repetitive element; contains element MER9 repetitive element;
4941	14723	24505	0.82	3.0E-14	AW363541	EST_HUMAN	Homo sapiens a disintegrin and metalloprotease domain 26 (ADAM26), mRNA
4844	14725	24607	1.1	3.0E-14	7665864	NT	X60471.1 NCI CGAP_Gd11 Homo sapiens cDNA clone IMAGE:3195501.3 similar to contains MER14.2 MER14
5104	14972		1.28	3.0E-14	OE36372.1	EST_HUMAN	DFCUMBP002001E PROTEIN PRECURSOR (CS)
5157	15624	24791	1.8	3.0E-14	P02894	SWISSPROT	Ap016724.1 NCI CGAP_HN11 Homo sapiens cDNA clone IMAGE:2743343.3 similar to contains Alu repetitive element; contains element MER9 repetitive element;
8863	14722	24505	7.89	3.0E-14	AW363541	EST_HUMAN	Homo sapiens X4 pseudocatalytic region, segment 22
3841	10331	20154	3.98	2.0E-14	AJ271758.1	NT	Homo sapiens X4 pseudocatalytic region, segment 22
3841	10331	20155	3.98	2.0E-14	AJ271758.1	NT	Homo sapiens X4 pseudocatalytic region, segment 22
375	12673	20428	6.35	2.0E-14	A153933.2	NT	Homo sapiens chromosome 21 segment RS210103

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
2359	12219		1.36	2.0E-14	AW372688.1	EST_HUMAN	RC5-BT077-091295-031D12 BT077 Homo sapiens cDNA
2416	12293		1.09	2.0E-14	7657526	NT	Homo sapiens (inbred) tumor deletion region protein 1 (RTDR1), mRNA
2470	12355	22246	1.24	2.0E-14	AL482309.2	NT	Homo sapiens chromosome 21 segment HS21C009
2601	12607		0.95	2.0E-14	P08435	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
5595	15423	25485	2.96	2.0E-14	U01317.1	NT	Human beta globin region on chromosome 11
6114	15908		2.16	2.0E-14	BE000559.1	EST_HUMAN	RC5-BN072-240200-011-a05 BN072 Homo sapiens cDNA
6423	12293	28454	19.91	2.0E-14	BE13759.1	EST_HUMAN	L2-HT0397-077299-024D04 HT0397 Homo sapiens cDNA
6423	12293	28455	19.91	2.0E-14	BE13759.1	EST_HUMAN	L2-HT0397-077299-024D04 HT0397 Homo sapiens cDNA
8160	18046	28360	4.75	2.0E-14	AW316890.1	EST_HUMAN	U14-BT1-adv-a-10-01-011 NCI CGAP S3a33 Homo sapiens cDNA clone IMAGE2718284.3
8791	15423	234651	1.81	2.0E-14	U01317.1	NT	Human beta globin region on chromosome 11
1051	10965	20310	1.31	1.0E-14	AL183246.2	NT	Homo sapiens chromosome 21 segment HS21C045
1354	11289	21145	7.97	1.0E-14	AL183268.2	NT	Homo sapiens chromosome 21 segment HS21C058
1354	11289	21141	7.97	1.0E-14	AL183268.2	NT	Homo sapiens chromosome 21 segment HS21C058
1956	11851	21738	21.54	1.0E-14	AL144140.1	NT	Homo sapiens chromosome X region from flamm (FLN) gene to glucose-6-phosphate dehydrogenase (G6PD) gene on the X chromosome
2137	12025	21921	6.17	1.0E-14	AL183303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2358	12238	22134	6.43	1.0E-14	AF001699.1	NT	Homo sapiens chromosome 21 segment HS21C103
2974	12841		1.38	1.0E-14	P16527	SWISSPROT	HISTONE H3H PROTEIN PRECURSOR (CLONE PHRP-1)
3130	13055	22654	4.67	1.0E-14	BF33527.1	EST_HUMAN	RC5-CT0432-310700-015-439.1 CT0432 Homo sapiens cDNA
3130	13055	22655	4.67	1.0E-14	BF33527.1	EST_HUMAN	RC5-CT0432-310700-015-439.1 CT0432 Homo sapiens cDNA
3811	13723	23912	2	1.0E-14	A4682994.1	EST_HUMAN	bedet12.41 Staphylococcus aureus strain S11 Homo sapiens cDNA clone IMAGE597185.3
4374	14270	24051	1.74	1.0E-14	A1275952.1	EST_HUMAN	apopto10.1 NCI CGAP L205 Homo sapiens cDNA clone IMAGE270309.3
5550	15466	25538	1.67	1.0E-14	AF128145.1	NT	Box taurine xenobiotic-inducible chain fatty acid CoA ligase from XL-111 mRNA, nuclear mRNA encoding mitochondrial protein, complete cds
6012	16457	20045	10.41	1.0E-14	11437150	NT	Homo sapiens primate (mouse)-like 1 (PROML1), mRNA
6012	16457	20046	10.41	1.0E-14	11437150	NT	Homo sapiens primate (mouse)-like 1 (PROML1), mRNA
1159	11493	21320	2.85	9.0E-15	7427622	NT	Homo sapiens protein tyrosine phosphatase, receptor type 1 (PTPRN1), mRNA
2126	12014		1.64	9.0E-15	BF19779.1	NT	Homo sapiens transcription factor GCM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, type LIM domain protein 6, and synapophycin genes, complete cds, and L-type calcium channel α_2
6427	16288	20749	4.28	9.0E-15	BE000559.1	EST_HUMAN	GAG POLYPROTEIN [CONTAINS CORE PROTEINS P16, P12, P30, P10]
6473	16553	20748	1.93	9.0E-15	BE000559.1	EST_HUMAN	8016777007 NH_MGC_21 Homo sapiens cDNA clone IMAGE3960159.5
2780	10415		1	8.0E-15	BE281462.1	EST_HUMAN	8011466325 NH_MGC_19 Homo sapiens cDNA clone IMAGE3164025.5

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7963	17613		2.63	7.0E-15	AW241958.1	EST_HUMAN	sn77402.4 Spores, NFE1_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2700483 3' similar to contains THR12 THR repetitive element;
978	19071	20748	6.12	6.0E-15	AJ271756.1	NT	Homo sapiens Xq pseudobisubunit region, segment 2/2
8622	19470		1.86	6.0E-15	AF535643.1	EST_HUMAN	QV14.1T0035:150200-076-010 T0036 Homo sapiens cDNA
9946	19415		1.97	6.0E-15	BF432200.1	EST_HUMAN	ml81412.11 Spores, NSF_F8_WT_OT_PA_P S1 Homo sapiens cDNA clone IMAGE: 3'
484	10350	20177	5.76	5.0E-15	AL163308.2	NT	Homo sapiens chromosome 21 segment HS21C008
2733	12595		1.36	5.0E-15	U91326.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (H1A-H) gene, RNF41 gene, and sodium phosphate transporter (NPTS) gene, complete cds
3423	13340	22490	1	5.0E-15	AV726617.1	EST_HUMAN	U14-BV05-JB-pc-10-CJ1 s1 NGI CGAP S105 Homo sapiens cDNA clone IMAGE:2731219 3'
8063	17584		2.22	5.0E-15	AV730059.1	EST_HUMAN	AV730059 HTF Homo sapiens cDNA clone HTF-AVE09 5'
4231	9566	19770	2.5	4.0E-15	AL165353.2	NT	Homo sapiens chromosome 21 segment HS21C103
4039	13942	23720	0.76	4.0E-15	AL118594.1	EST_HUMAN	DKFZ751C0810 .1 T61 (synonym: ham2) Homo sapiens cDNA clone DKFZ751C0810 5'
8474	16438	26620	2.38	4.0E-15	AJ130944.1	NT	Homo sapiens mRNA for transcription factor
8414	16438	26624	2.38	4.0E-15	AJ130944.1	NT	Homo sapiens mRNA for transcription factor
4123	14023		5.93	3.0E-15	N90462.1	EST_HUMAN	LY1142F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone LY1142 5' similar to ANCH-UBIQUINONE OXIDOREDUCTASE
4643	14724		1.41	3.0E-15	P22345	SWISSPROT	ANCH-UBIQUINONE OXIDOREDUCTASE CHAIN 5
4851	14632	24556	0.88	3.0E-15	AJ078097.1	EST_HUMAN	PROT83 Chromosome 7 Placental cDNA Library Homo sapiens cDNA clone 7P01503
4851	14632	24600	0.88	3.0E-15	AJ078097.1	EST_HUMAN	PROT83 Chromosome 7 Placental cDNA Library Homo sapiens cDNA clone 7P01503
8314	16177	26538	2.86	3.0E-15	M27855.1	NT	Mus musculus ultra high pillar keratin gene, complete cds
8314	16177	26536	2.86	3.0E-15	M27855.1	NT	Mus musculus ultra high pillar keratin gene, complete cds
7769	17559		1.87	3.0E-15	AA607128.1	EST_HUMAN	cd0407.S1 NIG CGAP G061 Homo sapiens cDNA clone IMAGE:1931764 3' similar to contains MER16.11 MER17 repetitive element;
8173	16061	28311	2.71	3.0E-15	AB058888.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
250	10216	20033	3.26	2.0E-15	AF273391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-48, and partial cds, alternatively spliced
364	10320	20141	3.23	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-48, and partial cds, alternatively spliced
364	10320	20142	3.23	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-48, and partial cds, alternatively spliced
19312	11417		1.14	2.0E-15	B623201	NT	Homo sapiens hypothetical protein FLJ26212 (FLJ26212) mRNA

Table 4

Single Exon Probes Expressed In Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3465	13381	23186	1.04	2.0E-15	AF223391.1	NT	Homo sapiens sodium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
3465	13391	23187	1.04	2.0E-15	AF223391.1	NT	Homo sapiens sodium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
4522	14415		2.07	2.0E-15	AI060335.1	EST_HUMAN	wf700.xt Soares, NFL_T_GBC, S1 Homo sapiens cDNA clone IMAGE:2349823 3' similar to TR.Q01043
5097	14866	24741	1.33	2.0E-15	P13693	SWISSPROT	C61048 NININ-1
5097	14866	24742	1.33	2.0E-15	P13693	SWISSPROT	REPETITIVE PROLINE-RICH CELL WALL PROTEIN 2 PRECURSOR
8223	15069		1.71	2.0E-15	AJ400877.1	NT	Homo sapiens ASCL3 gene, CCGP1 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
8310	16173	28331	2.2	2.0E-15	AA704185.1	EST_HUMAN	z778d10.1 Soares, fetal liver, spleen, INFLS, S1 Homo sapiens cDNA clone IMAGE:400823 3'
8375	16237	28397	5.13	2.0E-15	W05064.1	EST_HUMAN	WP-FAF4.8 C20227 TRANSPOSASE ;
7163	17040	27232	2.72	2.0E-15	D14547.1	NT	Human DNA, SINE repetitive element
7410	17271	27484	1.26	2.0E-15	AIW37965.1	EST_HUMAN	CNACHT0244-201099-078-a12 HT0244 Homo sapiens cDNA
7410	17271	27485	1.26	2.0E-15	AIW37965.1	EST_HUMAN	CNACHT0244-201099-078-a12 HT0244 Homo sapiens cDNA
8212	18066		3.01	2.0E-15	AJ271355.1	NT	Homo sapiens X0 pseudobacterial region, segment 12
9799	13381	23186	2.22	2.0E-15	AF223391.1	NT	Homo sapiens sodium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
9799	13381	23187	2.22	2.0E-15	AF223391.1	NT	Homo sapiens sodium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
2747	12609		1.84	1.0E-15	AI699844.1	EST_HUMAN	SC285.xt NCI, C61P, Lu24 Homo sapiens cDNA clone IMAGE:2270745 3' similar to TR.Q13539 Q13539
2879	12908	22708	0.8	1.0E-15	BC043541.1	EST_HUMAN	WAB20.xt NCI, C61P, C61A Homo sapiens cDNA clone IMAGE:2999182 5'
3103	13028	22833	0.89	1.0E-15	BC057487	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
4262	14161	23839	0.8	1.0E-15	BC10386.1	EST_HUMAN	KC3-H0466 109939 022455110818 Homo sapiens cDNA
5068	14656	24131	1.15	1.0E-15	AI049428.1	EST_HUMAN	wf800.xt NCI, C61P, KRT11 Homo sapiens cDNA clone IMAGE:2944590 3'
5841	15750	25894	1.83	1.0E-15	U95763.1	EST_HUMAN	wf800.xt Soares, fetal liver, spleen, INFLS Homo sapiens cDNA clone IMAGE:2944590 3'
6122	16068		1.96	1.0E-15	BC074217.1	EST_HUMAN	QYD-BT10580-27100-074-g05 BT0559 Homo sapiens cDNA
6791	16670	28882	1.28	1.0E-15	AL162820.2	NT	Homo sapiens atrazine21 21 segment 15210380
6865	16783	28976	4.97	1.0E-15	AI020076.1	EST_HUMAN	gpro300.xt Soares, testis, NHT Homo sapiens cDNA clone IMAGE:1755227 3'
6865	16783	28977	4.97	1.0E-15	AI020076.1	EST_HUMAN	gpro300.xt Soares, testis, NHT Homo sapiens cDNA clone IMAGE:1755227 3'
7227	17104	27293	1.44	1.0E-15		NT	Homo sapiens spermidine synthase (SRM) mRNA

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
8193	19079	28331	8.81	1.0E-16	AF04083.1	NT	Homo sapiens major histocompatibility locus class III region h3-10a.1; NC_01_Ox23 Homo sapiens cDNA clone IMAGE:221992.3' similar to contains Alu repetitive element;
9887	19492	25131	3.71	1.0E-15	AF78944.1	EST_HUMAN	Homo sapiens rat (Ornithine) iso 1 (CCAAT displacement protein) (CUTL1) mRNA
4404	14298	24042	1.03	9.0E-10	4503168	NT	Homo sapiens rat (Ornithine) iso 1 (CCAAT displacement protein) (CUTL1) mRNA
8391	18238	28460	2.6	9.0E-10	F08588.1	EST_HUMAN	HS-C29F051 normalized infant brain cDNA Homo sapiens cDNA clone c-2305
9343	15209	23368	1.5	7.0E-10	O68807	SWISSPROT	PROTEIN-ARGININE DEIMINASE TYPE M (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4) (PEPTIDYLARGININE DEIMINASE TYPE ALPHA)
6343	15209	23369	1.5	7.0E-10	O68807	SWISSPROT	PROTEIN-ARGININE DEIMINASE TYPE M (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4) (PEPTIDYLARGININE DEIMINASE TYPE ALPHA)
6816	19285		6.8	7.0E-10	T84149.1	EST_HUMAN	h28-12.1 Stralagene lung (h27210) Homo sapiens cDNA clone IMAGE:118082.5'
2094	11983		8.32	0.0E-10	AW97281.1	EST_HUMAN	EST184702 IMAGE resources, MAC3, Homo sapiens cDNA
1477	11382	21246	1.09	5.0E-10	AL0251154.1	NT	Mus musculus olfactory receptor cluster, OR37A, OR37B, OR37C, OR37E genes and OR37D pseudogene dbDp4.1 Soares, Jodi, Feuts, Nilsa, 9v Homo sapiens cDNA clone IMAGE:1104128.5'
2047	12514	22404	1.79	5.0E-10	AA922175.1	EST_HUMAN	contains element L1, repetitive element
7804	17824	27887	1.09	5.0E-10	AL163249.2	NT	601857347F1 NIH MGC_57 Homo sapiens cDNA clone IMAGE:1104128.5'
8809	18238	28414	3.33	5.0E-10	EF21788.1	EST_HUMAN	Homo sapiens gene for TMEH and PwF2 complete and partial cds
9904	19381		8.34	5.0E-10	11418127	NT	Homo sapiens GTP binding protein 1 (GTPBP1), mRNA
2162	12079		1.37	4.0E-10	AB001523.1	NT	Homo sapiens gene for TMEH and PwF2 complete and partial cds
2328	12209	22107	1.32	4.0E-10	AW797168.1	EST_HUMAN	OV-1-UM035-20300-115-922 UN0036 Homo sapiens cDNA
2328	12209	22108	1.32	4.0E-10	AW797168.1	EST_HUMAN	OV-1-UM035-20300-115-922 UN0036 Homo sapiens cDNA
8411	13328	23120	3.85	4.0E-10	C03633	SWISSPROT	MYELIN OLIGODENDROCYTE GLYCOPROTEIN PRECURSOR
4050	13352	23728	3.95	4.0E-10	BE083875.1	EST_HUMAN	h4-AT (950-010400-002-003-01059) Homo sapiens cDNA
4050	13352	23728	3.95	4.0E-10	BE083875.1	EST_HUMAN	h4-AT (950-010400-002-003-01059) Homo sapiens cDNA
5082	14655	24731	1	4.0E-10	AB08348	SWISSPROT	LINE (REVERSE) TRANSCRIPTASE (HIV) LOG
5538	15395	25375	33.8	4.0E-10	AL163249.2	NT	Homo sapiens chromosome 21 segment 15321038
7537	17425	27425	1.22	4.0E-10	AL163249.2	NT	Homo sapiens chromosome 21 segment 15321038
8531	18421	28591	1.74	4.0E-10	AY700300.1	EST_HUMAN	Homo sapiens hypodermal protein PL-0024 (PL-0024), mRNA
9150	18509		1.94	4.0E-10	PM08548	SWISSPROT	AY700300 HIT Homo sapiens cDNA clone h17A1403.5'
9241	18557		1.94	4.0E-10	C03947.1	EST_HUMAN	LINE (REVERSE) TRANSCRIPTASE HOMOLOG
9255	18554	25516	2.04	4.0E-10	9612468	EST_HUMAN	CD347 Human pancreatic islet Homo sapiens cDNA clone h6c535
1225	18624	19624	1.89	3.0E-10	AW02862.1	EST_HUMAN	Homo sapiens cDNA associated linker 2 (L2) (L2) (L2), mRNA
128	10102	19625	1.59	3.0E-10	AW02862.1	EST_HUMAN	h4-AT (950-010400-002-003-01059) Homo sapiens cDNA clone IMAGE:24833.16.5'
459	10402		1.47	3.0E-10	AL046445.1	EST_HUMAN	h4-AT (950-010400-002-003-01059) Homo sapiens cDNA clone IMAGE:24833.16.5'

Single Exon Probes Expressed In Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) HIT BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
457	10410		1.6	3.0E-16	AF136416.1	NT	Homo sapiens TSX (TSX) pseudogene, exon 5
1435	11341	21207	2.01	3.0E-16	Q28883	SWISSPROT	ZONADHESIN PRECURSOR
2946	12873	22870	4.05	3.0E-16	P03200	SWISSPROT	ENVELOPE GLYCOPROTEIN GP340 (MEMBRANE ANTIGEN) (MA) [CONTAINS: GLYCOPROTEIN GP220]
3874	13785		8.18	3.0E-16	AF022903.1	NT	Homo sapiens FRA3B3 common fragile region, disadenosine triphosphate hydrolase (FHT) gene, exon 5
3875	13786		0.99	3.0E-16	U03887.1	NT	Human BXP20 gene
4891	14741	24521	1.01	3.0E-16	AF01393.1	EST_HUMAN	AV081935 GLC Homo sapiens cDNA clone GLC03A01.3'
5452	15373	25431	1.41	3.0E-16	AF038259.1	NT	Homo sapiens glycocalyx 3 (GPC3) gene, partial cds and flanking repeat regions
7031	15809	27028	4.72	3.0E-16	AF002838.1	EST_HUMAN	antiH05.01 Stridagene schizo yeast S11 Homo sapiens cDNA clone IMAGE:184186.3' similar to contains THR_L2 THS repetitive element;
7691	17541		1.27	3.0E-16	BF60017.1	EST_HUMAN	002246538F1 NH: MGCC 261 Homo sapiens cDNA clone IMAGE:433032.5'
7828	17578	27922	3.08	3.0E-16	U78810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
956	10860		1.18	2.0E-16	AF18379.2	EST_HUMAN	Homo sapiens chromosome 21 segment (HS21C079
2337	12217		0.96	2.0E-16	AA021795.1	EST_HUMAN	af02404.1 Soares, Jellis, NHT Homo sapiens cDNA clone IMAGE:1030655.3'
2467	12524		1.71	2.0E-16	J03091.1	NT	Human SSAN-related endogenous retroviral LTR-like element
4087	13087	23764	1.33	2.0E-16	X89211.1	NT	H. sapiens DNA for endogenous retroviral LTR-like element
6846	16526	28720	1.63	2.0E-16	AF139837.1	EST_HUMAN	est7018.45 NCL CQ4P2 Pr12 Homo sapiens cDNA clone IMAGE:120947 similar to TR-051849 054849 HYPOTHETICAL 0.9 Kbp transforming gene protein (PTTG) gene, complete cds
178	10149	19926	2.86	1.0E-16	AF200719.1	NT	Homo sapiens piliary tumor transforming gene protein (PTTG) gene, complete cds
371	10361		22.41	1.0E-16	AA62592.1	EST_HUMAN	af0711.41 Soares, Jellis, NHT, 253478, 546 Homo sapiens cDNA clone IMAGE:104004.3' similar to contains OFR 12 OFR repetitive element;
1826	11823	21704	2.41	1.0E-16	BF370462.1	EST_HUMAN	C10-1000 (40-0700-205-s10 BND146 Homo sapiens cDNA
3877	15783		23.72	1.0E-16	U45883.1	NT	Homo sapiens C23B8 chondrin receptor (CHKB8) gene, complete cds
5800	15886	28697	2.61	1.0E-16	Q02779	SWISSPROT	MITOCHONDIALLY ACTIVATED PROTEIN KINASE KINASE 2 (MINK2) (PROTEIN KINASE MS1)
6458	15783		0.39	1.0E-16	U45883.1	NT	Homo sapiens C23B8 chondrin receptor (CHKB8) gene, complete cds
7349	17217	27416	1.31	1.0E-16	AF187555.1	EST_HUMAN	C10-1000 (40-0700-205-s10 BND146 Homo sapiens cDNA
3878	15888	23379	2.84	9.0E-17	AF190048.1	EST_HUMAN	C10-1000 (40-0700-205-s10 BND146 Homo sapiens cDNA
6095	15938		2.02	9.0E-17	AF187555.1	EST_HUMAN	g0221.141 NCL CQ4P2 Pr12 Homo sapiens cDNA clone IMAGE:210624.3' similar to contains MER28.2 MER28 repetitive element;
6720	16000		4.87	9.0E-17	AF150257.1	EST_HUMAN	af04712.1 NCL CQ4P2 Pr12 Homo sapiens cDNA clone IMAGE:260960.3' similar to contains OFR 12 OFR repetitive element;

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7870	17726		2.18	6.0E-17	AF200719.1	NT	Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds
1001	10919		1.7	8.0E-17	AF680791.1	EST_HUMAN	Q10-OT0032-080300-155-401 OT0032 Homo sapiens cDNA
3817	13728		0.87	8.0E-17	AL193863.2	NT	Homo sapiens chromosome 21 segment H821C080
5427	15444	25402	3.58	8.0E-17	BE170981.1	EST_HUMAN	MRCH10650-060300-003-404 H10350 Homo sapiens cDNA
6311	16174		1.30	8.0E-17	AY730759.1	EST_HUMAN	AV730759 HTF Homo sapiens cDNA clone HTFAQ807.5
1442	11347		3.18	7.0E-17	6753097	NT	Manuscript: apolipoprotein B editing complex 2 (apoBc2), mRNA
5282	15194		3.05	7.0E-17	AF216953.1	NT	Homo sapiens putative NTAP (NTAP) mRNA, partial cds, alternatively spliced
6017	15921	20052	6.88	7.0E-17	AF229843.1	NT	Mus musculus WNT-2 gene, partial cds; putative erythropoietin-related protein and cyclic furanose transmembrane complex regulator (CFTR) gene, section 1 of 2 of the complete cds; and unknown gene
198	10108	15986	4.78	6.0E-17	AF068880.1	EST_HUMAN	BC1-HM003-220300-021-304 HN003 Homo sapiens cDNA
5812	15717	26830	1.91	6.0E-17	AY062772.1	EST_HUMAN	h81604.x1 Soares, NF1_T_OBC_S1 Homo sapiens cDNA clone IMAGE:2076865 3' similar to contains 1.12
415	9682	15773	2.31	5.0E-17	764101.1	EST_HUMAN	L11 repetitive element 1
6478	16335	26502	2.07	5.0E-17	781043.1	EST_HUMAN	720908-1 Straddling lung (8637210) Homo sapiens cDNA clone IMAGE:76335 5'
8783	18598	28887	2.12	4.0E-17	AL163247.2	NT	Y20804.1 Soares, fetal liver, spleen, thymus, testis, heart, brain, placenta, cDNA clone IMAGE:108327 5'
9171	18814		1.98	4.0E-17	AI073546.1	EST_HUMAN	045504.x1 Soares, testis, heart, thymus, spleen, thymus, testis, heart, brain, placenta, cDNA clone IMAGE:164238 3' similar to TR-Q16530
2051	11941	21836	1.35	3.0E-17	AY119123.1	EST_HUMAN	Q16530 PMS3 mRNA, contains MER10.2, MER10 repeats element
3157	13062		1.31	3.0E-17	P35410	SWISSPROT	X89505.x1 Soares, NF1_T_OBC_S1 Homo sapiens cDNA clone IMAGE:2504764 3'
3550	13504	23293	1.14	3.0E-17	BE326522.1	EST_HUMAN	W85004.x1 NC1 CGAP_L124 Homo sapiens cDNA clone IMAGE:3181569 3'
3550	13504	23294	1.14	3.0E-17	BE326522.1	EST_HUMAN	hW5004.x1 NC1 CGAP_L124 Homo sapiens cDNA clone IMAGE:3181569 3'
7554	17445	27690	4.72	3.0E-17	AB028888.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
9134	18650		3.15	3.0E-17	114170951	EST_HUMAN	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
5905	15386		15.82	3.0E-17	AV720324.1	EST_HUMAN	AV720324 GLC Homo sapiens cDNA clone GLCIDF08 5'
350	10309	20127	2.81	2.0E-17	AL270060.1	EST_HUMAN	q65a06.x1 NC1 CGAP_Enc2 Homo sapiens cDNA clone IMAGE:1959922 3' similar to contains ALU repetitive element
351	13009	20127	2	2.0E-17	AL270060.1	EST_HUMAN	q65a06.x1 NC1 CGAP_Enc2 Homo sapiens cDNA clone IMAGE:1959922 3' similar to contains ALU repetitive element
672	10968		1.27	2.0E-17	AA172593.1	EST_HUMAN	2581d04.x1 Soares, fetal heart, NHH1919 Homo sapiens cDNA clone IMAGE:369781 3'
2397	12275	22170	2.6	2.0E-17	Q28883	SWISSPROT	ZONADHESIN PRECURSOR
2397	12275	22171	2.6	2.0E-17	Q28883	SWISSPROT	ZONADHESIN PRECURSOR

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9636	10305	20121	5.73	7.0E-18	AW316976.1	EST_HUMAN	xt1004.x1 NCL CGAP_Pant Homo sapiens cDNA clone IMAGE:2837071 3' similar to gblD2688 60S
9638	10305	20122	5.73	7.0E-18	AW316976.1	EST_HUMAN	RIBOSOMAL PROTEIN L4 (HUMAN);
3255	13178	22976	1.16	6.0E-18	X71791.2	NT	xt1004.x1 NCL CGAP_Pant Homo sapiens cDNA clone IMAGE:2837071 3' similar to gblD2688 60S
4841	14529		3.37	6.0E-18	P32181	SWISSPROT	Ribosomal protein L4 (HUMAN); RIBOSOMAL PROTEIN L4 (HUMAN); Ratios nonreducing partial GlnPhe-1 gene for glia-derived neurotrophin neuron 1 enhancer region (TGASE C) (TGC)
6799	16678		2.69	6.0E-18	11428135	NT	Homo sapiens similar to high-mobility group (nucleosome chromosomal) protein 4 (H. sapiens) (LOC23446), mRNA
8470	18349	28914	1.75	3.0E-18	AL16326.2	NT	Homo sapiens chromosome 21 segment HS21C048
8642	18506	28794	1.78	6.0E-18	X97344.1	NT	H. sapiens DNA, DN6, HLA-21, PP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
9594	19552	25303	3.95	5.0E-18	U87828.1	NT	Human acyl-CoA oxidase 2 (ACOX2) gene, exon 4
1130	11044	20899	14.74	5.0E-18	A129274.1	EST_HUMAN	sim5g1.1 x1 Soares, glycemia, Schweska, 2NH-P6c6W Homo sapiens cDNA clone IMAGE:186368 3'
4217	14115	23893	0.92	5.0E-18	1094665	NT	muscle myosin heavy chain 11 (Myh11) mRNA
5058	14628	24700	1.76	5.0E-18	D81517.1	EST_HUMAN	muscle myosin heavy chain 11 (Myh11) mRNA
5224	15147	24914	1.38	5.0E-18	AF087913.1	NT	Human endogenous telomerase hERV-P-1.7D
7007	16939	27128	4.28	5.0E-18	BE14312.1	EST_HUMAN	MRD-H10161/22109-022-038 H10161 Homo sapiens cDNA
8345	18223	28474	4.33	5.0E-18	10242378	NT	Homo sapiens lymphocyte activation-associated protein (LOC51088), mRNA
8345	18223	28475	4.33	5.0E-18	10242378	NT	Homo sapiens lymphocyte activation-associated protein (LOC51088), mRNA
9512	19125		5.3	5.0E-18	AW807192.1	EST_HUMAN	MR1-SN06035-06040-001-g11 SN06035 Homo sapiens cDNA
9837	19339		13	5.0E-18	AW60547.1	EST_HUMAN	AV650347 GLC Homo sapiens cDNA clone GLC00A02 3'
119	10098	19915	1.39	4.0E-18	BC044076.1	EST_HUMAN	h39804.x1 NCL CGAP_UH Homo sapiens cDNA clone IMAGE:3039511 3' similar to contains MER29.b3
119	10098	19916	1.39	4.0E-18	BC044076.1	EST_HUMAN	h39804.x1 NCL CGAP_UH Homo sapiens cDNA clone IMAGE:3039511 3' similar to contains MER29.b3
1845	11742		1.06	4.0E-18	A1738592.1	EST_HUMAN	h39804.x1 NCL CGAP_UH Homo sapiens cDNA clone IMAGE:3039511 3' similar to contains MER29.b3
2154	12042	21940	0.96	4.0E-18	Q09430	SWISSPROT	N-Acetylgalactosaminide beta-1,6-N-acetylglucosaminyl transferase (N-Acetylgalactosaminyl transferase) (BRANCHING ENZYME) (IGIT)
2154	12042	21941	0.96	4.0E-18	Q09430	SWISSPROT	N-Acetylgalactosaminide beta-1,6-N-acetylglucosaminyl transferase (N-Acetylgalactosaminyl transferase) (BRANCHING ENZYME) (IGIT)
5203	13214	23014	2.55	4.0E-18	A1017565.1	EST_HUMAN	h39804.x1 NCL CGAP_UH Homo sapiens cDNA clone IMAGE:3039511 3' similar to contains MER29.b3

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6293	18214	26016	2.65	4.0E-18/0.7685.1	EST_HUMAN	EST_HUMAN	cd22603.1 Scores: NFI_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627138.3 ES193533 Pituitary gland, subadult (prolactin/growth hormone) Homo sapiens cDNA 5' end similar to EST containing O family repeat
8370	18247	28498	7.12	4.0E-18/0.517807.1	EST_HUMAN	EST_HUMAN	cd22603.1 Scores: NFI_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627138.3 ES193533 Pituitary gland, subadult (prolactin/growth hormone) Homo sapiens cDNA 5' end similar to EST containing O family repeat
831	10768	20609	2.38	3.0E-18/0.481406.1	EST_HUMAN	EST_HUMAN	cd22603.1 Scores: NFI_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627138.3 ES193533 Pituitary gland, subadult (prolactin/growth hormone) Homo sapiens cDNA 5' end similar to EST containing O family repeat
914	10839	20686	2.41	3.0E-18/0.481406.1	EST_HUMAN	EST_HUMAN	cd22603.1 Scores: NFI_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627138.3 ES193533 Pituitary gland, subadult (prolactin/growth hormone) Homo sapiens cDNA 5' end similar to EST containing O family repeat
3897	13778	23871	1.19	3.0E-18/0.163247.2	NT	NT	cd22603.1 Scores: NFI_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627138.3 ES193533 Pituitary gland, subadult (prolactin/growth hormone) Homo sapiens cDNA 5' end similar to EST containing O family repeat
6084	16029	26169	5.2	3.0E-18/0.601071.1	EST_HUMAN	EST_HUMAN	cd22603.1 Scores: NFI_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627138.3 ES193533 Pituitary gland, subadult (prolactin/growth hormone) Homo sapiens cDNA 5' end similar to EST containing O family repeat
6642	19210		4.92	3.0E-18/0.601071.1	EST_HUMAN	EST_HUMAN	cd22603.1 Scores: NFI_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627138.3 ES193533 Pituitary gland, subadult (prolactin/growth hormone) Homo sapiens cDNA 5' end similar to EST containing O family repeat
281	10217	20634	2.83	2.0E-18/0.638820.1	EST_HUMAN	EST_HUMAN	cd22603.1 Scores: NFI_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627138.3 ES193533 Pituitary gland, subadult (prolactin/growth hormone) Homo sapiens cDNA 5' end similar to EST containing O family repeat
1135	11049		47.22	2.0E-18/0.656097.1	EST_HUMAN	EST_HUMAN	cd22603.1 Scores: NFI_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627138.3 ES193533 Pituitary gland, subadult (prolactin/growth hormone) Homo sapiens cDNA 5' end similar to EST containing O family repeat
5327	15242		9.2	2.0E-18/0.688810.1	EST_HUMAN	EST_HUMAN	cd22603.1 Scores: NFI_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627138.3 ES193533 Pituitary gland, subadult (prolactin/growth hormone) Homo sapiens cDNA 5' end similar to EST containing O family repeat
5390	15299	25149	9.04	2.0E-18/0.14547.1	NT	NT	cd22603.1 Scores: NFI_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627138.3 ES193533 Pituitary gland, subadult (prolactin/growth hormone) Homo sapiens cDNA 5' end similar to EST containing O family repeat
5386	15299	25150	3.04	2.0E-18/0.14547.1	NT	NT	cd22603.1 Scores: NFI_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627138.3 ES193533 Pituitary gland, subadult (prolactin/growth hormone) Homo sapiens cDNA 5' end similar to EST containing O family repeat
5585	15500		1.07	2.0E-18/0.47229.1	EST_HUMAN	EST_HUMAN	cd22603.1 Scores: NFI_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627138.3 ES193533 Pituitary gland, subadult (prolactin/growth hormone) Homo sapiens cDNA 5' end similar to EST containing O family repeat
5814	15720	25934	3.83	2.0E-18/0.605853.1	EST_HUMAN	EST_HUMAN	cd22603.1 Scores: NFI_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627138.3 ES193533 Pituitary gland, subadult (prolactin/growth hormone) Homo sapiens cDNA 5' end similar to EST containing O family repeat
7779	17629	27801	1.53	2.0E-18/0.151673.1	EST_HUMAN	EST_HUMAN	cd22603.1 Scores: NFI_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627138.3 ES193533 Pituitary gland, subadult (prolactin/growth hormone) Homo sapiens cDNA 5' end similar to EST containing O family repeat
7779	17629	27862	1.53	2.0E-18/0.151673.1	EST_HUMAN	EST_HUMAN	cd22603.1 Scores: NFI_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627138.3 ES193533 Pituitary gland, subadult (prolactin/growth hormone) Homo sapiens cDNA 5' end similar to EST containing O family repeat
8340	18217	28409	5.32	2.0E-18/0.470791.1	EST_HUMAN	EST_HUMAN	cd22603.1 Scores: NFI_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627138.3 ES193533 Pituitary gland, subadult (prolactin/growth hormone) Homo sapiens cDNA 5' end similar to EST containing O family repeat
8089	18774	28065	4.44	2.0E-18/0.151299.1	EST_HUMAN	EST_HUMAN	cd22603.1 Scores: NFI_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627138.3 ES193533 Pituitary gland, subadult (prolactin/growth hormone) Homo sapiens cDNA 5' end similar to EST containing O family repeat
9325	11049		3.15	2.0E-18/0.625097.1	EST_HUMAN	EST_HUMAN	cd22603.1 Scores: NFI_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627138.3 ES193533 Pituitary gland, subadult (prolactin/growth hormone) Homo sapiens cDNA 5' end similar to EST containing O family repeat
4318	14215	24885	1.02	1.0E-18/0.735403.1	EST_HUMAN	EST_HUMAN	cd22603.1 Scores: NFI_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627138.3 ES193533 Pituitary gland, subadult (prolactin/growth hormone) Homo sapiens cDNA 5' end similar to EST containing O family repeat
6295	18238	28885	2.38	1.0E-18/0.685403.1	EST_HUMAN	EST_HUMAN	cd22603.1 Scores: NFI_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627138.3 ES193533 Pituitary gland, subadult (prolactin/growth hormone) Homo sapiens cDNA 5' end similar to EST containing O family repeat
8419	18340	28934	1.97	1.0E-18/0.00098.1	NT	NT	cd22603.1 Scores: NFI_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627138.3 ES193533 Pituitary gland, subadult (prolactin/growth hormone) Homo sapiens cDNA 5' end similar to EST containing O family repeat
8419	18340	28935	1.97	1.0E-18/0.00098.1	NT	NT	cd22603.1 Scores: NFI_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627138.3 ES193533 Pituitary gland, subadult (prolactin/growth hormone) Homo sapiens cDNA 5' end similar to EST containing O family repeat
8883	18190	28912	1.32	1.0E-18/0.163268.2	NT	NT	cd22603.1 Scores: NFI_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627138.3 ES193533 Pituitary gland, subadult (prolactin/growth hormone) Homo sapiens cDNA 5' end similar to EST containing O family repeat

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7695	17546	27769	4.4	1.0E-18	U91328.1	NT	Human hercillian/hemochromatosis region, histone 2A-like protein gene, hercillian/hemochromatosis (HLA-H) gene, RoRRA gene, and sodium phosphate transporter (NPT3) gene, complete cds
9277	18980	28924	2.63	1.0E-18	AF035261.1	NT	Human sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
533	10476	20289	4.28	9.0E-19	AA328196.1	EST_HUMAN	MER19 repetitive element ; MER19 repetitive element ;
534	10476	20289	3.19	9.0E-19	AA328196.1	EST_HUMAN	MER19 repetitive element ;
6894	15464		5.21	9.0E-19	F06988.1	EST_HUMAN	HSC23F0681 normalized infant brain cDNA Homo sapiens cDNA clone c-23105
7042	18919	27110	2.46	9.0E-19	AL183203.2	NT	Homo sapiens chromosome 21 segment H8210003
7042	18919	27111	2.46	9.0E-19	AL183203.2	NT	Homo sapiens chromosome 21 segment H8210003
8470	18343	25803	3.88	9.0E-19	AB023961.1	NT	Homo sapiens mRNA for KIAA1143 protein, partial cds
9042	10475	20289	8.80	9.0E-19	AA328196.1	EST_HUMAN	MER19 repetitive element ;
1032	10950		1.54	9.0E-19	AW374602.1	EST_HUMAN	MER19 repetitive element ;
2198	12085	21987	1.58	7.0E-19	4758139	NT	Homo sapiens DEAD/DAH (Aap-Glu-Ala-Asp) box polypeptide 6 (RNA helicase, 6kD) (DDX6) mRNA
5894	16791	25913	2.18	7.0E-19	AF520563.1	NT	Scylla rostrata cp181 mRNA, partial cds
9179	19742		2.98	7.0E-19	AA705684.1	EST_HUMAN	X60061.31 Source: GenBank; Acc: X60061.31
3713	13828		1.02	6.0E-19	AW853600.1	EST_HUMAN	PM-C0248-131059-001-g01 C0248 Homo sapiens cDNA
4360	14256	24041	1.36	6.0E-19	F34986	SWISSPROT	OLFACTORY RECEPTOR 6 (N60)
4360	14256	24042	1.36	6.0E-19	F34986	SWISSPROT	OLFACTORY RECEPTOR 6 (N60)
4894	14580		1.16	6.0E-19	AI271735.1	NT	Homo sapiens X4 pseudocatalase region, segment 1/2
4952	14829	24595	1.09	6.0E-19	AI120817.1	EST_HUMAN	DKFZ762F162.11762 (eponym: hms2) Homo sapiens cDNA clone DKFZ762F162.5
5571	15498	25692	5.24	6.0E-19	Q00193	SWISSPROT	ZONA PELLUCIDA SPERM-BINDING PROTEIN B PRECURSOR (ZONA PELLUCIDA GLYCOPROTEIN 2P-X) (R095)
5824	18937	28921	7.19	6.0E-19	AW189726.1	EST_HUMAN	X87402.41 Source: NFI_L_GBC_S1 Homo sapiens cDNA clone IMAGE:2694171.3 similar to contig element M8R1 repetitive element ;
9849	19495		1.52	6.0E-19	U69060.1	NT	Human germline T-cell receptor beta chain TCORBV1351, TCORBV659A21, TCORBV659A3N21, TCORBV1350A21, TCORBV659P, TCORBV653A21, TCORBV1358P, TCORBV653A1N1, TCORBV652, TCORBV659A21, TCORBV653P, TCORBV1354, TCORBV652A1N1, TCORBV654A21, TCORBV654A1, TCORBV2351A21, TCORBV12
542	10483	20293	1.45	4.0E-19	AE007970.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript UAA0801
2949	12516	22406	1.39	4.0E-19	BF597362.1	EST_HUMAN	60213010101 NFI_MGC_56 Homo sapiens cDNA clone IMAGE:4287674.5

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3776	13690	23475	1.74	3.0E-19	Q28897	SWISSPROT	RET-2 ADRENERGIC RECEPTOR
3778	13690	23476	1.74	3.0E-19	Q28897	SWISSPROT	RET-2 ADRENERGIC RECEPTOR
4345	14242	24024	1.18	3.0E-19	A1708136.1	EST_HUMAN	AY081583 Homo sapiens cDNA clone ACDAA11.9'
6370	16232		2.47	3.0E-19	11432214	NT	Human cDNA similar to adic-1-like reductase family 1, member B11 (adose reductase-like) (H. sapiens) (LOC33222), mRNA
7443	16456	28645	1.23	3.0E-19	Q89693.1	NT	Mus musculus protein 1 protein (P8) mRNA, complete cds
6416	19068		7.38	3.0E-19	AF65201.1	NT	Homo sapiens chromosom 21 segment H521C060
2513	12387	22719	17.57	2.0E-19	AL163201.2	NT	Homo sapiens chromosome 21 segment H521C060
6548	16728	26923	8.96	2.0E-19	AA012854.1	EST_HUMAN	BC346501.1 Soares ratina N264R Homo sapiens cDNA clone IMAGE:361880.6'
473	10417		1.6	1.0E-19	BE08811.1	EST_HUMAN	BC130472F1.NH.MGC.21 Homo sapiens cDNA clone IMAGE:363810.6'
2118	12007	21906		1.4	1.0E-19	H30765.1	Y079007.1 Homo sapiens adult brain N26-RB557 Homo sapiens cDNA clone IMAGE:184188.5 similar to contains MER10 repetitive element:
2855	12550		2.88	1.0E-19	D38044.1	NT	Human gene for Ahr-receptor, exon 7-9
2817	12746		5.03	1.0E-19	4758077	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
3355	13274	23075	1.27	1.0E-19	AA831967.1	EST_HUMAN	448012.1 Soares, beta1.NH.T Homo sapiens cDNA clone IMAGE:1393831.3 similar to contains MER37.2
5701	15909	25711	2.37	1.0E-19	U12186.1	NT	MER37 repetitive element:
6519	16797	26960	1.79	1.0E-19	M54657.1	NT	Oryzotilus curticulus sodium/dicarboxylate cotransporter mRNA, partial cds
							Rabbit phospholipase kinase beta subunit mRNA, complete cds
							Wt7302.1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:123248.6 similar to contains OFR repetitive element:
7076	16953		2.83	1.0E-19	T06020.1	EST_HUMAN	RC3-ST0174-101009-031-505 ST0174 Homo sapiens cDNA
7853	17703	27848	26.21	1.0E-19	AW012259.1	EST_HUMAN	W34505.1 Soares melanocyte 2N6HM Homo sapiens cDNA clone IMAGE:272872.6'
7857	17707	27853	1.79	1.0E-19	NA4831.1	EST_HUMAN	Mus musculus keratin-associated protein 8-1 (Krtap8-1), mRNA
6005	13910	26035	2.22	8.0E-20	7657296	NT	Mus musculus keratin-associated protein 8-1 (Krtap8-1), mRNA
6005	13910	26035	2.22	8.0E-20	7657296	NT	Mus musculus keratin-associated protein 8-1 (Krtap8-1), mRNA
6439	16300	26462	1.31	8.0E-20	A121371.1	EST_HUMAN	q98003.1 Soares, NHL.T. GBC.S1 Homo sapiens cDNA clone IMAGE:1842086.3'
6439	16300	26463	1.31	8.0E-20	A121371.1	EST_HUMAN	q98003.1 Soares, NHL.T. GBC.S1 Homo sapiens cDNA clone IMAGE:1842086.3'
3238	13181	22601	0.88	7.0E-20	BF326454.1	EST_HUMAN	PM-AN0096-030500-003-adj AN0096 Homo sapiens cDNA
6176	15133	24852	5.53	7.0E-20	AL18128.1	EST_HUMAN	DK172647.D092.1.1 547 (synonym: ltr1) Homo sapiens cDNA clone DKFZ557D092.6
							W4824.1 NCI COAP P14 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER23.b2
							MER23 repetitive element:
6947	18825	27018	10.99	7.0E-20	AA457857.1	EST_HUMAN	W4824.1 NCI COAP P14 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER23.b2
6947	18825	27019	10.99	7.0E-20	AA457857.1	EST_HUMAN	MER23 repetitive element:
8052	18759		10.45	7.0E-20	6912633	NT	Homo sapiens ribosomal protein, 13a (RP.13A), mRNA
3508	13424	23227	3.85	8.0E-20	P39188	SWISSPROT	ALU SURFAMILY Y SEQUENCE CONTAMINATION WARNING ENTRY

Table 4

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Probe SEQ ID NO.	Exon NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
4175	14075	23830	2.55	0.0E-20	BE622434.1	EST_HUMAN	3014411321 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916231.5'
4481	14385		1.17	5.0E-20	AV17523.1	EST_HUMAN	AV1752323 HTC Homo sapiens cDNA clone H1GTA001.5'
6634	16514	26704	4.66	5.0E-20	W10025.1	EST_HUMAN	3078408.41 Sources: fetal_liver, spleen, INFLS_S1 Homo sapiens cDNA clone IMAGE:418191.3' similar to contains MER30411 MER20. repetitive element.
6934	16514	26705	4.66	5.0E-20	W10025.1	EST_HUMAN	3078408.41 Sources: fetal_liver, spleen, INFLS_S1 Homo sapiens cDNA clone IMAGE:418191.3' similar to contains MER30411 MER20. repetitive element.
7128	17005	27197	1.44	5.0E-20	AB028174.1	EST_HUMAN	3078408.41 Sources: fetal_liver, spleen, INFLS_S1 Homo sapiens cDNA clone IMAGE:418191.3' similar to contains MER30411 MER20. repetitive element.
7128	17005	27198	1.44	5.0E-20	AB028174.1	NT	3078408.41 Sources: fetal_liver, spleen, INFLS_S1 Homo sapiens cDNA clone IMAGE:418191.3' similar to contains MER30411 MER20. repetitive element.
6824	18504		6.03	4.0E-20	AB74352.1	EST_HUMAN	3078408.41 Sources: fetal_liver, spleen, INFLS_S1 Homo sapiens cDNA clone IMAGE:418191.3' similar to contains MER30411 MER20. repetitive element.
7695	17845	29037	1.17	4.0E-20	AW132408.1	EST_HUMAN	3078408.41 Sources: fetal_liver, spleen, INFLS_S1 Homo sapiens cDNA clone IMAGE:418191.3' similar to contains MER30411 MER20. repetitive element.
2032	11881	21876	1.04	3.0E-20	U03883.1	EST_HUMAN	3078408.41 Sources: fetal_liver, spleen, INFLS_S1 Homo sapiens cDNA clone IMAGE:418191.3' similar to contains MER30411 MER20. repetitive element.
4115	14015	23766	1.69	3.0E-20	P23273	SWISSPROT	Human E2P27 gene
4324	14417	24201	0.86	3.0E-20	AA037618.1	EST_HUMAN	CLACTORY RECEPTOR-LIKE PROTEIN 1H4
7112	17049		3.20	3.0E-20	D14517.1	NT	263001221 Sources: pregnant_uterus, NBHPU Homo sapiens cDNA clone IMAGE:484895.3' similar to contains 1.15.1.1 repetitive element
8955	17946		2.08	3.0E-20	P11399	SWISSPROT	Human DNA, SINE repetitive element
9195	18929	25832	5.37	3.0E-20	BE586422.1	EST_HUMAN	RETROVIRUS-RELATED POLYPROTEIN (CONTAINS: REVERSE TRANSCRIPTASE)
813	10741		4.52	2.0E-20	AW30988.1	EST_HUMAN	001811801 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:391622.5'
1095	11011	20852	2.03	2.0E-20	AA516335.1	EST_HUMAN	x224e10.x1 NCI_GGAP_U4 Homo sapiens cDNA clone IMAGE:2781098.3' similar to SW.RS5_MOUSE
1095	11011	20853	2.03	2.0E-20	AA516335.1	EST_HUMAN	P97461.40S REBOSOMAL PROTEIN S5. ;
2786	10741	24625	2.72	2.0E-20	AW30688.1	EST_HUMAN	0069009.31 NCI_GGAP_L1p2 Homo sapiens cDNA clone IMAGE:340097 similar to TR.G1224066
4695	14746	24625	4.32	2.0E-20	O28983	SWISSPROT	G1224066 ORF2: FUNCTION UNKNOWN. ;
4695	14746	24626	4.32	2.0E-20	O28983	SWISSPROT	G1224066 ORF2: FUNCTION UNKNOWN. ;
5003	14860		11.36	2.0E-20		NT	0069009.31 NCI_GGAP_L1p2 Homo sapiens cDNA clone IMAGE:340097 similar to TR.G1224066
7301	17177	27376	2.96	2.0E-20	D10083.1	NT	x224e10.x1 NCI_GGAP_U4 Homo sapiens cDNA clone IMAGE:2781098.3' similar to SW.RS5_MOUSE
7301	17177	27379	2.96	2.0E-20	D10083.1	NT	G1224066 ORF2: FUNCTION UNKNOWN. ;
8993	18797	29069	1.99	2.0E-20	AA166755.1	EST_HUMAN	G1224066 ORF2: FUNCTION UNKNOWN. ;

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8093	18797	26090	1.95	2.0E-20	AA169755.1	EST_HUMAN	cd350a.81 NCL CGAP_G081 Homo sapiens cDNA clone IMAGE:1306935 3 similar to contains MER4.02 MER4 repeat element;
9574	18482	26129	1.5	2.0E-20	H5337.1	EST_HUMAN	CHR220310 Chromosome 22 exon Homo sapiens cDNA clone C22_361 5'
1967	12848	21751	5.25	1.0E-20	AA281961.1	EST_HUMAN	ZT1060471 NCL CGAP_G081 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER16.2 MER16 repetitive element;
4338	14235	24018	1	1.0E-20	BF115158.1	EST_HUMAN	h44603.X1 NCL CGAP_G081 Homo sapiens cDNA clone IMAGE:135165 3' similar to contains L112 L1 repetitive element;
7285	17161	27359	2.42	1.0E-20	11418491	NT	Homo sapiens Abdominal Highly Contracted Protein (AHCP) mRNA
8839	16552	26940	2.81	1.0E-20	AF22397.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-40, and partial cds, alternatively spliced
9321	19011		1.84	1.0E-20	AA420463.1	EST_HUMAN	nc0368.f1 NCL CGAP_571 Homo sapiens cDNA clone IMAGE:745694 similar to contains L118 L1 repetitive element;
2853	12910		1.09	9.0E-21	AJ003514.1	EST_HUMAN	AJ003514 Selected chromosome 21 cDNA library Homo sapiens cDNA clone M21p13.3.21
8945	18830		2.35	9.0E-21	AF169180.1	EST_HUMAN	RC3-NN0068-050900-021-403 NN058 Homo sapiens cDNA
7115	16902		1.74	8.0E-21	AF167489.1	EST_HUMAN	B330402.Y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2984714 5' similar to S1/NIAM_HUMAN
8925	18638	28922	3.42	8.0E-21	AA609411.1	EST_HUMAN	069169 NADH-UBIQUINONE OXOREDUCTASE-ASHI SUBUNIT PRECURSOR;
9207	19038		4.02	8.0E-21	Q21330	SWISSPROT	cd7106.f1 NCL CGAP_G081 Homo sapiens cDNA clone IMAGE:133695 3'
2023	19114	21803	2.07	7.0E-21	P11900	SWISSPROT	ATP SYNTHASE A CHAIN (PROTEIN 8)
2023	19114	21804	2.07	7.0E-21	P11900	SWISSPROT	LAMININ BETA-2 CHAIN PRECURSOR (SLAMININ) (LAMININ CHAIN B3)
4191	14061		4.98	7.0E-21	AA045502.1	EST_HUMAN	LAMININ BETA-2 CHAIN PRECURSOR (SLAMININ) (LAMININ CHAIN B3)
5687	16768	20952	1.43	7.0E-21	AJ277557.1	NT	2367ad6.f1 Source_pregnant_uterus_NKHPU Homo sapiens cDNA clone IMAGE:467856 5'
7098	18913	27102	5.84	7.0E-21	Q47418.1	NT	Homo sapiens dNT-2 gene for mitochondrial 5'(P)-deoxyribonucleoside (dNT-2) gene, exons 1-5
						NT	Human chromosomal protein HUG1 related gene
8090	17971	28220	2.94	7.0E-21	AA72404.1	EST_HUMAN	ph-MH4338 VITAMIN K-DEPENDENT PROTEIN 9 PRECURSOR (HUMAN); contains THR.3 OFR repetitive element;
8930	18458	28721	2.97	7.0E-21	7706568	NT	Homo sapiens PTDO17 protein (P1D013), mRNA
4304	19320	23865	0.94	6.0E-21	BE49891.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:363830 5'
907	10831	20578	1.15	5.0E-21	5802031	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type 21 (PTPN22), mRNA
2234	12119	22821	1.08	5.0E-21	AA281904.1	EST_HUMAN	env23403.s1 Scores_NFL2_GBC_S1 Homo sapiens cDNA clone IMAGE:1541908 3' similar to TBC02711 002711 PRO-POLYDIPYRIMIDINE POLYPROTEIN;
4296	14165	23942	2.95	5.0E-21	BE568630.1	EST_HUMAN	60164957.f1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:363886 5'
4696	14582	24375	5.98	5.0E-21	4685474	NT	Homo sapiens melanoma antigen, family C, 1 (MAGEC1), mRNA

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5109	14677		0.95	5.0E-21	D67075.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
1701	11802	21473	1.24	4.0E-21	AA970713.1	EST_HUMAN	h00403.x1 NCL CGAP Kid5 Homo sapiens cDNA clone IMAGE:1573094 3' similar to TRQ16330 Q16330
6105	16000	20138	3.06	4.0E-21	AB010576.1	NT	PKM3 mRNA, contains ORF1.1 ORF repetitive element;
2228	12113	22015	1.09	3.0E-21	AL163201.2	NT	Rattus norvegicus mRNA for rTMA, complete cds
3041	12968	22762	4.04	3.0E-21	ALJ007973.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C031
5749	15957		1.72	3.0E-21	AF146739.1	EST_HUMAN	Homo sapiens LGMD2B gene
9205	15955	23100	4.79	3.0E-21	BF181053.1	EST_HUMAN	h0184445F1 NIH MG2_54 Homo sapiens cDNA clone IMAGE:3054943 5'
7599	17440	27556	1.95	3.0E-21	AV1897760.1	EST_HUMAN	RC1-C710005-10050-016-008 OT10053 Homo sapiens cDNA
6924	18672	24862	1.32	3.0E-21	AL163210.2	NT	CM1-NN0085-280400-203408 NN0083 Homo sapiens cDNA
140	10114		14.75	2.0E-21	BE163247.1	EST_HUMAN	Homo sapiens chromosome 21 segment HST0313
919	10943	20988	0.85	2.0E-21	AB007657.2	NT	DV2-H70435-170300-025-112 H70435 Homo sapiens cDNA
919	10943	20986	0.85	2.0E-21	AB007657.2	NT	Homo sapiens mRNA for KIA0397 protein, partial cds
1190	11108		2.09	2.0E-21	BE304470.1	EST_HUMAN	Homo sapiens mRNA for KIA0397 protein, partial cds
2559	12468	22381	2.89	2.0E-21	Q23893	EST_HUMAN	RC4-B1031T-H189411-A09 B10311 Homo sapiens cDNA
2595	12468	22392	2.89	2.0E-21	Q23893	SWISSPROT	ZONADHESIN PRECURSOR
8370	12920	25126	1.77	2.0E-21	AB24562.1	EST_HUMAN	h39003.x1 NCL CGAP_Pant1 Homo sapiens cDNA clone IMAGE:2230109 3' similar to TRQ66664 Q66664
8373	10748	20644	4.96	2.0E-21	BE14783.1	EST_HUMAN	HYPOXETICAL 51.1 KO PROTEIN ;
7122	10869	27100	3.43	2.0E-21	AF159776.1	EST_HUMAN	QYDH10702-081199-050-g11 H70103 Homo sapiens cDNA
8412	16287		1.98	2.0E-21	BE390127.1	EST_HUMAN	AU190778 PLAC1 Homo sapiens cDNA clone PLACE1005032 3'
8536	19501	28776	1.92	2.0E-21	BE973526.1	EST_HUMAN	h00601.x1 NCL CGAP_K0R13 Homo sapiens cDNA clone IMAGE:3149256 3' similar to contains MER28.33
8536	19501	28777	1.92	2.0E-21	BE973526.1	EST_HUMAN	MER28 repetitive element ;
9425	19072		5.13	2.0E-21	AF170815.1	NT	h01800303F1 NIH MGCC_83 Homo sapiens cDNA clone IMAGE:3851005 5'
1235	11142	20904	1.98	1.0E-21	AA557097.1	EST_HUMAN	h01800303F1 NIH MGCC_83 Homo sapiens cDNA clone IMAGE:3851005 5'
1391	11286		2.46	1.0E-21	AI001264.1	EST_HUMAN	Homo sapiens putative 8-hydroxyguanine DNA glycosylase gene, complete cds
5907	19813		2.43	1.0E-21	AI070752.1	EST_HUMAN	h46d04.x1 NCL CGAP_P44 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER28.32
6299	16134	26298	4.43	1.0E-21	AI223104.1	EST_HUMAN	MER28 repetitive element ;
8021	17871		1.46	1.0E-21	5730038	NT	h68312.x1 Barleaded codon HPL187 Homo sapiens cDNA clone IMAGE:2152343 3'
4312	14209	23993	2.55	9.0E-22	AI020438.1	EST_HUMAN	q947605.x1 Soares, Keith, NHT Homosapiens cDNA clone IMAGE:1838330 3' similar to gbmM54241 QM
							PROTEIN (HUMAN);
							Homo sapiens SET domain and matrin transposase fusion gene (SETMAR) mRNA
							h594603.x1 NCL CGAP_K011 Homo sapiens cDNA clone IMAGE:2296204 3' similar to TRQ15408 Q15408
							NEUTRAL PROTEASE LARGE SUBUNIT ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Emission Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7002	16879	27070	1.26	6.0E-22	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
7002	16879	27071	1.26	9.0E-22	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
8171	18059	28309	3.65	9.0E-22	AF161874.1	EST_HUMAN	AV161874 MDS Homo sapiens cDNA clone MDSOC008 5'
8946	18753	20048	2.62	9.0E-22	AU140359.1	EST_HUMAN	AU140359 PLACE2 Homo sapiens cDNA clone PLACE2000394 5'
8997	18800		2.36	9.0E-22	9760256	NT	Mus musculus TF-1 cell apoptosis related protein-15 (Tfr15), mRNA
933	10568		4.55	8.0E-22	BE144748.1	EST_HUMAN	CMD-HT0179-281068-078-H08 HT0179 Homo sapiens cDNA
6009	16489		3.8	8.0E-22	AA04602.1	EST_HUMAN	2697760-1 Scores, segment, uterus, NHPU Homo sapiens cDNA clone IMAGE-487858 5'
649	10585	20401	4.25	7.0E-22	AL16346.2	NT	Homo sapiens chromosome 21 segment HS21C046
4180	14093	23861	2.32	7.0E-22	Q81638	SWISSPROT	ALPHA-2-MACROGLOBULIN PRECURSOR (ALPHA2M)
4895	14844	24613	1.18	7.0E-22	AB006881.1	SWISSPROT	Homo sapiens gene for actinin receptor type IIB, complete cds
7044	16921		1.34	7.0E-22	AF151064.1	NT	Homo sapiens HSPC220 mRNA, complete cds
7127	17004	27186	2.63	7.0E-22	AF178504.1	NT	EST100758 Fetal brain, Strabismus (catfish)2003 Homo sapiens cDNA clone HBC0617
7538	17398	27589	1.86	7.0E-22	AF09580.1	NT	Homo sapiens cDNA clone HBC0617
6798	14975		1.82	6.0E-22	AF029023.1	EST_HUMAN	w05507.x1 NQ1 CGAP Guest Homo sapiens cDNA clone IMAGE-4095434 5'
6977	15933	25955	2.55	8.0E-22	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
7912	17722	28001	3.97	6.0E-22	U06622.1	NT	Human, myoglobin (HMO) gene, exons 7, 8 and 9, and partial cds
9045	19213		2.03	6.0E-22	BF476511.1	EST_HUMAN	rac27003.x1 NQ1 CGAP P128 Homo sapiens cDNA clone IMAGE3255808 3' similar to contains ALU repetitive element
3584	13488		0.95	4.0E-22	AL271735.1	NT	Homo sapiens A21 pseudocytosine region, segment 1/2
6922	17677		2.71	4.0E-22	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
9105	17995	28244	2.97	4.0E-22	AF161800.1	EST_HUMAN	01602613P1 NHP1 MGC_57 Homo sapiens cDNA clone IMAGE-4095434 5'
9803	19315		1.51	4.0E-22	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C009
943	10868		1.2	3.0E-22	AF468679.1	EST_HUMAN	im4410.x1 NQ1 CGAP Cor4 Homo sapiens cDNA clone IMAGE2158611 3' similar to gbl16593 HIGH AFFINITY INTERLEUKIN-9 RECEPTOR B (HUMAN) contains 1.1x1.1 repetitive element
2523	12397	22988	1.89	3.0E-22	AF056038.1	EST_HUMAN	w05904.x1 NQ1 CGAP P128 Homo sapiens cDNA clone IMAGE2428839 3' similar to SW-AL21_HUMAN
3620	13534		1.49	3.0E-22	D141718.1	NT	Human chromosomal protein HMGP related gene
4095	14581	24374	2.72	3.0E-22	AF060123.1	EST_HUMAN	q02607.x1 Scores, segment, uterus, NHPU Homo sapiens cDNA clone IMAGE-1697560 3' similar to contains MERY12.6 MERY12.6 repetitive element
6793	10672	26964	2.75	3.0E-22	BE060641.1	EST_HUMAN	containing MERY12.6 MERY12.6 repetitive element
1910	11905		2.86	2.0E-22	N21942.1	EST_HUMAN	yc73005.e1 Scores melanocyte 2XRM Homo sapiens cDNA clone IMAGE-267368 3'
7476	12562	22244	1.33	2.0E-22	P24916	SWISSPROT	IMMEDIATE EARLY GENE 13 PROTEIN PRECURSOR
3373	13322	23001	4.09	2.0E-22	8394049	NT	Homo sapiens protein kinase, AMP-activated, gamma 3 non-catalytic subunit (PRKAG3), mRNA
4133	14033	23808	1.26	2.0E-22	AW817794.1	EST_HUMAN	PM1-ST0262-281189-001-1412 S10262 Homo sapiens cDNA

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Probe SEQ ID NO	Exon SEQ ID NO	ORF SEQ ID NO	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
5750	16447	25591	1.44	2.0E-22	W39456.1	EST_HUMAN	z00201.1 Scores: <i>senescence</i> , <i>fibroblasts</i> , <i>NH9SF</i> Homo sapiens cDNA clone IMAGE:322873 5' similar to
5747	15655	25763	3.39	2.0E-22	BF021116.1	EST_HUMAN	g0-X72208 MONOCYTE CHEMOTACTIC PROTEIN 3 PRECURSOR (HUMAN);
7595	17446	27691	1.49	2.0E-22	A127522.1	EST_HUMAN	q10K03.x1 Scores: <i>NH-HNF1A</i> , <i>S1</i> Homo sapiens cDNA clone IMAGE:1878559 3' similar to contains
7540	17460	27710	7.07	2.0E-22	AA715315.1	EST_HUMAN	nt04h11.11 NC1_OGAP_P122 Homo sapiens cDNA clone IMAGE:1219259 3'
7540	17460	27711	7.07	2.0E-22	AA715315.1	EST_HUMAN	nt04h11.11 NC1_OGAP_P122 Homo sapiens cDNA clone IMAGE:1219259 3'
8074	18776	29071	2.04	2.0E-22	AW418690.1	EST_HUMAN	h04h04.x1 NC1_OGAP_K12 Homo sapiens cDNA clone IMAGE:2874655 3'
8078	19304	25201	1.65	2.0E-22	AL16380.2	NT	Homo sapiens chromosome 21 segment HS21C080
1836	11733	21009	1.78	1.0E-22	AV1869517.1	EST_HUMAN	P14-SN0029-010400-009-102 SN0020 Homo sapiens cDNA
2536	12413	22303	2.65	1.0E-22	U16071.1	EST_HUMAN	Human familial Alzheimer's disease (STM2) gene, complete cds
3305	13284	23084	1.74	1.0E-22	U14547.1	NT	Human SINE repetitive element
9533	18411	23659	4.71	1.0E-22	BE004697.1	EST_HUMAN	MR0-ET0659-220300-002-007 BT0659 Homo sapiens cDNA
9533	18411	23659	4.71	1.0E-22	BE004697.1	EST_HUMAN	IL21.M0076-070400-051-F11 LM0076 Homo sapiens cDNA
9533	18411	23659	4.71	1.0E-22	BE004697.1	EST_HUMAN	Gallus gallus Dpb2 protein (Dpb2) mRNA, complete cds
3623	13450	23236	0.84	8.0E-23	AF108349.1	NT	Human fetal liver cDNA library/Homo sapiens cDNA
5241	15165	24935	1.48	8.0E-23	AI133716.1	EST_HUMAN	H42340 Homo sapiens fetal liver cDNA library/Homo sapiens cDNA
9241	15165	24936	1.48	8.0E-23	AI133716.1	EST_HUMAN	H42340 Homo sapiens fetal liver cDNA library/Homo sapiens cDNA
3271	12102	24438	1.45	7.0E-23	AF67246.1	EST_HUMAN	AV43245 (GLG) Homo sapiens cDNA clone GLC017007 3'
4754	14540	24438	1.04	7.0E-23	U062929.1	NT	Homo sapiens DXF21565/004/03 protein (DXF21565/004/03) mRNA
5396	14274	25326	3.91	7.0E-23	AF196333.1	NT	Homo sapiens NC155 (D) intron region 11a protein (NOT55L) mRNA
3357	13305	25797	1.52	6.0E-23	AF162460.2	NT	Rattus norvegicus RNU16 (RNU16) mRNA, complete cds
4171	14071	23946	3.12	6.0E-23	AF162460.2	NT	Homo sapiens chromosome 21 segment HS21C049
5146	18899	25338	1.96	6.0E-23	AF224699.1	NT	Homo sapiens mammoduct, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3
5146	18899	25339	1.96	6.0E-23	AF224699.1	NT	(UBE2D) genes, complete cds
5146	18899	25339	1.96	6.0E-23	AF224699.1	NT	Homo sapiens mammoduct, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3
6941	16021	25297	2.18	6.0E-23	AI209130.1	EST_HUMAN	ag0003.x1 Scores: <i>testis</i> , <i>NHT</i> Homo sapiens cDNA clone IMAGE:1695490 3' similar to
5341	15202	25088	3.51	5.0E-23	U62071.2	NT	SN.MY10 MOUSE P22249 PROTEIN MOV-10. ;
5341	15202	25088	3.51	5.0E-23	U62071.2	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2a), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2b), melanoma antigen family A3 (MAGEA3), cetractin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and J1>
5781	16454	25797	3.51	5.0E-23	AF179818.1	NT	Pongo pygmaeus diacyl receptor (PPY110) gene, partial cds
9387	16454	25797	3.04	5.0E-23	AF179818.1	NT	Pongo pygmaeus diacyl receptor (PPY110) gene, partial cds

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Probe SEQ ID NO.	Exon NO.	Q9F SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6580	16400	20653	3.56	3.0E-23	AA130165.1	EST_HUMAN	233969.1 Scores, pregnant, uterus, NHPPU Homo sapiens cDNA clone IMAGE:503968 5' similar to contains MER29.12 ZF702 repetitive element;
7329	17233	27435	3.61	3.0E-23	Z702654.1	NT	Human endogenous retroviral element HC2
7329	17233	27436	3.61	3.0E-23	Z702654.1	NT	Human endogenous retroviral element HC2
650	10586	20402	4.36	2.0E-23	AJ288890.1	NT	Homo sapiens KIA08051 clone (partial) XTS gene and LZTFL1 gene
1126	12644	26244	2.77	2.0E-23	M5270.1	NT	Human matrix Gla protein (MGP) gene, complete cds
2765	12627	22519	1.06	2.0E-23	P22105	SWISSPROT	TENASIN-X PRECURSOR (TN-X) (HEXABRACHIONLIKE)
2765	12627	22520	1.06	2.0E-23	P22105	SWISSPROT	TENASIN-X PRECURSOR (TN-X) (HEXABRACHIONLIKE)
3325	13245		1.46	2.0E-23	AJ201458.1	EST_HUMAN	973911.1 NCI CGAP P28 Homo sapiens cDNA clone IMAGE:194978 2' similar to TRC13837 Q13837
3655	13569		3.03	2.0E-23	BE16980.1	EST_HUMAN	MRS37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE.;
3804	13804	23589	2.98	2.0E-23	H69511.1	EST_HUMAN	371502.1 Scores fetal liver spleen, INFLS Homo sapiens cDNA clone IMAGE:205418 5'
3804	13804	23590	2.98	2.0E-23	H69511.1	EST_HUMAN	371502.1 Scores fetal liver spleen, INFLS Homo sapiens cDNA clone IMAGE:205418 5'
6595	14775		5.02	2.0E-23	AF26017.1	NT	Homo sapiens cyclochrome P-450 polypeptide 45 (CYP2A45) gene, partial cds
9131	18838		2.05	2.0E-23	M52053.1	NT	Polypeptide 9 (CYP3A7) gene, partial cds
9656	10218		2.47	2.0E-23	AF026680.1	NT	Human alcohol dehydrogenase gamma subunit (ADH3) gene, exon 1
9774	10770		2.02	2.0E-23	AJ133851.1	EST_HUMAN	Homo sapiens 1 cell receptor beta locus, TOR575332 to TOR571252 region
4428	14323	24110	1.03	1.0E-23	AL162552.2	NT	AU133851 OVARC1 Homo sapiens cDNA clone OVARC100046 5'
4557	14543		4.49	1.0E-23	AL162510.2	NT	Homo sapiens chromosome 21 segment HS21C002
6534	15937		2.91	1.0E-23	BE37471.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C010
6595	16744	20637	4.54	1.0E-23	AA448097.1	EST_HUMAN	2362062.1 Scores, testis, NIH Homo sapiens cDNA clone IMAGE:3068693 5'
540	10481		1.88	9.0E-24	AA603213.1	EST_HUMAN	ab75408.31 Stradiolene fetal retina 637202 Homo sapiens cDNA clone IMAGE:352785 3' similar to TRE16822 E16822 CA PROTEIN.;
4549	14442	24225	1.08	8.0E-24	P23269	SWISSPROT	OLFATORY RECEPTOR-LIKE PROTEIN I3
4549	14442	24226	1.08	8.0E-24	P23269	SWISSPROT	OLFATORY RECEPTOR-LIKE PROTEIN I3
3796	13708		1.31	7.0E-24	AW637654.1	EST_HUMAN	Q9V-DT0047-170200-122-405 D10047 Homo sapiens cDNA
690	10623		2.4	9.0E-24	AB001421.1	NT	Musca domestica mRNA for Testis-Specific Protein Y (TSPY), complete cds
820	10748	20895	10.14	6.0E-24	AL162463.2	NT	Homo sapiens chromosome 21 segment HS21C049
3889	13900	23585	7.18	5.0E-24	AJ22043.1	NT	Homo sapiens 689 kb contig between AM1.1 and CBR1 on chromosome 21q22, segment 3/3
5611	15526	25609	3.06	4.0E-24	AA594178.1	EST_HUMAN	m31063.1 NCI CGAP Case1 Homo sapiens cDNA clone IMAGE:1035529 3' similar to SW_POL_MLVYRK P31795 POL POLYPROTEIN.;

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Table 4

Single Exon Probes Expressed In Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9306	19121	26293	2.12	4.0E-24	AB029016.1	NT	Homo sapiens mRNA for KIAA1063 protein, partial cds
9748	19099	26293	1.83	4.0E-24	11418378	NT	Homo sapiens G-2 and S-phase expressed 1 (GISE1), mRNA
6748	16884	27463	3.02	3.0E-24	AW614871.1	EST_HUMAN	IMAGE281 NCI CGAP GU1 Homo sapiens cDNA clone IMAGE281950 3' similar to contains MER28 b2 IMAGE281 repetitive element
7449	17258	27463	4.12	3.0E-24	AL633502.2	NT	Homo sapiens chromosome 21 segment HS2T0682
9387	19171	28273	5.14	3.0E-24	BF127662.1	EST_HUMAN	601610448P1 NIH JGOC 46 Homo sapiens cDNA clone IMAGE4083308 5'
2268	12180	23078	2.33	2.0E-24	AA167839.1	EST_HUMAN	24P1104971 Sra gene full length 1377362 Homo sapiens cDNA clone IMAGE409101 5'
3728	13641	23078	1.01	2.0E-24	AV868189.1	EST_HUMAN	RG3889008-060500-021-463 NM00681 Homo sapiens cDNA
7075	16952	27148	3.14	2.0E-24	AL119158.1	EST_HUMAN	DKFZP611712.1 T1 707 (synonym: Hm1y2) Homo sapiens cDNA clone DKFZP611712 5'
9433	19717	27148	6.55	2.0E-24	U28877.1	NT	Human O family dispersed repeat element
1870	11572	21439	2.18	1.0E-24	7706340	NT	Homo sapiens CGH-127 protein (LOC31646), mRNA
2633	12605	22710	1.87	1.0E-24	AV820194.1	EST_HUMAN	QY6-ST0294-100400-165-210 ST0294 Homo sapiens cDNA
2987	12915	22710	0.91	1.0E-24	D64423.1	NT	Mus musculus mRNA for HCT1 keratin, partial cds
4179	14079	26484	1.63	1.0E-24	AF14313.1	NT	Homo sapiens PTER (PTEN) gene, exon 2
6456	16317	26484	4.07	1.0E-24	AL63303.2	NT	Homo sapiens chromosome 21 segment HS2T0682
6833	16813	26703	1.98	1.0E-24	AW301164.1	EST_HUMAN	QMS-NN1010-130300-281-407 NT1010 Homo sapiens cDNA
4928	14805	24575	2.32	7.0E-25	AA483944.1	EST_HUMAN	re52a10.41 NCI CGAP JKH1 Homo sapiens cDNA clone IMAGE311754 similar to contains MER1 b2 MER1 repetitive element
6785	16864	28855	3.75	7.0E-25	AA469461.1	EST_HUMAN	re52a10.41 NCI CGAP Cox3 Homo sapiens cDNA clone IMAGE380408 3' similar to contains THR b2 THR repetitive element
8642	18750	29045	7.48	7.0E-25	AA935540.1	EST_HUMAN	re2506a.31 NCI CGAP P71 Homo sapiens cDNA clone IMAGE314843 similar to 5W/R144_YEAST
6174	15131	28950	4.32	6.0E-25	W07623.1	EST_HUMAN	P36108 PROBABLE 66S RIBOSOMAL PROTEIN L14EA.1
6943	16401	28950	11.44	6.0E-25	W07623.1	EST_HUMAN	286507.T1 Soares, fetal liver, spleen, INFLS_S1 Homo sapiens cDNA clone IMAGE418869 5'
9186	15032	24799	0.96	8.0E-25	AV838171.1	EST_HUMAN	QV2L110035-290300-111-603 LT0051 Homo sapiens cDNA
8634	18499	28774	3.61	3.0E-25	AV879107.1	EST_HUMAN	EST391217 IMAGE resequences, MACP Homo sapiens cDNA
1430	11335	21201	2.08	4.0E-25	181807.1	EST_HUMAN	re52a10.41 Soares fetal liver, spleen, INFLS Homo sapiens cDNA
3386	13275	21201	2.78	4.0E-25	AV138767.1	EST_HUMAN	PMS-OT1065-200200-001-007 OT10653 Homo sapiens cDNA
4221	14119	22699	3.02	4.0E-25	BE170871.1	EST_HUMAN	QV3-HT10843-10400-148-e11 HT10543 Homo sapiens cDNA
3278	13109	29000	2.86	3.0E-25	8633241	NT	Homo sapiens hypothetical protein FL20344 (FL20344), mRNA
3278	13109	29000	2.86	3.0E-25	P25662	SWISSPROT	Homo sapiens hypothetical protein FL20344 (FL20344), mRNA
4798	14683	24470	0.86	3.0E-25	FL169210.2	SWISSPROT	KALLISTATIN PREGUCISOR (KALLIKREIN INHIBITOR) (PROTEASE INHIBITOR 4)
8854	16733	29526	2.47	3.0E-25	AL169210.2	NT	Homo sapiens chromosome 21 segment HS210010

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar Top Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
1160	11073	20316	3.33	5.0E-26	AF708235.1	EST_HUMAN	si39108.x1 Barasid axilla HPLR86 Homo sapiens cDNA clone IMAGE:2819519.3 similar to WP-F49C12.11 CE0374.1
1160	11073	20319	3.33	5.0E-26	AF708235.1	EST_HUMAN	WP-F49C12.11 CE0374.1
9876	19495		1.71	5.0E-26	AF71429.1	EST_HUMAN	WP5606.F1 Sorensen NIST F8 GW_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:286986.5 similar to contains Alu repetitive element
1526	11430		1.32	4.0E-26	AJ329548.1	EST_HUMAN	EST33446 Embryo, 12 week II Homo sapiens cDNA, 5' end
7416	17283		3.77	4.0E-26	7657670.NT	EST_HUMAN	Homo sapiens testicular binding transcription factor RNA polymerase I (UBTF), mRNA
8033	17944	28104	3.74	4.0E-26	BE268187.1	EST_HUMAN	80119134.F1 NIH IM6C.7 Homo sapiens cDNA clone IMAGE:385610.5
1958	11853	21740	1.5	3.0E-26	AL048895.2	EST_HUMAN	DKFZ4341068.t1.434 (synonym: hsc3) Homo sapiens cDNA, clone DK-FZ434106.5
1987	11880		2.41	3.0E-26	AA115895.1	EST_HUMAN	2550408.1 Strabagene protein NIT29A.M137224 Homo sapiens cDNA clone IMAGE:484948.5 similar to dbM44338 VITAMIN K-DEPENDENT PROTEIN 5 PRECURSOR (HUMAN);
3712	13525	23408	1.19	3.0E-26	AA1152464.1	EST_HUMAN	255010.1 Strabagene protein (957720) Homo sapiens cDNA clone IMAGE:588427.5 similar to TR-G960374
3712	13525	23409	1.19	3.0E-26	AA1152464.1	EST_HUMAN	G96574.1 THYROID RECEPTOR INTERACTOR
8131	15078	28114	4.35	3.0E-26	BF245464.1	EST_HUMAN	255010.1 Strabagene protein (957720) Homo sapiens cDNA clone IMAGE:588427.5 similar to TR-G960374
8108	17668		2.18	3.0E-26	AF326495.1	NT	G96574.1 THYROID RECEPTOR INTERACTOR
8853	18865	28651	1.99	3.0E-26	AW875951.1	EST_HUMAN	Homo sapiens KILL (KILL) gene, clones 133, and partial cds
8853	18865	28652	1.39	3.0E-26	AW875951.1	EST_HUMAN	CV25-10073-30400-124-403 P10012 Homo sapiens cDNA
8879	18901	28694	10.65	3.0E-26	AJ583173.1	EST_HUMAN	CV25-10073-30400-124-403 P10012 Homo sapiens cDNA
6568	10920	20418	5.81	2.0E-26	AF163522.2	NT	miR205.s1 NCL CGAP GC05 Homo sapiens cDNA clone IMAGE:1066057.3 similar to contains OPR1.h OPR1 repetitive element
1825	11722	22524	3.36	2.0E-26	AL163522.2	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C082
3193	13118		4.20	2.0E-26	X66694.1	NT	DKFZ568617.1 s1 588 (synonym: H1625) Homo sapiens cDNA clone DKFZ56861.171.3
8135	18823		2.88	2.0E-26	X66694.1	NT	Mus musculus mRNA for aminoacyl phosphoprotein, PEA-16
8549	18420	26880	4.55	2.0E-26	AB01412.1	EST_HUMAN	Homo sapiens DNA for amyloid precursor protein, complete cds
8720	18537		1.82	2.0E-26	AF163506.1	NT	103801.s1 NCL CGAP GC04 Homo sapiens cDNA clone IMAGE:216816.5 similar to contains Alu repetitive element/contains element MER20 MER20 repetitive element
1252	18862		2.19	2.0E-26	AF163506.1	NT	Homo sapiens MHC class I region
132	10166	19927	2.36	1.0E-26	BE1170371.1	EST_HUMAN	Homo sapiens mRNA for KIAA1439 protein, partial cds
2001	11884	21786	1.39	1.0E-26	AL103963.2	EST_HUMAN	QV4H170538-020309-123-402 HT658 Homo sapiens cDNA
2516	12390	22252	0.84	1.0E-26	BE14695.1	EST_HUMAN	DKFZ4341090.t1.434 (synonym: hsc3) Homo sapiens cDNA clone DKFZ434109.5
2654	12321		16.79	1.0E-26	AF261065.1	NT	MR2-BN0114-2-04000-409-607 BN0114 Homo sapiens cDNA
							Homo sapiens diphosphatidyl-3-phosphate dihydrogenase (GADPH) mRNA, complete cds

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Probe SEQ ID NO.	Exon SEQ ID	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Ht BLAST Value	Top Ht Accession No.	Top Ht Database Source	Top Ht Descriptor
6089	16034		2.76	1.0E-20	AL016980.1	EST_HUMAN	MR3-HT0487-150200-118-401 HT0487 Homo sapiens cDNA
8296	18149		3.17	1.0E-20	BC038487.1	EST_HUMAN	DKFZ565602146.11 5601 (synonym: htk22) Homo sapiens cDNA clone BKF256562.146.5
9483	19737		1.84	1.0E-28	H50933.1	EST_HUMAN	CHF220032 Chromosome 22, cent. Homo sapiens cDNA clone C22_45.5
7364	17342		3.11	9.0E-27	U63163.1	NT	Homo sapiens IMAGE-B2 (IMAGE-B2), IMAGE-B3 (IMAGE-B3), IMAGE-B4 (IMAGE-B4), and IMAGE-B1 (IMAGE-B1) genes, complete cds
8027	19470	28116	3.48	9.0E-27	P54296	SWISSPROT	MYOESIN 2 (M-PROTEIN) (165 KD TITIN-ASSOCIATED PROTEIN) (165 KD CONNECTIN-ASSOCIATED TROPOMYOSIN)
9013	18812		3.97	9.0E-27	BF445556.1	EST_HUMAN	aa0307.v1 NCL CGAP_P128 Homo sapiens cDNA clone IMAGE-2353544.3 similar to contains ORF.H
40	5956	10787	3.09	8.0E-27	AB831462.1	EST_HUMAN	THR repetitive element 1
545	10466		4.13	8.0E-27	AL163227.2	NT	THR repetitive element 1
1395	11300	21158	18.87	8.0E-27	AW162737.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS210227
1395	11300	21159	18.87	8.0E-27	AW162737.1	EST_HUMAN	aa07063.v1 Schneider fetal from 00004 Homo sapiens cDNA clone IMAGE-2763295.5 similar to gb1000658
2121	12069	21909	0.98	8.0E-27	AW854776.1	EST_HUMAN	TUBULIN ALPHA-1 CHAIN (HUMAN)
3148	13073	22874	3.31	8.0E-27	P11226	SWISSPROT	PUB1-SN01616-220300-002-407 SN0167 Homo sapiens cDNA
3309	13220	22035	0.91	8.0E-27	AF181897.1	NT	ADP-ATP CARRIER PROTEIN, LIVER ISOFORM T2 (ADPIATP TRANSLOCASE 3) (ADENINE NUCLEOTIDE TRANSLOCATOR 3) (ANT 3)
6165	15152		3.12	8.0E-27	BE029560.1	EST_HUMAN	Homo sapiens WRN (WRN) gene, complete cds
6166	15956	29068	4	8.0E-27	N64970.1	EST_HUMAN	MR4-BT0368-250800-004-005 BT03038 Homo sapiens cDNA
7310	17180	27368	1.68	8.0E-27	AW651579.1	EST_HUMAN	J1761F Human fetal liver, Lenticla ZAP Expressa Homo sapiens cDNA clone J1761.5 similar to
7310	17180	27367	1.68	8.0E-27	AW651579.1	EST_HUMAN	CM1-GT0315F-091259-003-007 GT0315 Homo sapiens cDNA
668	10922		1.22	7.0E-27	T00854.1	NT	CM1-GT0315F-091259-003-007 GT0315 Homo sapiens cDNA
8023	14856		2.69	7.0E-27	AW629172.1	EST_HUMAN	Homo endogenous retroviral element HC2
5232	18020		4.22	7.0E-27	AZ017155.1	EST_HUMAN	SH6H12.41 Spores NR_1, G50, S1 Homo sapiens cDNA clone IMAGE-2576919.5 similar to TR-O78040
8631	18204		2.07	7.0E-27	AZ123355.1	EST_HUMAN	078040 ORF2, FUNCTION UNKNOWN.1
6169	17559	28246	6.21	6.0E-27	AF230661.1	EST_HUMAN	AV723565 HTB Homo sapiens cDNA clone HTBARE02.5
7677	17727	27970	2.52	5.0E-27	BF068614.1	EST_HUMAN	Human nuclear protein (B23) mRNA, complete cds
7677	17727	27970	2.52	5.0E-27	BF068614.1	EST_HUMAN	00212149P11 NH1.MGC 56 Homo sapiens cDNA clone IMAGE-4278527.5
7677	17727	27971	2.52	5.0E-27	BF068614.1	EST_HUMAN	00212149P11 NH1.MGC 56 Homo sapiens cDNA clone IMAGE-4278527.5
9046	11549	20080	1.54	4.0E-27		NT	Mus musculus sperm tail associated protein (Ssp), mRNA

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Probe SEQ ID NO.	Exon NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hitt BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6659	15538		1.23	4.0E-27	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
6850	18552	28451	2.56	4.0E-27	X60211.1	NT	Hsapiens DNA for endogenous retinoid like element
1965	11850	21752	5.62	3.0E-27	X06058.1	NT	Rattus RY13 mRNA for a potential ligand-binding protein
4174	14074	23849	1.27	3.0E-27	BC071924.1	EST HUMAN	PLOC1D-027-069100-001 cDNA (191827) Homo sapiens cDNA
5278	15200	24976	5.13	3.0E-27	AA071705.1	EST HUMAN	7B44208 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B44208
7355	17343	27549	2.68	3.0E-27	B1935327.1	EST HUMAN	891456331 FT NHX1 NCSC 66 Homo sapiens cDNA clone IMAGE366208 6'
36	10023	19520	7.66	2.0E-27	AF054187.1	NT	Homo sapiens alpha-NAC mRNA, complete cds
							NC150 rat NC1 CGAP_P111 Homo sapiens cDNA clone IMAGE1000659 similar to gbM17899 60S
1953	11749		18.58	2.0E-27	AA556345.1	EST HUMAN	AC100 RBOSOMAL PROTEIN P1 (HUMAN);
3071	12698		10.27	2.0E-27	AV520172.1	EST HUMAN	165112 rat Sorensen, NPL, T, GBC S1 Homo sapiens cDNA clone IMAGE 2876576 3' similar to TR-078040
							070040 ORF2: FUNCTION UNKNOWN.;
3187	13112	22916	1.43	2.0E-27	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds, cfos gene, complete cds; and unknown gene
3187	13112	22917	1.43	2.0E-27	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds, cfos gene, complete cds; and unknown gene
3944	13552	23027	1.09	2.0E-27	AF000358.1	NT	Rattus norvegicus voltage-gated sodium channel mRNA, complete cds
6712	16552	28750	1.3	2.0E-27	AB65947.1	EST HUMAN	428507.1 NC1 CGAP_P111 Homo sapiens cDNA clone IMAGE2423298 3' similar to
							nc09405.1 NC1 CGAP_P111 Homo sapiens cDNA clone IMAGE343757 similar to contains L1181.1
7338	17206		2.3	2.0E-27	AA551597.1	EST HUMAN	EST100738 Fetal brain, Striatum (Cat933205) Homo sapiens cDNA clone HFB07
7338	17618	27847	1.22	2.0E-27	MT6590.1	EST HUMAN	EST100738 Fetal brain, Striatum (Cat933205) Homo sapiens cDNA clone HFB07
7705	17618	27848	1.22	2.0E-27	MT6590.1	EST HUMAN	EST100738 Fetal brain, Striatum (Cat933205) Homo sapiens cDNA clone HFB07
8324	15211	25450	2.89	2.0E-27	AF121086.1	EST HUMAN	AUT121685 MAMMA1 Homo sapiens cDNA clone MAMMA100746 5'
							nc071510.1 NC1 CGAP_P111 Homo sapiens cDNA clone IMAGE1000659 similar to gbM17899 60S
9778	11749		20.82	2.0E-27	AA556345.1	EST HUMAN	AC100 RBOSOMAL PROTEIN P1 (HUMAN);
429	10374		1.56	1.0E-27	AF103246.2	NT	Homo sapiens chromosome 21 segment HS21C046
							Homo sapiens DNA, DLEC1 to ORC1L4 gene region, section 1/2 (DLEC1, ORC1L3, ORC1L4 genes, complete cds)
590	10903	20749	1.41	1.0E-27	AB028888.1	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
5943	15948	25972	6.31	1.0E-27	8009855	NT	HSPD0461 H1G3 Homo sapiens cDNA clone s4000305C10
6105	15959	26136	2.2	1.0E-27	F30168.1	EST HUMAN	HSPD0461 H1G3 Homo sapiens cDNA clone s4000305C10
6105	15959	26137	2.2	1.0E-27	F30168.1	EST HUMAN	Homo sapiens mRNA for KIAA0654 protein, partial cds
7005	16882	27075	1.72	1.0E-27	AB07923.1	NT	RC6-BT0627-140200-01-EX6 BT0627 Homo sapiens cDNA
7194	17071		1.86	1.0E-27	BC070760.1	EST HUMAN	Homo sapiens mRNA for KIAA0230 gene, partial cds
7806	17457	27872	2.68	1.0E-27	DE7449.1	NT	Bos taurus laophillin 3 splice variant b5ash mRNA, complete cds
8943	18751	29046	3.14	1.0E-27	AF111093.1	NT	

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF/SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
136	10109		2.32	9.0E-28	BE34399.1	EST_HUMAN	hw17d1.x1 NCL CGAP_Luc2 Homo sapiens cDNA clone IMAGE:3183168 3' similar to TR-Q07314 Q07314
308	10270	20089	3.01	9.0E-28	AI126200.1	EST_HUMAN	SECRETED NITROSPINALPH-C-RECEPTOR-3; TRC07260 TRC07310
5118	14969	24760	1.21	9.0E-28	AI690115.1	EST_HUMAN	lot 2499.x1 NCL CGAP_U2 Homo sapiens cDNA clone IMAGE:2178903 3' similar to contains OFR.H1 OFR repetitive element 1
5118	14966	24761	1.21	9.0E-28	AI690115.1	EST_HUMAN	lot 2499.x1 NCL CGAP_U2 Homo sapiens cDNA clone IMAGE:2178903 3' similar to contains OFR.H1 OFR repetitive element 1
9093	18895		3.74	8.0E-28	BF37689.1	EST_HUMAN	CH2-17047-070000-372.g01 TN0440 Homo sapiens cDNA
9418	19602		1.97	8.0E-28	AI157574.1	EST_HUMAN	sw6003.x1 Sommerfeld train 00040 Homo sapiens cDNA clone IMAGE:2762911 3' similar to TR-Q06502 Q06502 KIAA0655 PROTEIN, contains element MER22 repetitive element 1
1184	11077	26922	2.54	7.0E-28	AI142750.1	EST_HUMAN	AI142750-17947 Homo sapiens cDNA clone Y79AA1000824 5'
8523	18365	26660	2.54	7.0E-28	AI147886	NT	Homo sapiens gamma-glutamyltransferase-like actin NY1 (GGT1A1), mRNA
6083	18364		1.44	7.0E-28	AI738348.1	EST_HUMAN	AY738348 CB Homo sapiens cDNA clone CBFA2A12 5'
3937	13894	29670	1.27	6.0E-28	AB020673.1	NT	Homo sapiens mRNA for KIAA0695 protein, complete cds
3937	13894	29671	1.27	6.0E-28	AB020673.1	NT	Homo sapiens mRNA for KIAA0695 protein, complete cds
9673	19222		2.73	8.0E-28	AI604662.1	EST_HUMAN	sw6003.x1 NCL CGAP_G081 Homo sapiens cDNA clone IMAGE:8265340 5' similar to contains Alu repetitive element/contains element PTR3 repetitive element 1
315	10277		3.06	5.0E-28	AI92405.1	EST_HUMAN	hw18007.x1 NCL CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2465932 3' similar to contains THR.b1 THR repetitive element 1
3927	13836	23515	1.95	5.0E-28	RY7972.1	EST_HUMAN	sw6003.x1 NCL CGAP_X411 Homo sapiens cDNA clone IMAGE:2095604 3' similar to SW:GG05_HUMAN Q08379 GOLGN-96.1
2564	12455	22347	1.42	4.0E-28	AI196066.1	EST_HUMAN	001300707F NIH MQC_21 Homo sapiens cDNA clone IMAGE:3393305 5'
3070	12457	22768	3.39	4.0E-28	BE409100.1	EST_HUMAN	001300707F NIH MQC_21 Homo sapiens cDNA clone IMAGE:1755019 3' similar to gcbM19603 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN)
6336	16199	26359	1.56	4.0E-28	AI198941.1	EST_HUMAN	001300707F NIH MQC_21 Homo sapiens cDNA clone IMAGE:1755019 3' similar to gcbM19603 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN)
8299	18116		4.26	4.0E-28	AF033038.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and lymphogen gene families
8371	10240		93.0	4.0E-28	AB030241.1	NT	h-rts caltar GAPDH mRNA for glyceraldehyde-3-phosphate dehydrogenase, complete cds
8388	16166	26359	2.94	4.0E-28	AI198941.1	EST_HUMAN	001300707F NIH MQC_21 Homo sapiens cDNA clone IMAGE:1755019 3' similar to gcbM19603 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN)
1202	11186		1.89	3.0E-28	AF15382.1	NT	Homo sapiens metalloprotease-five, disintegrin-like, cysteine-rich protein 2 epsilon (ADAM22) mRNA, complete cds
7124	17001	27193	2.19	3.0E-28	BF356030.1	EST_HUMAN	MR3-H10713-265900-013-003 H10713 Homo sapiens cDNA
8306	18183	26430	1.84	3.0E-28	U63668.1	NT	Homo sapiens MHC class 1 region

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Probe SEQ ID NO.	Exon NO.	ORF SEQ ID NO.	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9489	19109		2.44	3.0E-28	AIK31991.1	EST_HUMAN	MB007.41 NCL CGAP Lym12 Homo sapiens cDNA clone IMAGE:2410885 3' similar to contains Alu repetitive element/containing element BGTG34 Homo sapiens cDNA
83	10097	16884	6.45	2.0E-28	BE062167.1	EST_HUMAN	RC1-UT0254-22000-019-c05 BT0254 Homo sapiens cDNA
11461	11042	20095	10	2.0E-28	Y11107.3	NT	Homo sapiens TGS4 gene for Hsp70 beta 4 subunit, exon 3-41
2427	12304	22200	2.1	2.0E-28	AI34834.1	EST_HUMAN	pc98408.41 NCL CGAP Lys1 Homo sapiens cDNA clone IMAGE:1910483 3' similar to contains L1 b2.L1 repetitive element
8821	15727		4.28	2.0E-28	BT123905.1	EST_HUMAN	801811986F1 NH_MGC_54 Homo sapiens cDNA clone IMAGE:048751 5'
7528	17379		5.66	2.0E-28	AW172805.1	EST_HUMAN	EST354394 IMAGE ressequencing, IMAGE Homo sapiens cDNA
8937	18368	28922	2.27	2.0E-28	AF224699.1	NT	Homo sapiens introns, beta A1, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D) genes, complete cds
1463	11368	21233	2.42	1.0E-28	D89044.1	NT	Human gene for Ahr receptor, exon 7-9
2173	12090	21683	1.55	1.0E-28	BF33328.1	EST_HUMAN	QV1-BT10251-22000-360-503 BT10251 Homo sapiens cDNA
2650	12517	22407	1.03	1.0E-28	AF000955.1	NT	Homo sapiens ubiquitin TPR motif, Y isodrom (UTY) mRNA, alternative transcript 2, complete cds
6937	18437		4.48	1.0E-28	11426883	NT	Homo sapiens similar to ribosomal protein L12 (H. sapiens) (LOC69091), mRNA
6875	18555		3.02	1.0E-28	8622793	NT	Homo sapiens hypothetical protein FLJ110058 (FLJ10988), mRNA
7346	17214	27413	2.63	1.0E-28	AA305744.1	EST_HUMAN	EST1179015 HCC cell line (metastasis to liver in mouse) (l Homo sapiens cDNA 5' and similar to similar to serotinal LTR
7878	17528	27783	8.13	1.0E-28	4758431	NT	Homo sapiens gamma-glutamyltransferase-like activity1 (GGT1A1), mRNA
7878	17528	27794	3.15	1.0E-28	4759431	NT	Homo sapiens gamma-glutamyltransferase-like activity1 (GGT1A1), mRNA
8059	18340		3.95	1.0E-28	AA054182.1	EST_HUMAN	25T601.17 Soares alpha h2b-4HR Homo sapiens cDNA clone IMAGE:380448 5'
8797	18435	24896	1.43	1.0E-28	AL103427.2	NT	Homo sapiens chromosome 21 segment HS21C047
8832	18581		2.8	9.0E-28	AW169987.1	EST_HUMAN	h76640.x1 Soares NHL_T_OBC_S1 Homo sapiens cDNA clone IMAGE:2878295 3'
9355	15169		2.92	8.0E-28	Q00180	SWISSPROT	HYPOTHETICAL GENE 50 PROTEIN
1354	11488	21349	0.91	7.0E-28	AW166447.1	EST_HUMAN	RC1-UT00621 IMAGE ressequencing, IMAGE Homo sapiens cDNA
9442	18410		5.08	7.0E-28	AJ432352.1	NT	Rattus norvegicus mRNA for 45 kDa secretory protein, partial
580	10518	28325	6.52	6.0E-28	AI693748.1	EST_HUMAN	WU89041.x1 NCL CGAP Bm25 Homo sapiens cDNA clone IMAGE:2460985 3' similar to TR-O15475
9353	18028		3.88	6.0E-28	BE04436.1	EST_HUMAN	O15475 UNANIMED HERV-H PROTEIN; contains LTR7.b1 LTR1 repetitive element;
9439	15076		1.96	6.0E-28	BF168097.1	EST_HUMAN	RC3-UT100622-210600-021-c05 UT00621 Homo sapiens cDNA
4628	14807		0.95	5.0E-28	AL163203.2	NT	662184062P1 NH_MGC_42 Homo sapiens cDNA clone IMAGE:4000078 5'
7008	10945		7.61	5.0E-28	AW187541.1	EST_HUMAN	RC3-OT0091-170300-011-c12 OT0091 Homo sapiens cDNA
3104	13119		1.69	4.0E-28	AF12367.1	EST_HUMAN	on1502.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC on1502 random
5896	15568		6.65	4.0E-28	BE16450.1	EST_HUMAN	QV1-BT0471-280300-121-c05 HT0471 Homo sapiens cDNA

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon ID NO.	ORF SEQ ID NO.	Expression Signal	Mean Similar Clust Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7079	10956	27149	4.71	4.0E-29	J04988.1	NT	Human 160 kD heat shock protein gene, complete cds
4317	14214	23997	1.45	3.0E-29	A3042297.1	NT	Human sapiens P15 gene for 6-pyruvate/hydroxycarboxyl synthase, complete cds
4626	14514	24305	1.31	3.0E-29	BF333293.1	EST_HUMAN	QV4-BT0821-126500-300-503 BT0821 Homo sapiens cDNA
7070	19547	27138	2.07	3.0E-29	D38044.1	NT	Human gene for Ah receptor, exon 2-9
7392	17229	27429	1.6	3.0E-29	AW30317.1	EST_HUMAN	wt703.x1 Soares, NFL_T_GBC, S1 Homo sapiens cDNA clone IMAGE:2613403 3' similar to contains AU repetitive di-nucleotide MER19.12 MER19 repetitive element;
7492	17392		1.64	3.0E-29	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C046
8591	18459	28728	2.22	3.0E-29	AA40393.1	EST_HUMAN	af5241.1 Soares, NFL_T_GBC, S1 Homo sapiens cDNA clone IMAGE:726869 5' similar to TR.G153769
9248	18659		1.51	3.0E-29	D63892.1	NT	Human HALLM15 mRNA for HALM15, complete cds
484	10427	20240	1.43	2.0E-29	A7604699.1	NT	Homo sapiens envelope protein RC-8 (env) gene, complete cds
484	10427	20241	1.43	2.0E-29	A7604699.1	NT	Homo sapiens envelope protein RC-8 (env) gene, complete cds
1616	11421	21276	8.12	2.0E-29	A1963504.1	EST_HUMAN	wf6610.x1 NCL CGAP, LRT Homo sapiens cDNA clone IMAGE:2492563 3' similar to TR.O15548 O15548
1516	11421	21279	8.12	2.0E-29	A1963504.1	EST_HUMAN	HERV-E ENVELOPE GLYCOPROTEIN;
4182	14082	23555	2.03	2.0E-28	AL163263.2	NT	Homo sapiens chromosome 21 segment HS21C088
5750	15558	25765	1.43	2.0E-29	A1938418.1	EST_HUMAN	wf2707.x1 Soares, NFL_T_GBC, S1 Homo sapiens cDNA clone IMAGE:2356890 3' similar to contains element MER6 repetitive element;
6461	15658	25766	1.43	2.0E-29	A1938418.1	EST_HUMAN	wf2707.x1 Soares, NFL_T_GBC, S1 Homo sapiens cDNA clone IMAGE:2356890 3' similar to contains element MER6 repetitive element;
7474	17334	27539	2.95	2.0E-29	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
7474	17334	27540	2.95	2.0E-29	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
7879	17729	27973	3.39	2.0E-29	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
7879	17729	27974	3.39	2.0E-29	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
8804	18818		1.96	2.0E-29	AW66070.1	EST_HUMAN	QV0-OT0932-093300-155-491 O10032 Homo sapiens cDNA
9004	18807		1.73	2.0E-29	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
7105	16982	27174	5.41	1.0E-29	AW663880.1	EST_HUMAN	RC1-HN0003-230300-021-504 HN0003 Homo sapiens cDNA
5696	15871	25995	3.04	9.0E-30	AA761215.1	EST_HUMAN	m20607.s1 NCL CGAP, GQ31 Homo sapiens cDNA clone IMAGE:1288332 3' similar to contains MER1b1 MER4 repetitive element;
9132	18889		1.5	9.0E-30	11422745	NT	Homo sapiens zinc finger regulated transporter-like (ZIRT1), mRNA
5815	15721		8.81	8.0E-30	F00988.1	EST_HUMAN	HSC232F051 normalized infant brain cDNA Homo sapiens cDNA clone c-2305
6812	16691	26880	3.37	8.0E-30	AA935873.1	EST_HUMAN	EST197317 Thymsus 1 Homo sapiens cDNA 5' and similar to EST containing O family repeat
7039	13916	27105	3.53	8.0E-30	AL157072.1	EST_HUMAN	PT12.1_13 BT1.1 tumor 2 Homo sapiens cDNA 3'

Table 4.

Table 4.

Probe SEQ ID NC:	Exon SEQ ID NC:	ORF SEQ ID NC:	Expression Signal	Most Similar (Top) HT BLAST Value	Top HT Accession No.	Top HT Database Source	Top HT Descriptor
1498	11403		1.16	7.0E-30	BE6091133.1	EST_HUMAN	PM4-BT0724-150400-001-411 BT0724 Homo sapiens cDNA
1549	11654		0.95	5.0E-30	X51755.1	NT	Human luteal-immunoglobulin constant region complex (germline)
1753	11637	21505	1.26	6.0E-30	D52300.1	NT	Human mRNA for integrin alpha subunit, complete cds
3153	13078	22878	2.41	6.0E-30	BE008026.1	EST_HUMAN	Y10-BN047-250400-21412 BT0177 Homo sapiens cDNA
9915	11454		3.15	6.0E-30	X51755.1	NT	Human luteal-immunoglobulin constant region complex (germline)
3931	13540	23920	31.23	5.0E-30	AF069692.1	EST_HUMAN	hg2503.3 x1 NC1 CGAP cDNA11 Homo sapiens cDNA clone IMAGE:2116276 3' similar to contains Au repetitive element
5206	16922		7.35	5.0E-30	U87931.1	NT	Human acitlate hydratase (ACOD) gene, exon 7
8291	18141		3.55	5.0E-30	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C0378
8495	18398	26532	6.68	5.0E-30	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C0310
8495	18398	26532	6.68	5.0E-30	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C0310
2096	11885	21850	1.84	4.0E-30	AW89747.1	EST_HUMAN	QY3-DT0045-090200-089-c08 DT0043 Homo sapiens cDNA
2096	11885	21850	1.84	4.0E-30	AW89747.1	EST_HUMAN	QY3-DT0045-090200-089-c08 DT0043 Homo sapiens cDNA
2096	11885	21851	1.64	4.0E-30	AW142488.1	EST_HUMAN	CH1-ST0181-1691-035-c08 ST0181 Homo sapiens cDNA
7162	17039	27231	1.49	4.0E-30	AW142488.1	EST_HUMAN	q5303.31 Scores: full, full, N52HF3_gov Homo sapiens cDNA clone IMAGE:1938820 3' similar to contains MER29.1 MER29 repetitive element
1134	11049		1.71	3.0E-30	AB38555.1	EST_HUMAN	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-6
3697	13911	23365	0.81	3.0E-30	AF172683.1	SW_BSPROT	TRANSCRIPTION FACTOR AP-2
8536	18410	28676	2.38	2.0E-30	P34205	EST_HUMAN	CHD-C03037-3100100-184-035 CT0307 Homo sapiens cDNA
650	10593	20411	1.18	2.0E-30	AW857915.1	EST_HUMAN	HS2C2F057, normalised infant brain cDNA Homo sapiens cDNA clone c-23505
1068	10584		2.32	2.0E-30	F068383.1	EST_HUMAN	RC5-H105652-100400-013-H08 H10562 Homo sapiens cDNA
1404	11269	21234	5.91	2.0E-30	BE175977.1	EST_HUMAN	LC5N10101-260700-116-040 NT10101 Homo sapiens cDNA
2563	12349	22433	10.37	2.0E-30	BE1766232.1	EST_HUMAN	Homo sapiens Y-linked zinc finger protein (ZFY) gene, complete cds
3790	12916	22619	6.38	2.0E-30	AF114156.1	NT	Human Y-linked zinc finger protein (ZFY) gene, complete cds
3721	13533	23409	2.11	2.0E-30	AW206281.1	EST_HUMAN	UH-HB1-afcc-12-011-11 NT CGAP Sub3 Homo sapiens cDNA clone IMAGE:2722563 3'
4663	14554	24546	1.72	2.0E-30	BE126846.1	EST_HUMAN	U1116980F1 NH, MSC, 17 Homo sapiens cDNA clone IMAGE:3029438 5'
4698	14554	24547	1.72	2.0E-30	BE126846.1	EST_HUMAN	U1116980F1 NH, MSC, 17 Homo sapiens cDNA clone IMAGE:3029438 5'
6966	18944	27036	3.46	2.0E-30	C18303.1	EST_HUMAN	C18303 Human placenta cDNA (TF-IIIw) Homo sapiens cDNA clone GEN-5760571 5'
7019	13990	27095	1.55	2.0E-30	BE570617.1	EST_HUMAN	C765712 x1 NT CGAP L124 Homo sapiens cDNA clone IMAGE 3284462 3' similar to SW.DHSA, HUMAN P31040 SUCONATE NUCLEOTIDE FLAVOPROTEIN SUBUNIT PRECURSOR ;
7019	16966	27096	1.55	2.0E-30	BE570617.1	EST_HUMAN	C765712 x1 NT CGAP L124 Homo sapiens cDNA clone IMAGE 3284462 3' similar to SW.DHSA, HUMAN P31040 SUCONATE NUCLEOTIDE FLAVOPROTEIN SUBUNIT PRECURSOR ;
7243	17814	27814	3.3	2.0E-30	AW571598.1	EST_HUMAN	EST1336557 IMAGE: mesencephalon, MAGL Homo sapiens cDNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7602	17652	27659	4.47	2.0E-30	AW147091.1	EST_HUMAN	hs33406.x1 NQI_OGAP_K012 Homo sapiens cDNA clone IMAGE:2875498 3' similar to contains THR L33
284	10249	20099	10.22	1.0E-30	CT18939.1	EST_HUMAN	THR repetitive element;
699	10532	20457	2.62	1.0E-30	AL163203.2	EST_HUMAN	C18939 Human placenta cDNA (TP-14ara) Homo sapiens cDNA clone GEN-370201 5'
2195	12052	21953	3.24	1.0E-30	AA064377.1	EST_HUMAN	hs30044.x1 Scores_NFL_1_GBC_31 Homo sapiens cDNA clone IMAGE:2910891 3' similar to contains
2413	12290	22187	2.57	1.0E-30	BF347728.1	EST_HUMAN	MER1.13 MER1 MER1 repetitive element;
2973	12900	22699	1.03	1.0E-30	5830291	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C003
3015	12943	22736	0.89	1.0E-30	AA315045.1	EST_HUMAN	hs30044.x1 Striagenes lung (#637210) Homo sapiens cDNA clone IMAGE:988559 3'
3645	16403	25932	2.32	1.0E-30	BF18320.1	EST_HUMAN	80022560F NQI_OGAP_Emi67 Homo sapiens cDNA clone IMAGE:4157991 5'
9733	18415	25932	5.1	1.0E-30	H45593.1	EST_HUMAN	Homo sapiens methionine aminopeptidase, eIF-2-associated p67 (MANPEP), mRNA
7013	18980	10977	2.04	9.0E-31	Z38293.1	EST_HUMAN	EST189808 HCG cell line (maternalist to liver in mouse) II Homo sapiens cDNA 5' end
1090	10977	20820	1.94	8.0E-31	8823390	EST_HUMAN	CHR220332 Chromosome 22 exon Homo sapiens cDNA clone C22_728 5'
2362	12243	20820	5.14	8.0E-31	AL163203.2	EST_HUMAN	HS08F032 normalised infant brain cDNA Homo sapiens cDNA clone c-05003 3'
694	10927	22932	1.72	7.0E-31	AA372657.1	EST_HUMAN	Homo sapiens lysophospholipid protein FL20426 (FL20426), mRNA
2633	12500	22932	1.7	7.0E-31	BE32657.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C008
9583	19188	23272	2.56	7.0E-31	X51755.1	EST_HUMAN	EST84556 Oocyte adhesion protein IV Homo sapiens cDNA 5' end
3625	13539		2.79	8.0E-31	AF223391.1	NT	hs05411.x1 NQI_OGAP_L024 Homo sapiens cDNA clone IMAGE:3182012 3'
8739	16618		3.68	8.0E-31	AF233053.1	NT	hs05411.x1 NQI_OGAP_L024 Homo sapiens cDNA clone IMAGE:3182012 3'
8120	18038	26235	2.11	8.0E-31	AA101905.1	EST_HUMAN	Human limbic system cytochrome P-450 (CYP2A6) gene, exons 7-9, and partial cdc, alternatively spliced
9191	18925	25951	1.88	8.0E-31	AA101905.1	EST_HUMAN	Homo sapiens MGC class 1 region
9319	19541		1.78	8.0E-31	BE384488.1	EST_HUMAN	AUT1018 HELM641 Homo sapiens cDNA clone HELM64105656 5'
185	10197	19873	2.85	8.0E-31	M00964.1	NT	RC151037/401288-051-D12 B10377 Homo sapiens cDNA
185	10197	19974	2.85	8.0E-31	M00964.1	NT	RC1430007F NH1_MGC_72 Homo sapiens cDNA clone IMAGE:391624 5'
8915	16793		1.21	5.0E-31	BF069540.1	EST_HUMAN	Homo sapiens type I DNA topoisomerase gene, exon 8
581	10519		3.78	4.0E-31	AJ271755.1	NT	Homo sapiens Xq pseudocistron region; segment 12
1694	11498	21357	1.04	4.0E-31	Q10473	SWISSPROT	7A0904.x1 NQI_OGAP_G03 Homo sapiens cDNA clone IMAGE:3449479 3' similar to TRC19337 Q19337
1775	11674		2.59	4.0E-31	AL163280.2	NT	SIMILAR TO POGD ELEMENT, contains L1.11.1 repetitive element;
							POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE (PROTEIN-UDP
							ACETYL GALACTOSAMINYLTRANSFERASE) (UDP-GALNAc POLYPEPTIDE, N-
							ACETYL GALACTOSAMINYLTRANSFERASE) (GALNAc-11)
							Homo sapiens chromosome 21 segment HS21C080

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2759	12621		1.38	4.0E-31	5730038	NT	Homo sapiens SET domain and murine transposase fusion gene (SETMAR) mRNA
9604	19186		1.92	4.0E-31	11430273	NT	Homo sapiens KIA00569 gene product (KIA00569) mRNA
9718	19259		1.38	4.0E-31	AB009881.1	NT	Homo sapiens gene for actinin receptor type IIB, complete cds
2550	12423	22314	1.42	3.0E-31	6005871	NT	Homo sapiens SEC8L, endoplasmic reticulum transition component (S. ocrevislae) [tag (SEC8L), mRNA
6341	16204	26366	9.03	3.0E-31	4826853	NT	Homo sapiens MADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8 (19kD, ASH) (NDUF9B) mRNA
6425	16290	26148	1.38	3.0E-31	11420328	NT	Homo sapiens hypothetical protein FLJ10842 (FLJ10842) mRNA
6745	16624		1.95	3.0E-31	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
7525	17370	27595	2.80	3.0E-31	DT4523.1	NT	Horse mRNA for ferritin L-chain, complete cds
8028	17020	28167	2.01	3.0E-31	PI1174	SWISSPROT	40S RIBOSOMAL PROTEIN S15 (RIG PROTEIN)
8403	18360		6.36	3.0E-31	BR03527.1	EST_HUMAN	OV2-1T0051-293300-111-403 LTO051 Homo sapiens cDNA clone IMAGE:3962090 5'
1875	11771	21647	1.83	2.0E-31	AV183871.1	EST_HUMAN	944905.x1 Scars, NFL, T, C8C S1 Homo sapiens cDNA clone IMAGE:2111972 3'
2197	12064	21945	1.31	2.0E-31	AI393388.1	EST_HUMAN	DKF267G1513.11 601 (synonym: ham2) Homo sapiens cDNA clone DKF267G1513 5'
2292	12174	22074	2.18	2.0E-31	AL118245.1	EST_HUMAN	ss8811.41 Stralagene fetal retina 837202 Homo sapiens cDNA clone IMAGE:838413 3' similar to contains THR_12 THR repetitive element;
2391	12256	22164	4.4	2.0E-31	AA498324.1	EST_HUMAN	ND901.x1 NCL CGAP_K413 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.13 MER29 negative element;
5502	15421	25483	3.6	2.0E-31	BE35127.1	EST_HUMAN	nt884.s1 NCL CGAP_C010 Homo sapiens cDNA clone IMAGE:1161055 3' similar to TR-Q1357 Q1367
7246	17120		1.8	2.0E-31	AA87784.1	EST_HUMAN	MER37 TRANSPARENT ELEMENT, COMPLETE CONSENSUS SEQUENCE ;
7309	17165	27395	3.99	2.0E-31	766183.1	EST_HUMAN	Homo sapiens B9 protein (B9) mRNA
7700	17850	27774	1.27	2.0E-31	AV170948.1	EST_HUMAN	AV170948.Os Homo sapiens cDNA clone CUALEB07 5'
7700	17850	27775	1.27	2.0E-31	AV170948.1	EST_HUMAN	AV170948.Os Homo sapiens cDNA clone CUALEB07 5'
7797	17647	27883	2.17	2.0E-31	BE408611.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
7797	17647	27884	2.17	2.0E-31	BE408611.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
9322	18853		2	2.0E-31	AF146512.1	NT	Homo sapiens translocase II gene, promoter region
9322	18759		1.81	2.0E-31	AF14527.1	EST_HUMAN	HA1110 Human fetal liver cDNA library Homo sapiens cDNA clone IMAGE:42 (IMAGE-42), IMAGE-83 (IMAGE-83), IMAGE-94 (IMAGE-94), and IMAGE-81 (IMAGE-81) genes, complete cds
16	10002	19794	8.34	1.0E-31	U63163.1	NT	QI-FACTORY RECEPTOR 2C1
1640	11544	21403	2	1.0E-31	O95571	SWISSPROT	QI-FACTORY RECEPTOR 2C1
1640	11544	21404	2	1.0E-31	O95571	SWISSPROT	QI-FACTORY RECEPTOR 2C1
1640	11544	21405	2	1.0E-31	O95571	SWISSPROT	QI-FACTORY RECEPTOR 2C1
4835	14428	24209	1.01	1.0E-31	AL134376.1	EST_HUMAN	DKF2667B235.11 547 (synonym: hfr-1) Homo sapiens cDNA clone DKF2667B235 5'

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4353	14428	24210	1.01	1.0E-31	AL134376.1	EST HUMAN	DNFZ64B235 JT 547 (synonym: hrb-1) Homo sapiens cDNA clone DNKJ65473236 5'
5235	15159	24827	3.15	1.0E-31	AV391076.1	EST HUMAN	MRC-51 0220-161260-028-08 1 510220 Homo sapiens cDNA
5728	15535	25736	1.57	1.0E-31	AF048727.1	NT	Homo sapiens trinitatillactin ccd1 repeat region
6295	18167	28411	2.72	1.0E-31	AI065434.1	EST HUMAN	Q16506 FRATAVIN ;
2635	12703		0.90	6.0E-32	U90071.1	NT	Human familial Alzheimer's disease (S1M2) gene, complete cds
6020	15505	29029	2.34	9.0E-32	AV729376.1	EST HUMAN	AV729376 HTB Homo sapiens cDNA clone HT9A001 5'
2032	11923	21615	3.32	8.0E-32	AI056770.1	EST HUMAN	act1509.x1 Scores, fetal liver spleen, INFLS 51 Homo sapiens cDNA clone IMAGE:1678354 3'
4754	14639	24426	1.17	7.0E-32	P62991	SWISSPROT	NUCLEAR ENVELOPE PORE MEMBRANE PROTEIN POM 121 (PORE MEMBRANE PROTEIN OF 121 KD) (P145)
6295	15972		2.77	7.0E-32	X17833.1	NT	Human chromosome 22 immunoglobulin V(κ) gene, part with 5' intracistern between option and neighbouring non-amplified region
2702	12566	22456	0.9	6.0E-32	AI478104.1	EST HUMAN	Im5410.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:218694 3' similar to contains MER28 IS
6359	16222		1.15	6.0E-32	BE589016.1	EST HUMAN	MER29 regulatory element ;
1018	10936	20778	29.97	5.0E-32	AF118627.1	NT	001611509F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:391367 5'
915	10930		1.24	4.0E-32	AL182463.2	NT	Homo sapiens chromosome 21 segment HS21G248
8454	16342	28510	2.82	4.0E-32	11432574	NT	Homo sapiens AT-binding transcription factor 1 (ATBF1) mRNA
8454	16342	28511	2.82	4.0E-32	11432574	NT	Homo sapiens AT-binding transcription factor 1 (ATBF1) mRNA
448	10392	20213	3.4	3.0E-32	Y17263.1	NT	Homo sapiens TLI gene, partial
1438	11343	21210	7.97	3.0E-32	AV715900.1	EST HUMAN	AV715100 HTT Homo sapiens cDNA clone HTFAK037 5'
7404	17271	27477	6.73	3.0E-32	AV796534.1	EST HUMAN	AV796534 BM Homo sapiens cDNA clone BMPBPH12 5'
7404	17271	27478	6.73	3.0E-32	AV796534.1	EST HUMAN	AV796534 BM Homo sapiens cDNA clone BMPBPH12 5'
5207	16176	29421	8.08	3.0E-32	AA177621.1	EST HUMAN	295d07.x1 Scores, fetal liver spleen, INFLS 51 Homo sapiens cDNA clone IMAGE:49500 3' similar to contains Thr to Thr repetitive element ;
5254	18565		3.04	3.0E-32	BE270066.1	EST HUMAN	001156285F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3139701 5'
9655	15090	24862	2.43	3.0E-32	5174574	NT	Homo sapiens myeloid/lymphoid or mixed lineage leukemia (t(11q24)) homolog, translocated to, 4 (MLL1) mRNA
9655	15090	24862	2.43	3.0E-32	5174574	NT	Homo sapiens myeloid/lymphoid or mixed lineage leukemia (t(11q24)) homolog, translocated to, 4 (MLL1) mRNA
9655	15090	24863	2.43	3.0E-32	5174574	NT	Homo sapiens myeloid/lymphoid or mixed lineage leukemia (t(11q24)) homolog, translocated to, 4 (MLL1) mRNA
9655	15090	24863	2.43	3.0E-32	BE270066.1	EST HUMAN	001156285F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3139701 5'
4763	14967	21454	0.91	2.0E-32	BE290613.1	EST HUMAN	00117363F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3529159 5'
5601	15068	25929	19.01	2.0E-32	Z38133.1	NT	H sapiens mRNA for myosin
5601	15068	25930	19.01	2.0E-32	Z38133.1	NT	H sapiens mRNA for myosin

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6815	13094	26894	3.41	2.0E-32	AA14294.1	EST_HUMAN	z76608.r1 Striatagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:593160 5'
6815	16694	26895	3.41	2.0E-32	AA14294.1	EST_HUMAN	z76608.r1 Striatagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:593160 5'
6908	19385	28175	1.91	2.0E-32	AV796449.1	EST_HUMAN	AV796449.CB Homo sapiens cDNA clone CBPJA08 5'
6908	19385	28176	1.91	2.0E-32	AV796449.1	EST_HUMAN	AV796449.CB Homo sapiens cDNA clone CBPJA08 5'
3055	12062		1.35	1.0E-32	BE743259.1	EST_HUMAN	601573207.F1 NIH: MGC 9 Homo sapiens cDNA clone IMAGE:3834433 5'
6198	15056	27090	7.04	1.0E-32	11439785	NT	Homo sapiens chromosome 11 open reading frame 9 (GTTORF9), mRNA
6927	16874	27095	5.18	1.0E-32	AA720574.1	EST_HUMAN	hw21402.at NCL CGAP_QG30 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains 1HR13 THR repetitive element: _
3435	13352		4.98	9.0E-33	BE327142.1	EST_HUMAN	hw705.e1 NCL CGAP_L124 Homo sapiens cDNA clone IMAGE:3182210 3' similar to ITC08539 O88539 WW DOMAIN BINDING PROTEIN 11: _
5927	15779		4.19	9.0E-33	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-18, and partial cds, alternatively spliced
7103	16260	27172	1.39	9.0E-33	BF547226.1	EST_HUMAN	602031164.F1 NCL CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4156970 5'
8177	18665		5.89	9.0E-33	AL163280.2	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C080
84	10441	18850	2.98	7.0E-33	5931768	NT	Homo sapiens short-chain alcohol dehydrogenase family member (HEP27) mRNA
54	10041	18851	2.98	7.0E-33	5931768	NT	Homo sapiens short-chain alcohol dehydrogenase family member (HEP27) mRNA
2115	12004	21992	2.71	7.0E-33	AL560115.1	EST_HUMAN	hs2506.x1 NCL CGAP_U2 Homo sapiens cDNA clone IMAGE:2178809 3' similar to contains ORF.H1 OFR
2612	12680		8.4	7.0E-33	AV730058.1	EST_HUMAN	AV730058.HTF Homo sapiens cDNA clone HTFAN508 5'
2800	11573	21439	1.78	7.0E-33	AV730058.1	EST_HUMAN	AV730058.HTF Homo sapiens cDNA clone HTFAN508 5'
3204	13128		12.85	7.0E-33	AA7971907.1	EST_HUMAN	EST383506 IMAGE:rescues, MGL Homo sapiens cDNA
8203	18067	28338	3.9	7.0E-33	BF547226.1	EST_HUMAN	602071044.F1 NCL CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4156970 5'
8573	18441	28709	2.15	7.0E-33	AV7971908.1	EST_HUMAN	EST383607 IMAGE:rescues, MGL Homo sapiens cDNA
6274	18078	25322	3.43	7.0E-33	AA601446.1	EST_HUMAN	nt01801.at NCL CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100891 3' similar to contains L1.H1 repetitive element: _
3676	13590		0.85	6.0E-33	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C085
6948	18965	27059	13.52	6.0E-33	JA0438.1	NT	Human glyceraldehyde 3-phosphate dehydrogenase (GAP3H) gene, complete cds
7049	18026	27117	2.57	6.0E-33	11429168	NT	Homo sapiens similar to RAC23 (S. cerevisiae) homolog B (H. sapiens) (LOC83277), mRNA
7150	17900	27822	1.24	6.0E-33	6755609	NT	Mus musculus SRV-box containing gene 6 (Sox6), mRNA
7750	17000	27823	1.24	6.0E-33	6755609	NT	Mus musculus SRV-box containing gene 6 (Sox6), mRNA
1739	11640		1.78	5.0E-33	BF372515.1	EST_HUMAN	QV4-FTD166-100700-271-402 FTD169 Homo sapiens cDNA
1838	11735		1.18	5.0E-33	11141884	NT	Homo sapiens solute carrier family 5 (cholesterol transporter), member 7 (SLC5A7), mRNA
1850	11752	21626	1.37	5.0E-33	4507208	NT	Homo sapiens spermidine synthase (SRM) mRNA
1856	11752	21627	1.37	5.0E-33	4507208	NT	Homo sapiens spermidine synthase (SRM) mRNA

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Probe SEQ ID No:	Exon SEQ ID No:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2226	12111		1.3	6.0E-33	AL16395.2	NT	Homo sapiens chromosome 21 segment HS21C065
9082	18958		1.62	5.0E-33	11433063	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), mRNA
1113	11027		3.26	4.0E-33	AL16307.2	NT	Homo sapiens chromosome 21 segment HS21C007
2078	11988	21661	1.77	4.0E-33	4759987	EST	Homo sapiens RAB1, member RAS oncogene family (RAB1), mRNA
2370	12250		7.39	4.0E-33	AA029821.1	EST_HUMAN	4d5191.11 Stratiagene lung carcinoma 837218 Homo sapiens cDNA clone IMAGE:844317 5' similar to
2468	12373	22265	3.71	4.0E-33	AL16310.2	NT	contains Alu repetitive element/contains MER28.k2 MER28 repetitive element;
4382	14278	24657	1.63	4.0E-33	AW29346.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C010
5918	15239	25943	20.94	4.0E-33	AA053053.1	EST_HUMAN	U1H-B12-39-43-33.1 x1 NC1 CGAP 5.3k4 Homo sapiens cDNA clone IMAGE:272749 3'
9007	18810	28102	1.72	4.0E-33	11425636	NT	471408.11 Stratiagene cdorf 460720.04 Homo sapiens cDNA clone IMAGE:840338 5' similar to
1073	10689		4.46	3.0E-33	BE350127.1	EST_HUMAN	pbx1/2671, ms1 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN X1 (HUMAN);
1074	10689		3.4	3.0E-33	BE350127.1	EST_HUMAN	Homo sapiens killer cell immunoglobulin-like receptor, three domains, long cytoplasmic tail, 1 (KIR3DL1),
2400	12721		1.48	3.0E-33	AV479571.1	EST_HUMAN	mRNA
69	10005		2.33	2.0E-33	AI100198.1	EST_HUMAN	HP0001.X1 NC1 CGAP Kdr13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER28.k3
4522	14219		4.27	2.0E-33	BE15939.1	EST_HUMAN	MER29, repetitive element;
4811	11790	24565	5.1	2.0E-33	AA029883.1	EST_HUMAN	HP0001.X1 NC1 CGAP Kdr13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to
5026	14699	24608	1.73	2.0E-33	11421332	NT	contains ORF11 ORF
5026	14699	24609	1.73	2.0E-33	11421332	NT	4d5191.11 Stratiagene lung carcinoma 837218 Homo sapiens cDNA clone IMAGE:844398 5' similar to
5989	15775	25894	1.01	2.0E-33	AI277462.1	EST_HUMAN	gp52007.34, cd11 TUBULIN BE-1A-S-161 (HUMAN);
7291	17138		1.8	2.0E-33	AA03276.1	EST_HUMAN	Homo sapiens hypodermal protein SRP-82 (SRP-82), mRNA
8	9894		1.44	1.0E-33	AF003528.1	NT	Homo sapiens hypodermal protein SRP-82 (SRP-82), mRNA
8937	18502	28778	2.02	1.0E-33	AV196818.1	EST_HUMAN	HP0001.X1 NC1 CGAP Kdr13 Homo sapiens cDNA clone IMAGE:1880161 3'
8921	18728	29024	5.33	1.0E-33	U06822.1	NT	4d21463.X1 Soares, Jena Jivar, sapien, INTUS.51 Homo sapiens cDNA clone IMAGE:1880161 3'
9553	19151		1.82	1.0E-33	AB22719.1	EST_HUMAN	gp52007.34, cd11 TUBULIN BE-1A-S-161 (HUMAN);
							HP0001.X1 NC1 CGAP Kdr13 Homo sapiens cDNA clone IMAGE:1880161 3'
							Homo sapiens X-linked androgenic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
							QY3-BN0047.230200-02-563 BN0047 Homo sapiens cDNA
							Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds
							wo85606.x1 NC1 CGAP Kdr13 Homo sapiens cDNA clone IMAGE:2462410 3'

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9723	9994		3.04	1.0E-33	AF003628.1	NT	Human sapiens X-linked arylidic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions	
9754	9278		1.34	1.0E-33	AF077690.1	EST_HUMAN	AV127959 HTO Homo sapiens cDNA clone HTCC012.5'	
9927	19309		25226	1.34	1.0E-33	AF077690.1	EST_HUMAN	AV127959 HTO Homo sapiens cDNA clone HTCC012.5'
1427	11332		21198	1.38	7.0E-34	U170945.1	EST_HUMAN	YF1605.1 Soares fetal liver spliced NPLS Homo sapiens cDNA clone IMAGE:108320.5'
9340	10020		3.08	7.0E-34	U170945.1	EST_HUMAN	YF1605.1 Soares fetal liver spliced NPLS Homo sapiens cDNA clone IMAGE:108320.5'	
483	10406		20226	1.46	6.0E-34	U10891.1	NT	Human G2 protein mRNA, partial cds
483	10406		20226	1.46	6.0E-34	U10891.1	NT	Human G2 protein mRNA, partial cds
9133	19503		25340	1.44	6.0E-34	U03596.1	NT	Human G2 protein mRNA, partial cds
1837	11734		2.23	5.0E-34	U03596.1	NT	Human G2 protein mRNA, partial cds	
4893	14399		24631	4	5.0E-34	U03596.1	NT	Human G2 protein mRNA, partial cds
7144	17021		27216	1.18	5.0E-34	AF078779.1	NT	Human sapiens NPLS3-binding protein NPLS3 (LOC51729), mRNA
9046	17637		25186	2.12	5.0E-34	AF078779.1	NT	Human sapiens NPLS3-binding protein NPLS3 (LOC51729), mRNA
9078	18440		2.01	5.0E-34	AF078779.1	NT	Human sapiens NPLS3-binding protein NPLS3 (LOC51729), mRNA	
1383	11948		21706	2.11	5.0E-34	AF094697.1	EST_HUMAN	Human sapiens NPLS3-binding protein NPLS3 (LOC51729), mRNA
2927	12952		22441	0.98	4.0E-34	AF094697.1	EST_HUMAN	Human sapiens NPLS3-binding protein NPLS3 (LOC51729), mRNA
5492	19306		4.81	3.0E-34	BF093327.1	EST_HUMAN	Human sapiens NPLS3-binding protein NPLS3 (LOC51729), mRNA	
1488	11393		21254	8.56	1.0E-34	P12238	SWISSPROT	Human sapiens NPLS3-binding protein NPLS3 (LOC51729), mRNA
3621	13535		23320	1.46	1.0E-34	AF003628.1	NT	Human sapiens WNT3 precursor (WNT3), mRNA, complete cds
3979	13561		23661	0.78	1.0E-34	AF003628.1	NT	Human sapiens WNT3 precursor (WNT3), mRNA, complete cds
3979	13561		23662	0.78	1.0E-34	AF003628.1	NT	Human sapiens WNT3 precursor (WNT3), mRNA, complete cds
4391	14277		4.02	1.0E-34	BE071414.1	EST_HUMAN	Human sapiens WNT3 precursor (WNT3), mRNA, complete cds	
4920	14760		0.86	1.0E-34	AF045706.1	EST_HUMAN	Human sapiens WNT3 precursor (WNT3), mRNA, complete cds	
5731	15559		25743	1.99	1.0E-34	BE574032.1	EST_HUMAN	Human sapiens WNT3 precursor (WNT3), mRNA, complete cds
6731	15639		25744	1.99	1.0E-34	BE574032.1	EST_HUMAN	Human sapiens WNT3 precursor (WNT3), mRNA, complete cds
7195	17032		27226	3.87	1.0E-34	AF098451.1	EST_HUMAN	Human sapiens WNT3 precursor (WNT3), mRNA, complete cds
7591	17442		27698	8.89	1.0E-34	AF098451.1	EST_HUMAN	Human sapiens WNT3 precursor (WNT3), mRNA, complete cds
9746	19307		2.92	1.0E-34	AF163210.2	NT	Human sapiens WNT3 precursor (WNT3), mRNA, complete cds	
3594	13508		23296	1.26	9.0E-35	AF069302.1	EST_HUMAN	Human sapiens WNT3 precursor (WNT3), mRNA, complete cds
219	10189		24.25	8.0E-35	AF069302.1	EST_HUMAN	Human sapiens WNT3 precursor (WNT3), mRNA, complete cds	
1703	11604		21475	3.3	8.0E-35	BF099637.1	EST_HUMAN	Human sapiens WNT3 precursor (WNT3), mRNA, complete cds

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1703	11604	21476	3.3	8.0E-36	BF58937.1	EST_HUMAN	hms3308.x1 NCL CGAP_Kdrl1 Homo sapiens cDNA IMAGE:288134.3 similar to TR-079612
4761	14646	24435	3.09	8.0E-36	BF183195.1	EST_HUMAN	OT5912 DIACYLGLYCEROL KINASE (OTA);
8075	17966	28217	3.19	8.0E-36	BE378490.1	EST_HUMAN	00180558F1 NH1.MGC_18 Homo sapiens cDNA clone IMAGE:4040324.5
9265	18669		3.49	8.0E-36	BF569282.1	EST_HUMAN	00123949F1 NH1.MGC_44 Homo sapiens cDNA clone IMAGE:3368513.5
9505	19311	25937	1.32	7.0E-35	11425417	NT	0021846241 NH1.MGC_42 Homo sapiens cDNA clone IMAGE:4300660.3
1391	11295	21154	1.28	6.0E-36	AA757115.1	EST_HUMAN	Homo sapiens phosphatidylinositol glycan, class L (PIGL), mRNA
1925	11820	21659	1.78	6.0E-36	6035975	NT	hfs3103.st Scores, testis, NHT Homo sapiens cDNA clone 1303937.3
6510	18460	26676	3.6	6.0E-36	6035921	NT	Homo sapiens zinc finger protein 208 (ZNF208), mRNA
7698	17548	27771	2.7	6.0E-36	AB377795.1	EST_HUMAN	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA
1691	11983	21454	2.28	5.0E-36	X63392.1	NT	Homo sapiens mRNA for KIAA1305 protein, partial cds
							H sapiens immunoglobulin kappa light chain variable region L14
4311	14208	23892	2.2	5.0E-36	AF023398.1	NT	Homo sapiens alkyl kinase (CLK2), prepro1, cdk5, glucocorticoid-induced (GBA), and melanin genes, complete cds; pathogenesis and glucocorticoid-induced pseudogene, and thymopodanthin (THBS3) gene, partial cds
6761	16640		3.14	5.0E-36	BE569292.1	EST_HUMAN	00143198F1 NH1.MGC_72 Homo sapiens cDNA clone IMAGE:3917220.5
6776	16658	28848	2.18	5.0E-36	AI200795.1	EST_HUMAN	008405.x1 Scores, testis, NHT Homo sapiens cDNA clone IMAGE:1837448.3 similar to SW1249_HUMAN_Q82830-HYPOTHETICAL PROTEIN KIAA0246.1
6779	16658	28849	2.18	5.0E-36	AI200795.1	EST_HUMAN	008405.x1 Scores, testis, NHT Homo sapiens cDNA clone IMAGE:1837448.3 similar to SW1249_HUMAN_Q82830-HYPOTHETICAL PROTEIN KIAA0246.1
8517	18389		3.42	5.0E-36	AA007183.1	EST_HUMAN	hms1721.1 Scores, fetal liver, spleen, INFLS S1 Homo sapiens cDNA clone IMAGE:428015.5
1415	11321	21186	14.91	4.0E-36	BE257607.1	EST_HUMAN	00110671F1 NH1.MGC_10 Homo sapiens cDNA clone IMAGE:339405.5
1778	11675	21552	5.1	4.0E-36	H91183.1	EST_HUMAN	ptd8007.1 Scores fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:241236.5 similar to contains PTD8007 negative element
5042	14914		1.29	4.0E-36	BE450102.1	EST_HUMAN	00130070F1 NH1.MGC_21 Homo sapiens cDNA clone IMAGE:3934641.5
6280	16144		1.82	4.0E-36	BC390127.1	EST_HUMAN	hms601.x1 NCL CGAP_Kdrl13 Homo sapiens cDNA clone IMAGE:3740256.3 similar to contains MER26103 MER202 negative element
6957	16835	27030	0.84	4.0E-36	AB046596.1	EST_HUMAN	DNFZP454L148.J1 494 (synonym: hms3) Homo sapiens cDNA clone DKFZp454L148.5
1561	11466	21324	9.93	3.0E-35	BE378162.1	EST_HUMAN	001123200F1 NH1.MGC_3 Homo sapiens cDNA clone IMAGE:3345003.5
2283	12167		2.42	3.0E-35	AF224492.1	NT	Homo sapiens phosphatidyl scramblase 1 gene, complete cds
4793	14978	24465	1.06	3.0E-35	BF376402.1	EST_HUMAN	MR1-TN0046-130000-010-401 TN0046 Homo sapiens cDNA
5275	15197	24971	22.73	3.0E-35	BF433100.1	EST_HUMAN	7b26069.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3365391.3 similar to TR-QBQZH7 QBQZH7 F-BOX PROTEIN FBL2.1
5276	15197	24972	22.73	3.0E-35	BF433100.1	EST_HUMAN	7b26069.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3365391.3 similar to TR-QBQZH7 QBQZH7 F-BOX PROTEIN FBL2.1

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7405	17325		1.61	3.0E-35	AF22391.1	NT	Homo sapiens calcium channel alpha1E subunit (CAVNA1E) gene, exons 7-49, and partial cds, alternatively spliced
103	12659	19902	1.74	2.0E-35	NE6965.1	EST_HUMAN	K693ZF Human fetal heart, Lambda Zap Express Homo sapiens cDNA clone K6932 5' similar to
1171	11093	20028	1.35	2.0E-35	T11803.1	EST_HUMAN	REPETITIVE ELEMENT
2171	12056	21941	5.2	2.0E-35	A3018413.1	NT	AG71F Heart Homo sapiens cDNA clone A971
3272	13193	22691	0.97	2.0E-35	6912458	NT	Homo sapiens mRNA for Gab2, complete cds
3272	13193	22692	0.97	2.0E-35	6912458	NT	Homo sapiens Ch22-associated binder 2 (KIAA0571), mRNA
3511	13427		0.88	2.0E-35	A3020702.1	NT	Homo sapiens mRNA for KIAA0854 protein, partial cds
							TOBA-PZE-4328 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HQSC project-TGBA Homo sapiens cDNA clone TCBAF-4328
3935	13747	20339	1.06	2.0E-35	BE247575.1	EST_HUMAN	TOBA-PZE-4328 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HQSC project-TGBA Homo sapiens cDNA clone TCBAF-4328
3935	13747	20340	1.06	2.0E-35	BE247575.1	EST_HUMAN	TOBA-PZE-4328 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HQSC project-TGBA Homo sapiens cDNA clone TCBAF-4328
4670	14402		2.55	2.0E-35	H46239.1	EST_HUMAN	Y10A12.1 Scores fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:274078 5'
8438	15347	25401	1.66	2.0E-35	BF332417.1	EST_HUMAN	OV01-BT071-210-000-185-04 BT0701 Homo sapiens cDNA
8175	16093	26912	3.72	2.0E-35	X58417.1	NT	H sapiens PROS-37 mRNA
3038	13193	20391	1.36	2.0E-35	6912458	NT	Homo sapiens Ch22-associated binder 2 (KIAA0571), mRNA
3038	13193	20392	1.36	2.0E-35	6912458	NT	Homo sapiens Ch22-associated binder 2 (KIAA0571), mRNA
8295	16350	23354	1.91	2.0E-35	BE504978.1	EST_HUMAN	60149874F1 NH1_MGC_70 Homo sapiens cDNA clone IMAGE:366659 5'
8295	16350	23355	1.91	2.0E-35	BE504978.1	EST_HUMAN	60149874F1 NH1_MGC_70 Homo sapiens cDNA clone IMAGE:366659 5'
9725	16264		3.97	2.0E-35	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
							K693ZF Human fetal heart, Lambda Zap Express Homo sapiens cDNA clone K6932 5' similar to
8602	12859	19902	4.17	2.0E-35	NE6965.1	EST_HUMAN	REPETITIVE ELEMENT
40	10028	18628	4.38	1.0E-35	A0651945.1	EST_HUMAN	hncr1c Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
40	10028	18629	4.38	1.0E-35	A0651945.1	EST_HUMAN	hncr1c Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
735	10067	20500	44.43	1.0E-35	AV386473.1	EST_HUMAN	U2-S10762-131068-006-417 S10167 Homo sapiens cDNA
735	10067	20501	44.43	1.0E-35	AV386473.1	EST_HUMAN	U2-S10762-131068-006-417 S10167 Homo sapiens cDNA
6951	10817		1.16	1.0E-35	T87047.1	EST_HUMAN	y83d01.1 Scores fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:115752 5' similar to
8495	12369	22392	2.31	1.0E-35	7705954	NT	SP-A44262 A44262 NEI HOVPR103-RELATED POLY(ADP-RIBOSE) POLY(ADP-RIBOSE) HUMAN
2740	12002	22496	1.11	1.0E-35	BE39072.1	EST_HUMAN	Homo sapiens hypothetical protein (LOC51733), mRNA
							MER20 repetitive element;
							h00g01.x1 NC1_CGAP_KG13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3
2740	12002	22497	1.11	1.0E-35	BE39072.1	EST_HUMAN	MER20 repetitive element;
							h00g01.x1 NC1_CGAP_KG13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) HIT BLAST E Value	Top HIT Accession No.	Top HIT Database Source	Top HIT Descriptor
3104	13030	22826	1.07	1.0E-35	600806	NT	Homo sapiens transcription elongation factor B (SII), polypeptide 1-like (TCIEB1) mRNA
3126	13051	22848	2.2	1.0E-35	AV590422.1	EST_HUMAN	AV590422 GLC Homo sapiens cDNA clone GLOC908 3'
3126	13051	22849	2.2	1.0E-35	AV590422.1	EST_HUMAN	AV590422 GLC Homo sapiens cDNA clone GLOC908 3'
4325	14222	24003	4.7	1.0E-35	7655005	NT	Mus musculus actinin receptor interacting protein 1 (Arip1-pending), mRNA
4325	14222	24004	4.7	1.0E-35	7655005	NT	Mus musculus actinin receptor interacting protein 1 (Arip1-pending), mRNA
5392	15001	28154	1.43	1.0E-35	11532026	EST_HUMAN	AU165505 PLACE3 Homo sapiens cDNA clone PLACE3000382 3'
7591	19469	27878	2	1.0E-35	AU165505.1	EST_HUMAN	AU165505 PLACE3 Homo sapiens cDNA clone PLACE3000382 3'
7591	19469	27879	2	1.0E-35	AU165505.1	EST_HUMAN	AU165505 PLACE3 Homo sapiens cDNA clone PLACE3000382 3'
8077	18782	27676	4.16	1.0E-35	AK23119.1	EST_HUMAN	promoter 7 D017 b1vmmr Homo sapiens cDNA 5'
8198	23260	22282	1.89	1.0E-35	770564	NT	Homo sapiens hypothetical protein (LOC31233), mRNA
9267	18971		1.37	1.0E-35	11418110	NT	Homo sapiens casain kinase 1, epsilon (CSNK1E), mRNA
9630	19168		2.38	1.0E-35	BE72632.1	EST_HUMAN	801834535.1 NH, MGCG 39 Homo sapiens cDNA clone IMAGE393658 5'
2830	12821	22822	0.94	7.0E-35	AV165759.1	EST_HUMAN	CH, CT0315-061530-063-207 CT0315 Homo sapiens cDNA
3080	13007	28548	4.03	7.0E-35	4857468	NT	Homo sapiens C-terminus binding protein 2 (CTBP2), mRNA
6512	16711	28549	6.04	7.0E-35	U06572.1	NT	Homo sapiens C-terminus binding protein 2 (CTBP2), mRNA
6512	16711	28549	6.04	7.0E-35	U06572.1	NT	Human carcinoembryonic antigen gene family member 12 (CGM12) gene, exon 1 and 2
9423	19071	25279	5.23	7.0E-35	AF20051.1	NT	Human carcinoembryonic antigen gene family member 12 (CGM12) gene, exon 1 and 2
1959	11854	21741	1.88	6.0E-35	770622	NT	Homo sapiens glutathione S-transferase A4 gene, exon 1
2357	12247		6.17	6.0E-35	AB038346.1	NT	Homo sapiens albumin 2 (ALB2), mRNA
3367	13501	23260	0.91	6.0E-35	BF15101.1	EST_HUMAN	Homo sapiens TGL3 gene, exon 12
6288	15160	24965	10.79	6.0E-35	AK43616.1	EST_HUMAN	UHRBW1-serv-cv-124-Jul1 NCI, CGAP, Sub7 Homo sapiens cDNA clone IMAGE308542 3'
6221	19067	26237	3.34	6.0E-35	AY1780143.1	EST_HUMAN	h00306.x1 Soares, NGF, FGF, GW, OT, PA, P-31 Homo sapiens cDNA clone IMAGE2126166 3' similar to gM11949 PANCREATIC SECRETORY TRYPSIN INHIBITOR PRECURSOR (HUMAN);
7027	16904	27050	2.21	6.0E-35	AF208161.1	NT	h006402.x1 NCI, CGAP, C-044 Homo sapiens cDNA clone IMAGE309327 3' similar to SW:IMA2_HUMAN
8813	16848	26931	2.74	6.0E-35	AB60460.1	EST_HUMAN	Homo sapiens synaptin precursor, mRNA, complete cds
9821	16880	28071	1.99	6.0E-35	BE737154.1	EST_HUMAN	h00306.x1 Soares, NGF, FGF, GW, OT, PA, P-31 Homo sapiens cDNA clone IMAGE309327 3' similar to gM11949 PANCREATIC SECRETORY TRYPSIN INHIBITOR PRECURSOR (HUMAN);
1331	10107	19926	6.69	5.0E-35	AJ271735.1	NT	h00306.x1 Soares, NGF, FGF, GW, OT, PA, P-31 Homo sapiens cDNA clone IMAGE309327 3' similar to gM11949 PANCREATIC SECRETORY TRYPSIN INHIBITOR PRECURSOR (HUMAN);
2722	12884	22476	7.71	5.0E-35	BE398436.1	NT	Homo sapiens Xq pseudautosomal region, segment 12
3581	13475	23284	1.96	5.0E-35	AL16209.2	NT	Homo sapiens Xq pseudautosomal region, segment 12
4678	14564	24350	1.42	5.0E-35	5729729	NT	Homo sapiens chromosome 21 segment HS21C009
4678	14564	24350	1.42	5.0E-35	5729729	NT	Homo sapiens chromosome 21 segment HS21C009
9028	10107	19926	2.54	5.0E-35	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 12

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Mean Similar (Top) HL BLAST E Value	Top HL Accession No.	Top Hit Database Source	Top Hit Descriptor
6816	19010	25337	2.36	5.0E-36	11417602	NT	Homo sapiens calcitriol binding protein 1 (KAA0339), mRNA
1205	11115	20961	1.49	4.0E-39	BE010033.1	EST_HUMAN	PM3-BN0176-100490-001-p4l BN0176 Homo sapiens cDNA
1424	11929	21196	1.64	4.0E-39	P10268	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN (CONTAINS: REVERSE TRANSCRIPTASE); ENDONUCLEASE
1628	11330	21359	1.60	4.0E-39	BE33827.1	EST_HUMAN	601295547F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE362536 5'
2175	12962	21389	1.63	4.0E-39	AW24777.2	EST_HUMAN	2520020 SpHme NIH_MGC_7 Homo sapiens cDNA clone IMAGE292020 5'
3310	13231	23036	3.21	4.0E-39	BE39529.1	EST_HUMAN	601282266F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE3014166 5'
3310	13231	23037	3.21	4.0E-39	BE39529.1	EST_HUMAN	601282266F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE3014166 5'
5693	15902	25704	2.21	4.0E-39	1149704.1	NT	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), transcript variant 3, mRNA
6511	16370	26547	1.74	4.0E-39	M33320.1	EST_HUMAN	Human placental Glycodelin, 1b (GP1b) gene, exons 2-29
6979	16568	27050	1.41	4.0E-39	D37675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
6979	16568	27051	1.41	4.0E-39	D37675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
8366	16233	25481	2.19	4.0E-39	AA400370.1	EST_HUMAN	208610.1 Scores, Islets, NHT Homo sapiens cDNA clone IMAGE_743250 5'
9334	19015	25481	1.31	4.0E-39	114205168	NT	Homo sapiens nuclear factor of activated T-cells, cytoplasmic 2 (NFATC2), mRNA
9360	19548	25481	2.65	4.0E-39	AV759329	EST_HUMAN	AV759329 TP Homo sapiens cDNA clone TP-CABH01 5'
681	10814	20437	2.73	3.0E-39	AF099810.1	EST_HUMAN	Homo sapiens nucleoside 11-sigma gene, partial cds
2362	12108	23933	0.99	3.0E-39	786240.1	NT	Homo sapiens (KIA03952) protein (KIA03952), mRNA
4402	14297	24084	5.15	3.0E-39	0918133	NT	Major nucleoside diphosphate 1 (Dp-terminus), mRNA
8452	15225	25684	1.75	3.0E-39	BF03527.1	EST_HUMAN	601455351F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE362056 5'
3132	13037	22587	2.71	2.0E-39	BE259237.1	EST_HUMAN	601106943F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE3342708 5'
4877	14797	24634	4.82	2.0E-39	AF160376.1	EST_HUMAN	Mus musculus P47-phox gene, complete cds
5371	15291	25127	2.16	2.0E-39	AF297747.1	NT	EST106848 Infant Brain, Dentis Secret Homo sapiens cDNA clone IMAGE33908 5'
5567	15483	25566	3.99	2.0E-39	T69525.1	EST_HUMAN	RC1100069F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE369450 5'
5962	15597	25569	11.62	2.0E-39	T69525.1	EST_HUMAN	RC1100069F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE369450 5'
867	10793	20943	1.9	1.0E-39	BE409310.1	EST_HUMAN	RCH107217-131169-02-107 HT0217 Homo sapiens cDNA
2096	11987	21684	0.86	1.0E-39	BE146823.1	EST_HUMAN	RCH107217-131169-02-107 HT0217 Homo sapiens cDNA
2096	11987	21685	0.86	1.0E-39	BE146823.1	EST_HUMAN	RCH107217-131169-02-107 HT0217 Homo sapiens cDNA
2155	12043	21842	1.31	1.0E-39	BF073161.1	EST_HUMAN	602199493F1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE_4272866 5'
5762	16980	26711	6.94	1.0E-39	AA1867714.1	EST_HUMAN	W637C12.x1 NC1_OCAP_G03 Homo sapiens cDNA clone IMAGE_2307862 3' similar to contains Alu repetitive element
9840	16920	26711	2.03	1.0E-39	AA148034.1	EST_HUMAN	z051612.1 Striatum endothelial cell 507223 Homo sapiens cDNA clone IMAGE_590386 5'
6640	16920	26712	2.03	1.0E-39	AA148034.1	EST_HUMAN	z051612.1 Striatum endothelial cell 507223 Homo sapiens cDNA clone IMAGE_590386 5'
7220	17097	27287	2.84	1.0E-39	AF103956.1	EST_HUMAN	xe82007.x1 NC1_OCAP_Bn03 Homo sapiens cDNA clone IMAGE_2614567 3'
7624	17674	27917	2.45	1.0E-39	BF364186.1	EST_HUMAN	QV3-NM1023-01060-199-101 NM1023 Homo sapiens cDNA

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8317	18194	28444	3.43	1.0E-50	AW897056.1	EST_HUMAN	CM3-NN0001-140400-147-1412.NN0001 Homo sapiens cDNA
8366	18674	28657	3.91	1.0E-36	AW14143.1	EST_HUMAN	UHF-BND-abc-03-04.1-1.NH_UGC_50 Homo sapiens cDNA clone IMAGE:3079277.5'
9203	18634		3.74	1.0E-36	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
9374	19024	28305	1.29	1.0E-36	11418121	NT	Homo sapiens chromosome 22 open reading frame 2 (C22ORF2), mRNA
9547	19214		3.07	1.0E-36	AL163213.2	NT	Homo sapiens chromosome 21 open reading frame 2 (C21ORF2), mRNA
9650	19271		2.95	1.0E-36	AF207223.1	NT	Homo sapiens Srd1 unc-34 domain protein 2 (SUN2) mRNA, partial cds
9358	19231	28390	1.96	9.0E-37	AW00927.1	EST_HUMAN	w83007.x1 NCL CGAP_C03 Homo sapiens cDNA clone IMAGE:2504245.3'
9358	19231	28391	1.96	9.0E-37	AW00927.1	EST_HUMAN	w83007.x1 NCL CGAP_C03 Homo sapiens cDNA clone IMAGE:2504245.3'
9442	19063		2.79	9.0E-37	W22918.1	EST_HUMAN	7304 Homo sapiens retina cDNA Tsp501-cleaved auxiliary Homo sapiens cDNA not directional
9143	19010	24781	1.38	8.0E-37	AB020984.1	NT	Homo sapiens mRNA for KIAA0877 protein, partial cds
9213	15136		1.7	8.0E-37	BE598077.1	EST_HUMAN	CM0-UT0003-050003-503-039.UT0003 Homo sapiens cDNA
5559	15475	25547	4.1	8.0E-37	BE330127.1	EST_HUMAN	MR29 repetitive element
5559	15475	25546	4.1	8.0E-37	BE330127.1	EST_HUMAN	MR29 repetitive element
5594	15469	25576	5.63	8.0E-37	AW84040.1	EST_HUMAN	MR29 repetitive element
5602	18462	26570	6.26	8.0E-37	X87344.1	NT	H sapiens DMA, DM8, HLA-2b, 1.PP2, LUP2, TAP2, DOB, DOB2 and RING8, 8, 10 and 14 genes
1253	11170		2.81	7.0E-37	AL042600.1	EST_HUMAN	RC1-CH0006-210100-012-029.1.CH0006 Homo sapiens cDNA
8140	18028	28274	6.77	7.0E-37	AI817700.1	EST_HUMAN	DKFZ494540.22.1.84 (synonym: hnc3) Homo sapiens cDNA clone DKFZ494540.22.5'
8288	18146	28388	4.16	7.0E-37	AI530702.1	EST_HUMAN	W62511.X1 NCL CGAP_Pmc02 Homo sapiens cDNA clone IMAGE:2475341.3' similar to contains PTRK2
9775	19252		2.48	6.0E-37	AF207223.1	NT	Imf07603.X1 NCL CGAP_Pmc02 Homo sapiens cDNA clone IMAGE:2165140.3' similar to contains L1.03.L1
5707	19515	28716	3.37	5.0E-37	AA307123.1	EST_HUMAN	Homo sapiens Srd1 unc-34 domain protein 2 (SUN2) mRNA, partial cds
5707	19515	28717	3.37	5.0E-37	AA307123.1	EST_HUMAN	EST178005 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
8282	18171		4.17	5.0E-37	7057117	NT	EST178005 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
9198	18631		3.57	5.0E-37	AF140773.1	NT	Homo sapiens glycine C-acetyltransferase (2-amino-3-ketobutyrate-CoA ligase) (GCA1), mRNA
2374	12254	22145	2.23	4.0E-37	AA702794.1	EST_HUMAN	2950504.31 Scores: Jctd Liver, spleen, INFLS_S1 Homo sapiens cDNA clone IMAGE:448015.3'
5100	19027		1.11	4.0E-37	NK02051.1	EST_HUMAN	EST25910 WATM1 Homo sapiens cDNA clone 52g10 similar to human STS 004101
1970	11863	21755	2.85	3.0E-37	AL046956.1	EST_HUMAN	DKFZ49454L2418.1.1.84 (synonym: hnc3) Homo sapiens cDNA clone DKFZ49454L2418
1970	11863	21756	2.85	3.0E-37	AL046956.1	EST_HUMAN	DKFZ49454L2418.1.1.84 (synonym: hnc3) Homo sapiens cDNA clone DKFZ49454L2418
2405	12241		3.02	3.0E-37	AW991100.1	EST_HUMAN	EST373222 IMAGE repeats, MAGF Homo sapiens cDNA
2536	12653		1.97	3.0E-37	AW991150.1	EST_HUMAN	EST373222 IMAGE repeats, MAGF Homo sapiens cDNA

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1064	10680	20824	1.94	2.0E-37	AL131202.1	EST_HUMAN	AL131202.1 NT2P3 Homo sapiens cDNA clone NT2P3002106 5'
1064	10860	20825	1.94	2.0E-37	AL131202.1	EST_HUMAN	AL131202.1 NT2P3 Homo sapiens cDNA clone NT2P3002106 5'
1821	11816	21695	1.47	2.0E-37	AF163247.2	NT	Homo sapiens chromosome 21 segment HS21C047 varianthomals), polypeptide 1 (CYP27A1b) mRNA
3818	13730	22519	5.05	2.0E-37	4930210	NT	EST52521 fetal heart II Homo sapiens cDNA 5' end
6007	15912	20039	3.36	2.0E-37	AA346720.1	EST_HUMAN	6018691971 NH1.MGC.17 Homo sapiens cDNA clone IMAGE:4111406 5'
6595	16565	26759	3.23	2.0E-37	BF204032.1	EST_HUMAN	Homo sapiens 1 domain containing protein 1 isoform 5 (DPF1) mRNA, complete cds
8545	18657	28945	16.4	2.0E-37	AF176013.1	NT	Homo sapiens pectadillo (zebrin) homolog 1, containing BRCT domain (PEST1), mRNA
9523	19403		3.15	2.0E-37	11417972	NT	Homo sapiens chromosome 21 segment HS21C081
2041	11923	21828	3.91	1.0E-37	AF163281.2	NT	Homo sapiens ribonuclease III (RN3) mRNA, complete cds
3878	13766	23577	22.51	1.0E-37	AF180011.1	NT	601448610P1 NH1.MGC.65 Homo sapiens cDNA clone IMAGE:3852582 5'
4072	13974	23763	0.95	1.0E-37	BS672395.1	EST_HUMAN	OV0-ENR180-260700-318<-10 FN0750 Homo sapiens cDNA
4827	14767	24617	2.13	1.0E-37	BF537178.1	EST_HUMAN	3271b02-r1 Striata neuroepithelium (R67231) Homo sapiens cDNA clone IMAGE:810059 5' similar to contains L1, L2, L1 repeat element:
7072	18946	27141	2.95	1.0E-37	AA171406.1	EST_HUMAN	Human somatic cyclohexa (HSC) processed pseudogene, complete cds
9382	17973	28222	20.59	1.0E-37	U2376.1	NT	CH2E17008-140700-243-397 FN0398 Homo sapiens cDNA
9598	19122		2.48	1.0E-37	BE771814.1	EST_HUMAN	Human nervous multidomain protein Pico (LOC56758), mRNA
5533	19447	28514	3.05	8.0E-38	10449482	NT	Homo sapiens GNAI1-AS1 (GNAI1-AS1), mRNA
1203	11113	20536	1.90	8.0E-38	11439955	NT	602016401T1 UCL CGAP_Bio67 Homo sapiens cDNA clone IMAGE:415992 5'
2449	12326	22225	1.44	8.0E-38	BF346221.1	EST_HUMAN	Homo sapiens GNAI1-AS1 (GNAI1-AS1), mRNA
9558	11113	20590	1.38	7.0E-38	AF192025.1	EST_HUMAN	EST1384620 MAGI2 resequencing, MAGI2 Homo sapiens cDNA
2159	12021	21920	1.38	6.0E-38	BF050033.1	EST_HUMAN	601465722P1 NH1.MGC.65 Homo sapiens cDNA clone IMAGE:3855348 5'
3005	12553	22726	1.76	6.0E-38	BF050033.1	EST_HUMAN	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
5432	13352	25407	1.95	6.0E-38	11425114	NT	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
5432	13352	25408	1.69	6.0E-38	11425114	NT	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
9000	18842		4.46	8.0E-38	11435947	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
9542	19143	25266	6.86	6.0E-38	A9002059.1	NT	Homo sapiens DNA for Human PDXM, complete cds
710	10042	21468	1.15	5.0E-38	AF071919.1	EST_HUMAN	Homo sapiens RHR gene (partial), exon 8
2404	12281	22178	1.79	5.0E-38	AJ237440.1	NT	601490148P1 NH1.MGC.65 Homo sapiens cDNA clone IMAGE:3854074 5'
6191	16076	28225	2.42	5.0E-38	BE871610.1	EST_HUMAN	B human mitochondrial aspartate aminotransferase mRNA, complete cds
113	10052	19009	2.96	4.0E-38	725466.1	NT	B human mitochondrial aspartate aminotransferase mRNA, complete cds
113	10062	19910	2.36	4.0E-38	725466.1	NT	B human mitochondrial aspartate aminotransferase mRNA, complete cds
1141	11055	20897	0.82	3.0E-38	11435947	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
2033	11943		4.39	3.0E-38	AF063530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions

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Table 4
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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3638	13652		1.11	3.0E-36	7549807	NT	Homo sapiens HIRA interacting protein 4 (dms-like) [HIRP4], mRNA
3781	13663	23460	1.05	3.0E-36	P53338	SWISSPROT	SSU72 PROTEIN
3781	13663	23461	1.85	3.0E-36	P53338	SWISSPROT	SSU72 PROTEIN
4513	14406		0.85	3.0E-36	BE770301.1	EST_HUMAN	00117633P1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3504272 5'
6050	19450	28043	7.17	3.0E-36	BE770300.2	NT	Homo sapiens chromosome 21 segment HS21C100
6478	18337	26504	7.84	3.0E-36	BF37664.1	EST_HUMAN	CX3-FT0181-140700-241407-170181 Homo sapiens cDNA
7025	16902	27094	1.78	3.0E-36	H54594.1	EST_HUMAN	Y68804.11 Soares melanocyte ZN81M Homo sapiens cDNA clone IMAGE:240776 5'
7025	16902	27095	1.78	3.0E-36	H54594.1	EST_HUMAN	Y68804.11 Soares melanocyte ZN81M Homo sapiens cDNA clone IMAGE:240776 5'
7727	17671		1.38	3.0E-36	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
44	10032	19636	1.41	2.0E-36	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
1358	11284	21120	2.6	2.0E-36	5902267	NT	Homo sapiens SMY3 (suppressor of mit two 3, yeast) homolog 2 [SMT3H2], mRNA
1627	11831	21390	1.66	2.0E-36	AA437353.1	EST_HUMAN	2603001.1 Soares ovary tumor NHHOT Homo sapiens cDNA clone IMAGE:770765 5' similar to
1627	11831	21391	1.66	2.0E-36	AA437353.1	EST_HUMAN	2603001.1 Soares ovary tumor NHHOT Homo sapiens cDNA clone IMAGE:770765 5' similar to
8941	16819		4.7	2.0E-36	BE105980.1	EST_HUMAN	SW MA12, RABIT P45701 MANNOsyl-OLIGOSACCHARIDE ALPHA-1,3-MANNOSIDASE ;
7316	17102		1.47	2.0E-36	BE22255.1	EST_HUMAN	SW MA12, RABIT P45701 MANNOsyl-OLIGOSACCHARIDE ALPHA-1,3-MANNOSIDASE ;
7970	17820	28043	1.85	2.0E-36	D58479.2	NT	MR3-HT0437: 50200-113-201 HT0437 Homo sapiens cDNA
8781	18586	28865	5.24	2.0E-36	BE172700.1	EST_HUMAN	GAG POLYPROTEIN ;
8807	18715	29008	3.86	2.0E-36	AF193501.1	NT	Homo sapiens cDNA clone IMAGE:3180100 3' similar to TR-02710 C02710
8807	18715	29009	3.86	2.0E-36	AF193501.1	NT	Homo sapiens leucine-rich repeat-containing G protein-coupled receptor 8 (LGR8) mRNA, partial cds
9112	18876		4.05	2.0E-36	AF193501.1	NT	Homo sapiens leucine-rich repeat-containing G protein-coupled receptor 8 (LGR8) mRNA, partial cds
9115	18878		4.05	2.0E-36	AF193501.1	NT	AV20586 HIC Homo sapiens cDNA clone HTCA007 5'
9412	19364	29313	3.86	2.0E-36	H55941.1	EST_HUMAN	Homo sapiens gene for kinin-like protein, complete cds
9472	19069		2.26	2.0E-36	S74906.1	NT	CHP20580 Chromosome 22 exon Homo sapiens cDNA clone G22.788 5'
9024	18966		2.85	2.0E-36	11418249	NT	E1 beta-primase dehydrogenase beta (primase) Human, placenta, Genomic, 1280 nt
1077	10663		2.29	1.0E-36	AA401570.1	EST_HUMAN	Homo sapiens sulfotransferase-related protein (SULTX3) mRNA
1854	11849	21736	0.84	1.0E-36	4863288	NT	236202.1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:742639 5' similar to contains element
1973	11866	21738	1.0E-36	1.0E-36	7661969	NT	MER10 repetitive element ;
2445	12221		1.88	1.0E-36	AF270631.1	NT	Homo sapiens guanine nucleotides binding protein-like 1 (GNL1), mRNA
							Homo sapiens KIA0073 gene product (KIA0073), mRNA
							Homo sapiens cydin K (COCK) gene, exon 7

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4053	13665	23743	1.41	1.0E-36	AB037863.1	NT	Homo sapiens mRNA for KIAA1442 protein, partial cds
4223	14121	23856	0.93	1.0E-36	4805016	NT	Homo sapiens low density lipoprotein receptor-related protein 6 (LRP6) mRNA, and translated products
4226	14127	23902	1.31	1.0E-36	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4228	14127	23903	1.31	1.0E-36	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4463	14387	24173	1.21	1.0E-36	8022543	NT	Homo sapiens hypothetical protein FLJ10800 (FLJ10800), mRNA
4573	15582	25662	3.61	1.0E-36	7305360	NT	Mus musculus diaphanin (Dpfn), mRNA
4573	15582	25683	3.61	1.0E-36	7305360	NT	Mus musculus diaphanin (Dpfn), mRNA
6376	16240	28400	2.78	1.0E-36	AB014612.1	NT	Homo sapiens mRNA for KIAA0572 protein, partial cds
7414	17281	27486	6.23	1.0E-36	BE330127.1	EST_HUMAN	NR0921 v1 NCL CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER26.83
9254	19461	19461	2.33	1.0E-36	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
948	19368	1942	6.14	8.0E-36	460212	NT	Homo sapiens ATPase, H+ transporting, lysosomal (vacuolar protein pump) 16G (ATP6C) mRNA
1372	11275	21134	1.31	8.0E-36	4755223	NT	Homo sapiens estrogen receptor-binding fragment-associated gene 6 (EBAG6) mRNA
1768	11686		1.06	8.0E-36	AB22304.1	EST_HUMAN	W55870 v1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:288491 3' similar to TRP-p7890 P67890
2047	11938	21832	5.34	7.0E-36	AL163272.2	NT	POL PROTEIN 1
6164	18070	28319	2.12	8.0E-36	AF531623.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C027
6808	16537		2.23	8.0E-36	BE579384.1	EST_HUMAN	QY-1510531 CG0000367-462 BT0031 Homo sapiens cDNA
691	10012	20757	1.3	5.0E-36	AF069528.1	NT	7464033.X1 NCL CGAP_L104 Homo sapiens cDNA clone IMAGE:3284366 3' similar to WIP-R151.6
2067	12584	22652	5.13	5.0E-36	AF1790194.1	EST_HUMAN	Homo sapiens X-linked arylidic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat
9546	19154		1.54	5.0E-36	11420296	NT	af59604.v1 Barleaded codon IPI-RE7 Homo sapiens cDNA clone IMAGE:2374083 3' similar to TR-Q15408
538	10-78	20281	10.53	4.0E-36	AF016910.1	NT	Q15408 NEUTRAL PROTEINASE LARGE SUBUNIT: contains LTR/1 LTR repetitive element:
3625	13-41	23238	0.86	4.0E-36	AL163210.2	NT	Homo sapiens hypothetical protein FLJ10803 (FLJ10803), mRNA
6707	16587	28775	1.46	4.0E-36	AF692490.1	EST_HUMAN	Chlorococcus arbuscule mRNA for ribosomal protein S42, complete cds
9575	19164		2.03	4.0E-36	11418177	NT	Homo sapiens chromosome 21 segment HS21C010
9857	19240		3.08	4.0E-36	BE336452.1	EST_HUMAN	Homo sapiens schizo brain S11 Homo sapiens cDNA clone IMAGE:1020438 3' similar to contains
41	10025	19830	11.27	3.0E-36	AF631949.1	EST_HUMAN	OPR-1.1 OPR repetitive element;
41	10025	19831	11.27	3.0E-36	AF631949.1	EST_HUMAN	Homo sapiens brain GTPase activating protein 1 (RANGAP1), mRNA
							QY-PN0058-26600-278-058 FN0063 Homo sapiens cDNA
							Imf1c16 Regional genomic DNA specific cDNA Library Homo sapiens cDNA clone CR12-1
							Imf1c16 Regional genomic DNA specific cDNA Library Homo sapiens cDNA clone CR12-1

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41	10026	18832	11.27	3.0E-39	AA631849.1	EST_HUMAN	IMR16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1 063a10.81 Soares, NHMPU, S1 Homo sapiens cDNA clone IMAGE:1800980 3' similar to SW/GTR5_RAT
9104	18871	28781	5.91	3.0E-39	A094557.1	EST_HUMAN	P43427 GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE: 063a10.81 Soares, NHMPU, S1 Homo sapiens cDNA clone IMAGE:1800980 3' similar to SW/GTR5_RAT
9104	18871	28782	5.91	3.0E-39	A094557.1	EST_HUMAN	P43427 GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE: 063a10.81 Soares, NHMPU, S1 Homo sapiens cDNA clone IMAGE:1800980 3' similar to SW/GTR5_RAT
8127	18600		4.42	3.0E-39	A078903.1	EST_HUMAN	063a10.81 Soares, NHMPU, S1 Homo sapiens cDNA clone IMAGE:1800980 3' similar to SW/GTR5_RAT
879	18665		4.05	2.0E-39	BE08203.1	EST_HUMAN	063a10.81 Soares, NHMPU, S1 Homo sapiens cDNA clone IMAGE:1800980 3' similar to SW/GTR5_RAT
884	18620		17.24	2.0E-39	A125816.1	EST_HUMAN	063a10.81 Soares, NHMPU, S1 Homo sapiens cDNA clone IMAGE:1800980 3' similar to SW/GTR5_RAT
1015	18633		3.91	2.0E-39	A150073.1	EST_HUMAN	063a10.81 Soares, NHMPU, S1 Homo sapiens cDNA clone IMAGE:1800980 3' similar to SW/GTR5_RAT
1513	11418		10.15	2.0E-39	AV322916.1	EST_HUMAN	063a10.81 Soares, NHMPU, S1 Homo sapiens cDNA clone IMAGE:1800980 3' similar to SW/GTR5_RAT
1890	11825	21707	10.03	2.0E-39	AA72874.1	EST_HUMAN	063a10.81 Soares, NHMPU, S1 Homo sapiens cDNA clone IMAGE:1800980 3' similar to SW/GTR5_RAT
2587	12458	22349	1.75	2.0E-39	AL16243.2	NT	063a10.81 Soares, NHMPU, S1 Homo sapiens cDNA clone IMAGE:1800980 3' similar to SW/GTR5_RAT
4393	14201	23865	1.36	2.0E-39	BF37037.1	EST_HUMAN	063a10.81 Soares, NHMPU, S1 Homo sapiens cDNA clone IMAGE:1800980 3' similar to SW/GTR5_RAT
5375	15395	25142	3.4	2.0E-39	AA08980.1	EST_HUMAN	063a10.81 Soares, NHMPU, S1 Homo sapiens cDNA clone IMAGE:1800980 3' similar to SW/GTR5_RAT
6560	16223	20364	2.17	2.0E-39	AA08987.1	EST_HUMAN	063a10.81 Soares, NHMPU, S1 Homo sapiens cDNA clone IMAGE:1800980 3' similar to SW/GTR5_RAT
8173	18387	28874	2.33	2.0E-39	D89564.1	NT	063a10.81 Soares, NHMPU, S1 Homo sapiens cDNA clone IMAGE:1800980 3' similar to SW/GTR5_RAT
9622	18394		2.31	2.0E-39	11425464	NT	063a10.81 Soares, NHMPU, S1 Homo sapiens cDNA clone IMAGE:1800980 3' similar to SW/GTR5_RAT
1497	11401	21251	1.78	1.0E-39	AJ00345.1	NT	063a10.81 Soares, NHMPU, S1 Homo sapiens cDNA clone IMAGE:1800980 3' similar to SW/GTR5_RAT
1497	11401	21252	1.78	1.0E-39	AJ00345.1	NT	063a10.81 Soares, NHMPU, S1 Homo sapiens cDNA clone IMAGE:1800980 3' similar to SW/GTR5_RAT
1514	11419	21275	4.95	1.0E-39	7657020	NT	063a10.81 Soares, NHMPU, S1 Homo sapiens cDNA clone IMAGE:1800980 3' similar to SW/GTR5_RAT
4581	14453	24239	5.49	1.0E-39	AW651995.1	EST_HUMAN	063a10.81 Soares, NHMPU, S1 Homo sapiens cDNA clone IMAGE:1800980 3' similar to SW/GTR5_RAT
4581	14453	24240	5.49	1.0E-39	AW651995.1	EST_HUMAN	063a10.81 Soares, NHMPU, S1 Homo sapiens cDNA clone IMAGE:1800980 3' similar to SW/GTR5_RAT
4604	14492	24279	8.88	1.0E-39	7857020	NT	063a10.81 Soares, NHMPU, S1 Homo sapiens cDNA clone IMAGE:1800980 3' similar to SW/GTR5_RAT
5459	15579	25339	1.54	1.0E-39	T81876.1	EST_HUMAN	063a10.81 Soares, NHMPU, S1 Homo sapiens cDNA clone IMAGE:1800980 3' similar to SW/GTR5_RAT
5475	15395	25460	4.36	1.0E-39	AJ278170.1	NT	063a10.81 Soares, NHMPU, S1 Homo sapiens cDNA clone IMAGE:1800980 3' similar to SW/GTR5_RAT
5475	15395	25461	4.36	1.0E-39	AJ278170.1	NT	063a10.81 Soares, NHMPU, S1 Homo sapiens cDNA clone IMAGE:1800980 3' similar to SW/GTR5_RAT
6033	16028		1.66	1.0E-39	11436739	NT	063a10.81 Soares, NHMPU, S1 Homo sapiens cDNA clone IMAGE:1800980 3' similar to SW/GTR5_RAT
6357	16020	26382	1.75	1.0E-39	D78132.1	NT	063a10.81 Soares, NHMPU, S1 Homo sapiens cDNA clone IMAGE:1800980 3' similar to SW/GTR5_RAT
543	10484	20294	1.67	9.0E-40	5803210	NT	063a10.81 Soares, NHMPU, S1 Homo sapiens cDNA clone IMAGE:1800980 3' similar to SW/GTR5_RAT
1215	11123	20671	10.19	9.0E-40	4755145	NT	063a10.81 Soares, NHMPU, S1 Homo sapiens cDNA clone IMAGE:1800980 3' similar to SW/GTR5_RAT
1215	11123	20672	10.19	9.0E-40	4755145	NT	063a10.81 Soares, NHMPU, S1 Homo sapiens cDNA clone IMAGE:1800980 3' similar to SW/GTR5_RAT

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Mean Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1433	11338	21285	5.04	9.0E-40	4507512	NT	Homo sapiens tissue inhibitor of metalloproteinase 3 (Sorcery fundus dysplastic, pseudoinflammatory) (TIMP3) mRNA
3852	15069	23486	3.88	9.0E-40	A9033070.1	NT	Homo sapiens mRNA for KIAA1244 protein, partial cds
4250	14149	23923	0.82	9.0E-40	4507948	NT	Homo sapiens ubiquitin specific protease 13 (isopapillae T-3) (USP13) mRNA
4365	14149	23923	1.12	9.0E-40	4507948	NT	Homo sapiens ubiquitin specific protease 13 (isopapillae T-3) (USP13) mRNA
3004	12632	22725	0.95	8.0E-40	AA078165.1	EST_HUMAN	Homo sapiens cDNA clone IMAGE3918164
3847	13758		2.41	8.0E-40	5E396541.1	EST_HUMAN	HT126933P1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE3918166 5'
8541	16359	28578	1.56	7.0E-40	U60326.1	NT	Human DNA polymerase gamma mRNA, nuclear gene encoding mitochondrial protein, complete cds
8541	16359	28578	1.56	7.0E-40	U60326.1	NT	Human DNA polymerase gamma mRNA, nuclear gene encoding mitochondrial protein, complete cds
8270	18150	28391	2.83	7.0E-40	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
2595	12580	22448	3.88	6.0E-40	AA391275.1	EST_HUMAN	EST170527 T-cell lymphoma Homo sapiens cDNA 5' end similar to zho finger protein family
2595	12580	22448	3.88	6.0E-40	AA391275.1	EST_HUMAN	EST170527 T-cell lymphoma Homo sapiens cDNA 5' end similar to zho finger protein family
6816	16531		2.07	6.0E-40	5E504786.1	EST_HUMAN	h54407.1 NCI CGAP G05 Homo sapiens cDNA clone IMAGE3310480 3'
8141	15968	28124	3.08	6.0E-40	11139783	NT	Homo sapiens fatty acid desaturase 1 (FADS1) mRNA
8141	15968	28125	3.08	6.0E-40	11139783	NT	Homo sapiens fatty acid desaturase 1 (FADS1) mRNA
7131	17881	27804	0.82	6.0E-40	AV65028.1	EST_HUMAN	AV65028 GLO Homo sapiens cDNA clone GLODGR04 3'
7131	17881	27805	0.82	6.0E-40	AV65028.1	EST_HUMAN	AV65028 GLO Homo sapiens cDNA clone GLODGR04 3'
2591	12453	22326	1.89	5.0E-40	AL162852.2	NT	Homo sapiens chromosome 21 segment HS21C038
1634	11731	21607	1.38	4.0E-40	AI68006.1	EST_HUMAN	h51641.x1 NCI CGAP J728 Homo sapiens cDNA clone IMAGE2246873 3' similar to TRO73568 O73565 POL PROTEIN 1;
2061	11951		2.67	4.0E-40	AF06523.1	NT	Homo sapiens X-linked antidiabetic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
4251	14189	23973	7.85	4.0E-40	7662117	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
0682	16542	28738	3.76	4.0E-40	AA742669.1	EST_HUMAN	h54407.1 NCI CGAP B47 Homo sapiens cDNA clone IMAGE1227122
7237	17114	27968	4.87	4.0E-40	5E009418.1	EST_HUMAN	P40-B0167.070500-002-H12 BN0167 Homo sapiens cDNA
7237	17114	27968	4.87	4.0E-40	5E009418.1	EST_HUMAN	P40-B0167.070500-002-H12 BN0167 Homo sapiens cDNA
8099	17669	28238	4.07	4.0E-40	AA184185.1	EST_HUMAN	RCT1 CN00177:12000-012 g4 CN00177 Homo sapiens cDNA
4040	13943	23721	0.86	3.0E-40	AI625649.1	EST_HUMAN	WT12607.x1 NCI CGAP K611 Homo sapiens cDNA clone IMAGE2300440 3'
8001	15906	26030	6.25	3.0E-40	11417942	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A), mRNA

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6882	16761	26856	4.28	3.0E-40	5454167	NT	Homo sapiens HBV associated factor (XAP4) mRNA
7186	17083	27253	1.46	3.0E-40	AF078776.1	NT	Rattus norvegicus putative four repeat bin channel mRNA, complete cds
7312	17188	27389	1.52	3.0E-40	AF078778.1	NT	Rattus norvegicus putative four repeat bin channel mRNA, complete cds
8387	18264	28515	1.93	3.0E-40	BE330127.1	EST_HUMAN	MG95.01.x1 NGL CGAP K413 Homo sapiens cDNA clone IMAGE:3146266 3' similar to contains MER29.B3
8588	18456	28725	11.23	3.0E-40	6005913	NT	MER29 repetitive element;
							Homo sapiens serine threonine protein kinase (NDR), mRNA
8855	18667	28954	1.96	3.0E-40	AW118799.1	EST_HUMAN	xd89402.x1 Scores, NGL_T_OBC_S1 Homo sapiens cDNA clone IMAGE:2605491 3' similar to TRC16804
322	10263		12.99	2.0E-40	AI223036.1	EST_HUMAN	Q19504 SIMILAR TO ENV OF TYPE A AND TYPE B RETROVIRUSES AND TO CLASS II HERV3 ;
							9525208.x1 Scores, testis, NHT Homo sapiens cDNA clone IMAGE:1838847 3'
777	10707		2.72	2.0E-40	AW303698.1	EST_HUMAN	9524010.x1 NGL CGAP UM Homo sapiens cDNA clone IMAGE:2781068 3' similar to SW_RSS_MOUSE
1783	11681		1.4	2.0E-40	AV71601.1	EST_HUMAN	P97481.4S RIBOSOMAL PROTEIN S5 ;
1822	11787	21684	2.16	2.0E-40	4505188	NT	AV731601.1HTF Homo sapiens cDNA clone HTFZC05 5'
							Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 7 (PSMA7) mRNA, and translated products
1832	11787	21685	2.16	2.0E-40	4506188	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 7 (PSMA7) mRNA, and translated products
							958411.x1 NGL CGAP G06 Homo sapiens cDNA clone IMAGE:2514716 3' similar to TR-Q81929 Q81929
2028	11917	21807	1.08	2.0E-40	A965562.1	EST_HUMAN	ZINC FINGER PROTEIN ;
2123	12011	21910	2.81	2.0E-40	5435592	NT	Homo sapiens cDNA/MY cyclase-associated protein 2 (CAP2) mRNA
2333	12214	22112	2.35	2.0E-40	AJ277652.1	NT	Homo sapiens cardiac TTN gene for titin
2658	12526		1.08	2.0E-40	BE276932.1	EST_HUMAN	601121567.1 NH_MGC_20 Homo sapiens cDNA clone IMAGE:3045784 5'
3097	13014	22906	3.86	2.0E-40	5435592	NT	Homo sapiens cDNA/MY cyclase-associated protein 2 (CAP2) mRNA
4607	14691	24478	1.49	2.0E-40	AL163280.2	NT	Homo sapiens chromosome 21 segment158210350
4607	14691	24479	1.46	2.0E-40	AL163280.2	NT	Homo sapiens chromosome 21 segment158210350
886	10791		1.95	1.0E-40	AD23966.1	EST_HUMAN	nc83608.x1 NGL CGAP-F11 Homo sapiens cDNA clone IMAGE:3853503 5'
2560	12451	22343	1.91	1.0E-40	59036851.1	EST_HUMAN	60146037.7 NH_MGC_09 Homo sapiens cDNA clone IMAGE:3046870 5' similar to TR-Q82168 Q82168
2653	12520		1.92	1.0E-40	BE018348.1	EST_HUMAN	SYNTAXIN 17 ;
2707	12570	22460	0.82	1.0E-40	BF541030.1	EST_HUMAN	60266604.1 NH_MGC_58 Homo sapiens cDNA clone IMAGE:4067758 5'
2707	12570	22461	0.82	1.0E-40	BF541030.1	EST_HUMAN	60266604.1 NH_MGC_58 Homo sapiens cDNA clone IMAGE:4067758 5'
3258	13181		1.81	1.0E-40	4507142	NT	Homo sapiens sorting nexin 3 (SNX3) mRNA
4505	14398	24184	6.28	1.0E-40	4506012	NT	Homo sapiens zinc finger protein 200 (ZNF200) mRNA, and translated products
4892	14772	24650	0.86	1.0E-40	7705776	NT	Homo sapiens C9orf68 protein (LOC51103), mRNA

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Table 4

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Mean Similarity Top Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8215	16081	26230	2.03	1.0E-40	AA573201.1	EST_HUMAN	H12604.x1 NCI CGAP_AAT1 Homo sapiens cDNA clone IMAGE:395167 3'
8215	16091	26231	2.03	1.0E-40	AA573201.1	EST_HUMAN	H12604.x1 NCI CGAP_AAT1 Homo sapiens cDNA clone IMAGE:395167 3'
8265	18166	28412	6.72	1.0E-40	AJ1169346.1	EST_HUMAN	AJ146345 N12R04 Homo sapiens cDNA clone NT2RM4002/22 3'
8355	18233	28450	6.33	1.0E-40	AJ235572.1	EST_HUMAN	q311n10.x1 Soares_NFL1_GSC_S1 Homo sapiens cDNA clone IMAGE:1846339 3'
8521	18223		3.93	1.0E-40	BF334112.1	EST_HUMAN	MF2-CT0222-211099-002-w10 CT0222 Homo sapiens cDNA
8521	16051	26689	1.73	8.0E-41	AL193203.2	NT	Homo sapiens chromosome 21 segment HS21C003
811	12678	20585	2.36	7.0E-41	A634394.1	EST_HUMAN	W04404.x1 NCI CGAP_K411 Homo sapiens cDNA clone IMAGE:2403865 3'
811	12678	20586	2.36	7.0E-41	A634394.1	EST_HUMAN	W04404.x1 NCI CGAP_K411 Homo sapiens cDNA clone IMAGE:2403865 3'
8555	15567	25663	3.27	7.0E-41	1118206	NT	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), mRNA
8531	19218		4.82	7.0E-41	11181972	NT	Homo sapiens pascadriol (zabrafish) homolog 1, containing BRCT domain (PES1), mRNA
270	10244	20064	1.72	6.0E-41	AB007163.1	NT	Homo sapiens DSCR5b, mRNA, complete cds
2034	11954	21851	2.19	6.0E-41	7687043	NT	Homo sapiens Down syndrome candidate region 1 (DSOR1), mRNA
4324	11260	24041	0.34	8.0E-41	3E557676.1	EST_HUMAN	60734045F1 NHL_MGC_53 Homo sapiens cDNA clone IMAGE:3582677 5'
1761	11660	21932	1.31	5.0E-41	T62628.1	EST_HUMAN	Y37810.31 Sijpe's lung (4537210) Homo sapiens cDNA clone IMAGE:79528 3'
4018	13622		0.38	5.0E-41	4885330	NT	Homo sapiens lung (4537210) Homo sapiens cDNA clone IMAGE:79528 3'
5946	15850		2.85	5.0E-41	BE607042.1	EST_HUMAN	PALC1T0341.251102-002-F11 BT0341 Homo sapiens cDNA
385	10532		1.91	4.0E-41	15E136718.1	EST_HUMAN	Q10-IT0361 50200-114-261 IT0361 Homo sapiens cDNA
1082	10666	26859	1.28	4.0E-41	AU119344.1	EST_HUMAN	AU119344 HENB1 Homo sapiens cDNA clone HENB1035863 5'
1388	11293	21148	9.42	4.0E-41	AB271171.1	EST_HUMAN	hw4508.s1 Soares_parrathyroid_tumor_NHAPA Homo sapiens cDNA clone IMAGE:1646794 3' similar to TRC006807/006807 CYTOCHROME C-LIKE POLYPEPTIDE; contains LTR3.5' LTR3' repetitive element;
1388	11293	21150	9.42	4.0E-41	AB271171.1	EST_HUMAN	hw4508.s1 Soares_parrathyroid_tumor_NHAPA Homo sapiens cDNA clone IMAGE:1646794 3' similar to TRC006807/006807 CYTOCHROME C-LIKE POLYPEPTIDE; contains LTR3.5' LTR3' repetitive element;
1404	11309	21170	2.12	4.0E-41	AB500681.1	NT	Homo sapiens gene for action receptor type IIB, complete cds
1018	11622	21380	8.5	4.0E-41	AI500406.1	EST_HUMAN	hw6604.x1 NCI CGAP_Bln25 Homo sapiens cDNA clone IMAGE:216959 3' similar to contains ORF.b1 ORF repetitive element;
2859	12787	22578	3.03	4.0E-41	AJ225041.1	NT	Homo sapiens 550 kb contig between AML1 and OBR1 on chromosome 21q22; segment 1/3
2859	12787	22578	3.03	4.0E-41	AJ225041.1	NT	Homo sapiens 550 kb contig between AML1 and OBR1 on chromosome 21q22; segment 1/3
4052	13554	23730	1.89	4.0E-41	X92885.1	NT	H. sapiens DNase I hypersensitive site (HSS-3) enhancer element
5920	15625		1.39	4.0E-41	AV1759256.1	EST_HUMAN	AV1759256 BM Homo sapiens cDNA clone BMFH006 5'
7500	17441	27657	6.01	4.0E-41	BF304683.1	EST_HUMAN	607168009F1 NHL_MGC_17 Homo sapiens cDNA clone IMAGE:4122119 5'
8625	18733		7.02	4.0E-41	AV170480.1	EST_HUMAN	AV170480 Qu Homo sapiens cDNA clone CuaACC07 5'
9559	19510		2.31	4.0E-41	AV708431.1	EST_HUMAN	AV708431 ADC Homo sapiens cDNA clone ADCAC02 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
632	10857	20704	1.94	3.0E-41	AB000176.1	NT	Homo sapiens PAD-H19 mRNA for peptidylarginine deiminase type II, complete cds
4240	14139	23914	3.08	3.0E-41	AB026896.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
5047	14619		0.85	3.0E-41	AB027748.1	NT	Homo sapiens mRNA for KIAA1327 protein, partial cds
5376	15296	25143	7.35	3.0E-41	X87689.1	NT	H. sapiens mRNA for putative p64 CLP protein
5849	15755	25873	1.48	3.0E-41	AB037808.1	NT	Homo sapiens mRNA for KIAA1387 protein, partial cds
1782	11443	21305	7.3	2.0E-41	U43701.1	NT	Human ribosomal protein L23a mRNA, complete cds
1915	11810	21984	2.03	2.0E-41	AA331940.1	EST_HUMAN	EST35818 Embryos, 8 week 1 Homo sapiens cDNA 5' end
2172	12059	21923	1.03	2.0E-41	D63682.1	NT	Human mRNA for KIAA0207 gene, complete cds
2224	12108	22010	4.07	2.0E-41	X86931.1	NT	Gordita DNA for ZNF80 gene homolog
2768	11443	21305	5.31	2.0E-41	U43701.1	NT	Human ribosomal protein L23a mRNA, complete cds
4521	14141	24198	1.06	2.0E-41	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C087
4621	14141	24200	1.06	2.0E-41	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C087
6521	16381	26398	0.99	2.0E-41	AF038404.1	NT	Homo sapiens homolog of Nucleo (Nucleo) mRNA, complete cds
9722	16382	26772	1.33	2.0E-41	X69944.1	NT	Human B-cell specific transcription factor (BS-TP) mRNA, complete cds
9722	16382	26773	1.33	2.0E-41	X69944.1	NT	Human B-cell specific transcription factor (BS-TP) mRNA, complete cds
9716	16396	26780	1.36	2.0E-41	AF328266.1	EST_HUMAN	EST371726 Embryos, 12 week 1 Homo sapiens cDNA 5' end
17188	17055	27255	1.77	2.0E-41	U52742.1	SWISSPROT	ZINC FINGER PROTEIN T55
8777	18554	26882	3.46	2.0E-41	AA372687.1	EST_HUMAN	EST184695 Colon adenocarcinoma IV Homo sapiens cDNA 5' end
4465	14359	24149	4.64	2.0E-41	AF078948	NT	Mus musculus tubulin alpha 0 (Tub60), mRNA
7420	17287	27464	1.8	1.0E-41	AL217893.1	EST_HUMAN	Human sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA
9197	18630		2.83	1.0E-41	U1526291	NT	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA
6958	16836		1.33	9.0E-42	BC178191.1	EST_HUMAN	RCU-H10613-210300-002-401 HT0613 Homo sapiens cDNA
7252	17168	27367	2.63	9.0E-42	U1600151	NT	Homo sapiens hypothetical C5H2 zinc finger protein FLJ22304 (FLJ22304), mRNA
7252	17168	27368	2.63	9.0E-42	U1600151	NT	Homo sapiens hypothetical C5H2 zinc finger protein FLJ22304 (FLJ22304), mRNA
455	10399	20216	5.37	8.0E-42	AF003830.1	NT	Homo sapiens homeobox protein, CDX4 (CDX4) gene, complete cds and flanking repeat regions
							Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
2062	11852	21849	1.32	8.0E-42	AB026896.1	NT	h07402 s1 NOL_OGAP_Thy1 Homo sapiens cDNA clone IMAGE:549580 similar to TR-G494304 G434304
9238	18625		32.6	8.0E-42	AA48386.1	EST_HUMAN	367BP EXPRESSED SEQUENCE TAG mRNA ;
916	10840		1.83	7.0E-42	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
1812	11709	21586	3.25	6.0E-42	AF072872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
1812	11709	21587	3.25	6.0E-42	AF072872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit BLAST Value)	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2244	12128		3.51	6.0E-42	AW238556.1	EST_HUMAN	xp0003.x1 NC_004910 Homo sapiens cDNA clone IMAGE:2741799 3' similar to contains L111 L1 repetitive element
4266	14814		1.04	6.0E-42	A284770.1	EST_HUMAN	Homo sapiens mRNA for KIAA1067 protein, partial cds
8355	15275	25105	1.81	6.0E-42	AB028690.1	NT	Homo sapiens mRNA for KIAA1067 protein, partial cds
5584	15276	25105	1.72	6.0E-42	AB028690.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
131	10169		5.44	3.0E-42	A2271738.1	NT	Homo sapiens SET domain and malher transposase fusion gene (SETWAR) mRNA
431	10378	20197	1.17	3.0E-42	B2E27933.1	EST_HUMAN	Homo sapiens SET domain and malher transposase fusion gene (SETWAR) mRNA
478	10423		2.94	6.0E-42	G700038	NT	Homo sapiens SET domain and malher transposase fusion gene (SETWAR) mRNA
479	10423		1.21	3.0E-42	G700038	NT	Homo sapiens SET domain and malher transposase fusion gene (SETWAR) mRNA
6016	15620	28050	1.76	5.0E-42	11433953	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), mRNA
6016	15620	28051	1.76	5.0E-42	11433953	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), mRNA
6072	16055	28051	2.75	5.0E-42	1141787	NT	Homo sapiens myxoidin-related protein 3 (MTRP3), mRNA
6274	16108	28094	1.57	5.0E-42	AF071599.1	NT	Homo sapiens multidomain calcium/calmodulin-dependent protein kinase II delta2 isoform mRNA, complete cds
7098	16975	27106	2.76	5.0E-42	AB037151.1	NT	Homo sapiens mRNA for KIAA1294 protein, partial cds
8360	18243	28464	2.15	5.0E-42	8629162	NT	Homo sapiens tyrosinase-related protein FLJ201 (3) (FLJ20163), mRNA
736	10668	20002	8.89	4.0E-42	AF055068.1	NT	Homo sapiens MHC class I region
736	10668	20003	8.89	4.0E-42	AF055068.1	NT	Homo sapiens MHC class I region
1050	10687	20009	2.67	4.0E-42	AF180011.1	NT	Homo sapiens ribonuclease III (RNS) mRNA, complete cds
4100	14000	23779	1.61	4.0E-42	X98417.1	NT	H sapiens PROS-27 mRNA
4156	14056	23850	4.82	4.0E-42	4596499	NT	Homo sapiens regulatory factor X, 4 (influences HLA class II expression) (RF4X) mRNA
4480	14374	24162	10.26	4.0E-42	4596008	EST	Homo sapiens zinc finger protein 177 (ZNF177) mRNA
8041	17932	28719	2.07	4.0E-42	AW818630.1	EST_HUMAN	RC1-310279.040400-018-H11 ST0278 Homo sapiens cDNA
8041	17932	28760	28.80	4.0E-42	AW818630.1	EST_HUMAN	RC1-310279.040400-018-H11 ST0278 Homo sapiens cDNA
8714	18531	28815	3.22	4.0E-42	BF035327.1	EST_HUMAN	60148603.1F1 NH1_MGC.06 Homo sapiens cDNA clone IMAGE:362086 5' adj14610.1 Stalagene lung (8637210) Homo sapiens cDNA clone IMAGE:840810 3' similar to contains THR12 THR repetitive element
98	10084		0.78	3.0E-42	AA48405.1	EST_HUMAN	RC0-NN0070-270400-024-407 TN0070 Homo sapiens cDNA
1467	11372	21239	3.63	2.0E-42	BF376834.1	EST_HUMAN	RC0-NN0070-270400-024-407 TN0070 Homo sapiens cDNA
2361	12241		3.86	2.0E-42	AW89344.1	EST_HUMAN	2818265.3prime NH1_MGC.7 Homo sapiens cDNA clone IMAGE:2819383 3'
2375	12265	22146	2.15	2.0E-42	AW250059.1	EST_HUMAN	2818265.3prime NH1_MGC.7 Homo sapiens cDNA clone IMAGE:2819383 3'
5519	15437	25500	10.2	2.0E-42	AW953568.1	EST_HUMAN	EST1297438 E5 sequences, MaGC Homo sapiens cDNA

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Probe Seq ID Seq ID NC:	Expr Seq ID Seq ID NC:	ORF Seq ID NC:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5519	15437	25501	10.2	2.0E-42	AIW95508.1	EST_HUMAN	EST3367438 IMAGE: ressequences, MAGO Homo sapiens cDNA
7653	17513	27758	1.27	2.0E-42	BE539918.1	EST_HUMAN	501067254F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3447928.6
7717	10084	20478	1.06	1.0E-42	X57147.1	NT	Human endogenous retrovirus PHE-1 (ERVH9)
1026	10844	20786	0.98	1.0E-42	AIW295809.1	EST_HUMAN	UHH81-afh-04-04-DL1-31 NCBI CGAP Sub3 Homo sapiens cDNA clone IMAGE:2721871.3
1065	11001	20542	1.11	1.0E-42	A251818.1	NT	Homo sapiens partial C9 gene for complement component C9, exon 1
1085	11001	20543	1.11	1.0E-42	A251818.1	NT	Homo sapiens partial C9 gene for complement component C9, exon 1
1222	12288	20863	12.78	1.0E-42	AF097185.1	NT	Homo sapiens NAU4-ubiquitome oxidoreductase AGGG substrate precursor homolog mRNA, nuclear gene encoding mitochondrial protein, complete cds
1222	12288	20864	12.78	1.0E-42	AF097185.1	NT	Homo sapiens NAU4-ubiquitome oxidoreductase AGGG substrate precursor homolog mRNA, nuclear gene encoding mitochondrial protein, complete cds
1873	11574	21443	1.46	1.0E-42	11423219	NT	Homo sapiens LOC512101, mRNA
1965	11879	21772	0.91	1.0E-42	AF110236.1	NT	Homo sapiens major histocompatibility complex, class II, DM alpha (HLA-DMA) mRNA
2467	12372	22284	1.88	1.0E-42	5174468	NT	Homo sapiens major histocompatibility complex, class II, D beta (HLA-DDB) mRNA
2951	12892	22992	8.82	1.0E-42	495524	NT	Homo sapiens major histocompatibility complex, class II, D beta (HLA-DDB) mRNA
3047	13391	23347	2.15	1.0E-42	7632027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
3549	13760	23563	1.02	1.0E-43	AI183267.2	NT	Homo sapiens chromosome 21 segment HS21C937
4153	14653	23827	1.72	1.0E-43	AI183260.2	NT	Homo sapiens chromosome 21 segment HS21C937
4489	14383	24170	0.98	1.0E-42	AIW813017.1	EST_HUMAN	FGS-ST0197-161099-012-03 ST0197 Homo sapiens cDNA
4540	14528	24310	2.86	1.0E-42	5803122	NT	Homo sapiens proteasome inhibitor (PSI), mRNA
4540	14528	24317	2.85	1.0E-42	5803122	NT	Homo sapiens proteasome inhibitor (PSI), mRNA
4650	14555	24348	5.35	1.0E-42	4506756	NT	Homo sapiens trypsinogen receptor 3 (TRY3) mRNA
4769	14654	24442	1.2	1.0E-42	45013174.1	NT	Homo sapiens trypsinogen receptor 3 (TRY3) mRNA
5048	14620	24663	0.98	1.0E-42	4501612	NT	Homo sapiens trypsinogen receptor 3 (TRY3) mRNA
5048	14620	24664	0.98	1.0E-42	4501612	NT	Homo sapiens trypsinogen receptor 3 (TRY3) mRNA
7605	17655	27963	2.94	9.0E-43	4757060	NT	Homo sapiens trypsinogen receptor 3 (TRY3) mRNA
8307	17873	28526	3.82	9.0E-43	AA345710.1	EST_HUMAN	274067.01 Soares, Iestis, NHT Homo sapiens cDNA clone IMAGE:728552.3
6316	10573	20396	12.13	9.0E-43	AV739682.1	EST_HUMAN	AV739682 CB Homo sapiens cDNA clone CBLAKH08.6
6316	10573	20397	12.13	9.0E-43	AV739682.1	EST_HUMAN	AV739682 CB Homo sapiens cDNA clone CBLAKH08.6
695	10018	20441	4.33	9.0E-43	8623276	NT	Homo sapiens hypothetical protein FJ20237 (FJ20237), mRNA
695	10018	20442	4.33	9.0E-43	8623276	NT	Homo sapiens hypothetical protein FJ20237 (FJ20237), mRNA
695	10018	20443	4.33	9.0E-43	8623276	NT	Homo sapiens hypothetical protein FJ20237 (FJ20237), mRNA
3559	13503	23262	6.05	7.0E-43	AW246142.1	EST_HUMAN	2822251.Sprime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3822251.5

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Mean Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7092	16069		1.76	7.0E-43	AI909748.1	EST_HUMAN	wp66001.x1 NOL_GCAP_Bm29 Homo sapiens cDNA clone IMAGE:246985 3' similar to TR:01475
1320	11227		10.17	6.0E-43	AA491890.1	EST_HUMAN	015475 UNLAMED HERV-H PROTEIN contains LTR7.1 LTR7 repetitive element;
2547	12421		4.15	6.0E-43	AV798201.1	EST_HUMAN	nef2306.x1 NOL_GCAP_Evi1 Homo sapiens cDNA clone IMAGE:908603 similar to gcl:05095 5'8S RIBOSOMAL PROTEIN L30 (HUMAN);
8511	15716		2.02	6.0E-43	9955973	NT	Homo sapiens A1P-binding cassette, sub-family C (CFH/NMRP), member 3 (ABC03), transcript variant MRP4B, mRNA
6128	15675	28111	2.02	6.0E-43	AW 68897.1	EST_HUMAN	h430304.x1 Sources_NELT_GBC_S1 Homo sapiens cDNA clone IMAGE:2370541 3' similar to contains MER10.13
7668	17518	27745	1.83	6.0E-43	AA189154.1	EST_HUMAN	z35506.x1 Sources_NHMFu_S1 Homo sapiens cDNA clone IMAGE:405410 5' similar to TR:G529441
8449	18322		6.54	6.0E-43	AL16188.1	EST_HUMAN	G529641 DB1, COMPLETE CDS, contains element P177 repetitive element;
137	10111		1.98	5.0E-43	AL16213.2	NT	DKF2791L1712.11 781 (synonym: ham2) Homo sapiens cDNA clone DKF2791L1712.5
484	10437	20246	3.01	5.0E-43	AA332780.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C013
2816	12748	22359	1.36	5.0E-43	AV792578.1	EST_HUMAN	EST169333 Testis1 Homo sapiens cDNA 5' end
7380	17208	27514	4.47	5.0E-43	AA46238.1	EST_HUMAN	AV739578 HTF Homo sapiens cDNA clone HTFANC08.5
7045	17795	28035	2.2	5.0E-43	AT33244.1	EST_HUMAN	ae3320.x1 NOL_GCAP_Lu8 Homo sapiens cDNA clone IMAGE:815055.5
7084	17814	28055	1.41	5.0E-43	AL06910.1	EST_HUMAN	PV14.5 GENE;
8148	18333	28260	5.46	5.0E-43	AW63307.1	EST_HUMAN	DKF2945D0119.11 434 (synonym: bac3) Homo sapiens cDNA clone DKF2945D0119
8338	18215	28468	2.87	5.0E-43	W25011.1	EST_HUMAN	W22-SN007-230305-004-022 SN0097 Homo sapiens cDNA
9793	17922	28146	2.6	5.0E-43	XT15804.1	NT	5544 Human testis cDNA randomly primed auxiliary/Homo sapiens cDNA Human mRNA for alpha-acutin
987	12543	20728	4.85	4.0E-43	AF063628.1	NT	Homo sapiens X-linked antidiabetic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
8321	16057		1.72	4.0E-43	11416793	NT	Homo sapiens proboscidean beta 6 (PQB48), mRNA
6757	16056	26824	4.46	4.0E-43	A244341.1	EST_HUMAN	qf7502.x1 NOL_GCAP_KG3 Homo sapiens cDNA clone IMAGE:160354.3 similar to contains MER10.13 MER10 repetitive element;
6757	16056	26825	4.46	4.0E-43	A244341.1	EST_HUMAN	qf7602.x1 NOL_GCAP_KG3 Homo sapiens cDNA clone IMAGE:160354.3 similar to contains MER10.13 MER10 repetitive element;
8624	18489	28761	1.8	4.0E-43	TT7390.1	EST_HUMAN	gdt2510.1 Sources fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:113827.5
9174	18815		1.86	4.0E-43	RC0660.1	EST_HUMAN	yf08005.1 Sources infant brain INB Homo sapiens cDNA clone IMAGE:31963.5 similar to contains MER10 repetitive element;
1185	11103		2.84	3.0E-43	AF22391.1	NT	Homo sapiens calcium channel alpha1E subunit (CAV1E) gene, exons 7-46, and partial cds, alternatively spliced

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1669	11671	21437	1.48	3.0E-43	X97689.1	NT	H sapiens gene encoding Lx auticalligen
3524	13440	23237	1.05	3.0E-43	S68002.1	NT	AML1-ETO1-AML1-ETO1 fusion protein (translocated translocation) [human, leukemia cell line SKH1, mRNA Mutant, 9398 nt]
4153	14093	23872	0.95	3.0E-43	AA548154.1	EST_HUMAN	nl55506.s1 NC1_GCAP_P77 Homo sapiens cDNA clone IMAGE:1017419
5637	15743	25655	1.71	3.0E-43	7305300	NT	Mus musculus ologalin (Olog), mRNA
5637	15743	25656	1.71	3.0E-43	7305360	NT	Mus musculus ologalin (Olog), mRNA
5637	15640	25672	3.78	3.0E-43	U95487.1	NT	Human fibronectin RNA (upstream binding transcription factor) (UBTF) gene, partial cds
9746	16625		6.88	3.0E-43	AA458824.1	EST_HUMAN	AB8811.s1 Striatum fold retina 897202 Homo sapiens cDNA clone IMAGE:834413 3' similar to contains
7120	16697	27188	1.18	3.0E-43	7961721	NT	THR12 THF repetitive element;
8842	18768	29001	2.02	3.0E-43	5730386	NT	Homo sapiens hypothetical protein (HSX011916), mRNA
177	10148		4.27	2.0E-43	AH190764.1	EST_HUMAN	Homo sapiens SET domain and nuclear transposase fusion gene (SETMAR) mRNA
8512	18175	25332	1.36	2.0E-43	AW207564.1	EST_HUMAN	PTR7 PTR7 repetitive element;
8536	18176		7.93	2.0E-43	U43701.1	NT	Homo sapiens PTPN13 protein (SH-PTPase), complete cds
8532	18404		3.39	2.0E-43	U03007.1	EST_HUMAN	Human fibronectin protein L23a, mRNA, complete cds
1030	11534	21364	2.22	1.0E-43	AF145936.1	NT	FBT5G fetal brain, Staphylococcus aureus cDNA clone FB_G8 3' end similar to LINE-1
1630	11534	21365	2.22	1.0E-43	AF145936.1	NT	Homo sapiens Ras-like GTP-binding protein (RASBP2A) gene, exons 1b and 2
1678	11580	21450	3.95	1.0E-43	AF164366.1	NT	Homo sapiens Ras-like GTP-binding protein (RASBP2A) gene, exons 1b and 2
2692	12557	22444	4.35	1.0E-43	BF346253.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C0384
5687	15692	26714	12.07	1.0E-43	4507168	NT	Human sapiens Spt transcription factor (SPT) mRNA
5687	15692	26715	12.07	1.0E-43	4507168	NT	Homo sapiens Spt transcription factor (SPT) mRNA
6159	15177	24960	1.63	1.0E-43	R19761.1	EST_HUMAN	y94001.r1 Sorens infant brain 1N8 Homo sapiens cDNA clone IMAGE:34752 5' similar to
6700	16880		1.63	1.0E-43	AF168490.1	NT	SP-BD38, MOUSE P26856 BRAIN PROTEIN DN38;
7129	17006	27166	25.23	1.0E-43	AW063976.1	EST_HUMAN	Homo sapiens Bq221 region and MTG8 (CBFA2T1) gene, partial cds
8331	18203	26458	6.76	1.0E-43	AB94991.1	EST_HUMAN	EST1375749 IMAGE: resutances, MACH Homo sapiens cDNA
8672	18650	28844	3.2	1.0E-43	11424378	NT	wf8701.x1 NC1_GCAP_Kut11 Homo sapiens cDNA clone IMAGE:246705 3'
9117	18980		3.96	1.0E-43	AF137944.1	EST_HUMAN	Homo sapiens calcium channel, voltage-dependent, alpha 1E subunit (CAONAE1), mRNA
9405	18958	25311	1.86	1.0E-43	AF167416.1	EST_HUMAN	DKF26761D1016.1 r1 781 (synonym: ham2) Homo sapiens cDNA clone IMAGE:2313778 3'
9618	19196	26245	2.82	9.0E-44	11418322	NT	wf86004.x1 NC1_GCAP_P128 Homo sapiens cDNA clone IMAGE:2313778 3'
9718	19768	26586	5.98	8.0E-44	AF222685.1	EST_HUMAN	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
872	10788	20549	6.98	8.0E-44	AF222685.1	EST_HUMAN	q128201.x1 Sorens_NFL_1, GBC_S1 Homo sapiens cDNA clone IMAGE:1846562 3'
8988	18845	27037	3.87	8.0E-44	X64354.1	NT	q128201.x1 Sorens_NFL_1, GBC_S1 Homo sapiens cDNA clone IMAGE:1846562 3'
							H sapiens DNA for Cone GMP-PDE gene

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Probe SEQ ID NO.	Exon ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8504	18077	28643	3.39	8.0E-44	Y10469.2	NT	Homo sapiens mRNA for thymidine kinase, partial
8505	18749	29038	5.06	8.0E-44	L29199.1	NT	Homo sapiens myosin mRNA, partial cds
8559	19031	29504	2.59	8.0E-44	11527388	NT	Homo sapiens polyoma virus (RNA) [1] (DNA directed) polypeptide P (POLP2P) mRNA
9400	18069	25161	1.80	8.0E-44	11418096	NT	Homo sapiens putative nuclear protein (HRJ-HF82122), mRNA
9742	16532	26559	1.75	8.0E-44	11418096	NT	Homo sapiens protein kinase C, alpha binding protein (PRKCABP), mRNA
9895	18069	25161	1.84	8.0E-44	11418096	NT	Homo sapiens putative nuclear protein (HRJ-HF82122), mRNA
6443	10580		0.85	7.0E-44	RC6535.1	EST_HUMAN	y68901.1 Sorex feta liver spleen 1NF.L3 Homo sapiens cDNA clone IMAGE 124920 5'
2197	10374	21978	1.2	7.0E-44	5031889	NT	Homo sapiens L1 domain-containing preferred translocation partner in lipoma (LPP) mRNA
2937	13964	22683	2.2	7.0E-44	AF048720.1	NT	Homo sapiens mitochondrial m32, nuclear region
2937	13964	22684	2.2	7.0E-44	AF048720.1	NT	Homo sapiens mitochondrial m32, nuclear region
2937	13964	22685	2.2	7.0E-44	AF048720.1	NT	Homo sapiens mitochondrial m32, nuclear region
4148	14048	23521	1.17	7.0E-44	AF231910.1	NT	Homo sapiens chromosome 21, unknown mRNA
4148	14048	23522	1.17	7.0E-44	AF231910.1	NT	Homo sapiens chromosome 21, unknown mRNA
4148	14048	23523	1.17	7.0E-44	AF231910.1	NT	Homo sapiens chromosome 21, unknown mRNA
6762	16541	26528	2.05	7.0E-44	AF196839.1	EST_HUMAN	EST159339 79AA1 Homo sapiens cDNA clone Y79AA1005466 3'
8886	18791	28590	2.81	8.0E-44	AF094050.1	EST_HUMAN	EST136120 MAGE-1, testis-specific, MAGE cDNA
300	10264		2.82	5.0E-44	AJ286960.1	NT	Homo sapiens KIA03851 gene (partial), X13 gene and L27-1 gene
326	10268		2.04	5.0E-44	AJ286960.1	NT	Homo sapiens KIA03851 gene (partial), X13 gene and L27-1 gene
6905	16485	26672	3.79	5.0E-44	AF158523.1	EST_HUMAN	h40402.x1 NCL CGAP Brn2 Homo sapiens cDNA clone IMAGE2170083 3' similar to contains OPR1
7359	17317		2.99	5.0E-44	AF154971.1	EST_HUMAN	h40402.x1 NCL CGAP Brn2 Homo sapiens cDNA clone N28R400218 5'
3398	13287	20386	2.6	4.0E-44	AF103303.2	NT	Homo sapiens chromosome 21 segment H221C103
8594	18433	28702	13.3	4.0E-44	L50378.1	NT	Homo sapiens carboxy terminal LIM domain protein (CLIM) mRNA, complete cds
1746	11646		1.07	3.0E-44	6912477	NT	Homo sapiens carboxy terminal LIM domain protein (CLIM) mRNA
2485	12860	22254	1.54	3.0E-44	BE890026.1	EST_HUMAN	601491502P1 NH1 MG2 89 Homo sapiens cDNA clone IMAGE069777 5'
3059	12886	22777	5.08	3.0E-44	AA116959.1	EST_HUMAN	601491502P1 NH1 MG2 89 Homo sapiens cDNA clone IMAGE069777 5'
1033	10851	20703	2.75	2.0E-44	4829683	NT	Homo sapiens DEADH (Asp-Glu-Ala-Asp) box polypeptide 1 (DDX1) mRNA
1033	10851	20704	2.75	2.0E-44	4829683	NT	Homo sapiens DEADH (Asp-Glu-Ala-Asp) box polypeptide 1 (DDX1) mRNA
1189	11099	20546	4.83	2.0E-44	5832000	NT	Homo sapiens transmembrane trafficking protein (TMP21), mRNA
1189	11099	20546	4.83	2.0E-44	5832000	NT	Homo sapiens transmembrane trafficking protein (TMP21), mRNA
1260	11197		2.79	2.0E-44	AF133380.1	NT	Homo sapiens transmembrane trafficking protein (TMP21), mRNA
1346	11262	21108	1.43	2.0E-44	BE485323.1	EST_HUMAN	h40402.x1 NCL CGAP Lu24 Homo sapiens cDNA clone IMAGE3182933 3' similar to SW102YB_HUMAN
2105	11994	21894	2.03	2.0E-44	AF070951.1	NT	P22025 OXYSTEROL-BINDING PROTEIN ;
2525	12403	22294	1.31	2.0E-44	D25003.1	NT	Homo sapiens tissue-type bone marrow zinc finger protein 4 mRNA, complete cds
							Human mRNA for integrin alpha subunit, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2567	12039		3.32	2.0E-44	5907933	NT	Homo sapiens adaptor-related protein complex 4, sigma 1 subunit (CLAPS4), mRNA
3425	13342	2347	1.36	2.0E-44	D87975.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4468	14362	24152	1.76	2.0E-44	AW68476.1	EST_HUMAN	PM4-SN0016-12050-003-044 SN0016 Homo sapiens cDNA
5709	15617	25719	1.36	2.0E-44	11146907	NT	Homo sapiens chitinase (C-C motif) receptor 9 (CCR9), mRNA
6097	15107	24670	1.46	2.0E-44	AF036568.1	NT	Homo sapiens general transcription factor 24 (GTF2D) mRNA, alternatively spliced product, complete cds
6363	16245	26406	3.96	2.0E-44	11149226	NT	Homo sapiens glutamate receptor, metabotropic 3 (GRAM3), mRNA
6363	16245	26407	3.96	2.0E-44	11149226	NT	Homo sapiens glutamate receptor, metabotropic 3 (GRAM3), mRNA
7069	16686	27078	1.86	2.0E-44	BE396058.1	EST_HUMAN	801286014F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3613586 5'
8022	18916		2.22	2.0E-44	BE246902.1	EST_HUMAN	TCBAP1E2795 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HSGC project cDNA clone TCBAP2795
8710	19736	24610	2.72	2.0E-44	AB02374.1	NT	Human mRNA for KIAA0376 gene, partial cds
8905	19833		3.88	2.0E-44	11590303	NT	Homo sapiens cat eye syndrome chromosome region, candidate 1 (CEOR1), mRNA
461	10034	19036	3.64	1.0E-44	7657334	NT	Homo sapiens Musashi3/NK-related kinase (MINK), mRNA
461	10034	19040	3.64	1.0E-44	7657334	NT	Homo sapiens Musashi3/NK-related kinase (MINK), mRNA
568	10065	20312	1.85	1.0E-44	AW65132.1	EST_HUMAN	EC1-CT0236-03050-036-112 CT0249 Homo sapiens cDNA
1179	11090		1.52	1.0E-44	AW94603.1	EST_HUMAN	RC1-BN0036-10300-012-501 BN0039 Homo sapiens cDNA
1655	11460		5.54	1.0E-44	AL163303.2	NT	Homo sapiens chromosome 21 segment RS21C163
2177	12064	21065	3.53	1.0E-44	AA45454.1	EST_HUMAN	253540211 Soares, Vol. 1, beta, N26ZF5_9W Homo sapiens cDNA clone IMAGE:775763 5' similar to correlates THR10 THR repetitive element;
2177	12064	21066	3.53	1.0E-44	AA49454.1	EST_HUMAN	253540211 Soares, Vol. 1, beta, N26ZF5_9W Homo sapiens cDNA clone IMAGE:775763 5' similar to correlates THR10 THR repetitive element;
2237	12716	22024	1.05	1.0E-44	AA398096.1	EST_HUMAN	25891111 Soares, beta5, NHT Homo sapiens cDNA clone IMAGE:729476 5'
2732	12694	22489	1.39	1.0E-44	AF106776.1	NT	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM5 protein, TS4 protein, JM10 protein, A4 differentiation-dependent protein, triple LM domain protein 6, and synapophycin genes, complete cds; and L-type calcium channel alpha-
3664	13578		6.08	1.0E-44	AA455980.1	EST_HUMAN	ad51030.11 Soares, NHHMPU_5T Homo sapiens cDNA clone IMAGE:811984 3'
6061	14931	24702	0.81	1.0E-44	AL130755.1	NT	Homo sapiens alpha satellite DNA, M1 monomer type
5061	14931	24703	0.81	1.0E-44	AL130755.1	NT	Homo sapiens alpha satellite DNA, M1 monomer type
8376	16255	26716	10.76	1.0E-44	AW14608.1	EST_HUMAN	AY714608 DDB Homo sapiens cDNA clone DDB3YC03 5'
8816	16629	26718	4.18	1.0E-44	10902664	NT	Homo sapiens Suniti domain (SCR repeat) containing (BK39A9.2), mRNA
8890	16861	26970	3.43	1.0E-44	AW84967.1	EST_HUMAN	RC1-CT0168-150666-011-C08 CT0168 Homo sapiens cDNA
8890	16861	26971	3.43	1.0E-44	AW84967.1	EST_HUMAN	RC1-CT0168-150666-011-C08 CT0168 Homo sapiens cDNA
4476	14370	24159	1.74	9.0E-45	8922301	NT	Homo sapiens hypothetical protein FL1037a (FL10379), mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4476	14370	24160	1.74	9.0E-48	8622394	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
2477	12353	22246	3.49	8.0E-48	5174719	NT	Homo sapiens TRC-like gene (NOTE: non-standard symbol and name) (TRC), mRNA
6075	14889	24966	7.48	8.0E-48	5174719	NT	Homo sapiens TRC-like gene (NOTE: non-standard symbol and name) (TRC), mRNA
3869	13806		5.26	6.0E-48	AW157570.1	EST_HUMAN	ab030747.1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2762909 3' similar to
9707	19718		1.46	6.0E-48	11418219	NT	SW-6103, HUMAN P-4029 60S RIBOSOMAL PROTEIN L19A ;
874	10800		1.11	5.0E-48	AL163203.2	NT	Homo sapiens ADP-ribosylation factor GTPase activating protein 1 (ARFGAP1), mRNA
1967	11652	21738	5.01	5.0E-48	BF333627.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C033
3173	13086	22904	2.01	5.0E-48	AI623796.1	EST_HUMAN	CM4-CH0044-180200-516-011 CN0044 Homo sapiens cDNA
9384	16503	25156	8.83	5.0E-48	AA39781.1	EST_HUMAN	964807.x1 NC, CGAP, CL1 Homo sapiens cDNA clone IMAGE:2116453 3' similar to SW-PAX1_MOUSE
7226	17103	27392	1.67	5.0E-48	4756223	NT	z172603.s1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:727877 3' similar to contains element
8640	11748	25043	2.87	5.0E-48	8623668	NT	TRAF1 repetitive element ;
1127	11441	20883	8.90	4.0E-48	X65523.8	NT	Homo sapiens programmed cell death 3 (PDCD3), mRNA
2246	12130	22027	1.98	4.0E-48	BE265022.1	EST_HUMAN	Homo sapiens golgi- like protein (GLP), mRNA
9613	15192		1.17	3.0E-48	BT76077.1	EST_HUMAN	H.sapiens ARLT4 gene
3527	13210		1.51	3.0E-48	AV729678.1	EST_HUMAN	601194402F1 NIH, MGCC, 7 Homo sapiens cDNA clone IMAGE:3639426 5'
7104	16681	27173	3.44	3.0E-48	AL163227.2	NT	902034052F1 NIH, MGCC, 83 Homo sapiens cDNA clone IMAGE:428253 5'
7607	17757	27966	8.37	3.0E-48	AL163227.2	NT	AB5607.r1 Soares fetal liver spleen, 1NFLS Homo sapiens cDNA clone IMAGE:110246 5'
7607	17757	27967	8.37	3.0E-48	X68211.2	NT	AV729678 H18 Homo sapiens cDNA clone HTBAAC001.5'
8814	19090		1.33	3.0E-48	X68211.2	NT	Homo sapiens golgi autotransfer, golgi subfamily A, 2 (GOLGA2), mRNA
2454	12331		2.17	2.0E-48	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C027
2966	13224	22716	0.93	2.0E-48	AJ243213.1	NT	H.sapiens DNA for endogenous retroviral like element
5929	15534	25657	4.82	2.0E-48	AL1695.1	NT	Homo sapiens partial 5-HT4 receptor gene, exon 2 to 5
6469	16327	26516	1.76	2.0E-48	BE702184.1	EST_HUMAN	Human osteopontin Chondrocyte crystal (GLC) protein (lyso-phospholipase) gene, promoter and exon 1
8178	19471	28315	27.04	2.0E-48	BE654360.1	EST_HUMAN	601467765F1 NIH, MGCC, 67 Homo sapiens cDNA clone IMAGE:3670858 5'
8516	16388	28552	3.96	2.0E-48	AA468770.1	EST_HUMAN	AF01070222-190000-261-423 HT0903 Homo sapiens cDNA
8794	16503	28566	2.13	2.0E-48	AW170260.1	EST_HUMAN	aa07121.1 Sturgeons fetal retina 037202 Homo sapiens cDNA clone IMAGE:683319 5' similar to
8794	16503	28569	2.13	2.0E-48	AW170260.1	EST_HUMAN	TRC1144688 G116668 R-SLT11 ;
8853	16548		2.76	2.0E-48	11418157	NT	972403.X1 NC, CGAP, Oyo40 Homo sapiens cDNA clone IMAGE:2746868 3'
							972403.X1 NC, CGAP, Oyo40 Homo sapiens cDNA clone IMAGE:2746868 3'
							Homo sapiens calcium channel, voltage-dependent, alpha 11 subunit (CACNA11), mRNA

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Probe SEQ ID NO.	Exon NO.	ORF SEQ ID NO.	Expression Signal	Max Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
118	10349		2.22	1.0E-46	BE389855.1	EST_HUMAN	801284305F1 NH1.MGC_44 Homo sapiens cDNA clone IMAGE:360183 5'
463	10349	20227	2.7	1.0E-45	BE389855.1	EST_HUMAN	801284305F1 NH1.MGC_44 Homo sapiens cDNA clone IMAGE:360183 5'
484	10467		1.5	1.0E-45	4505412	NT	Homo sapiens RAP1A, member of RAS oncogene family (RAP1A), mRNA
1157	11070	20915	1.7	1.0E-45	7857290	NT	Homo sapiens Langhans cell specific c-type lectin (LANGRIN), mRNA
3095	12892	22784	6.78	1.0E-46	U32169.1	NT	Human pro- $\alpha 2$ chain of collagen type XI (COL11A2) gene, complete cds
3447	13364	23171	1.04	1.0E-46	8656558	NT	Homo sapiens chromosome 21 open reading frame 1 (C21orf4), mRNA
3526	13442	23239	0.91	1.0E-46	AB040811.1	NT	Homo sapiens chromosome 21 open reading frame 1 (C21orf4), mRNA
4378	14274	24055	4.08	1.0E-46	BE389853.1	EST_HUMAN	801289116F1 NH1.MGC_8 Homo sapiens cDNA clone IMAGE:3618003 5'
4894	14785	24641	1.05	1.0E-45	11145726	NT	Homo sapiens ribon protein (NIBAN), mRNA
7274	17161	27347	5.22	1.0E-45	BE987843.1	EST_HUMAN	801511226F1 NH1.MGC_71 Homo sapiens cDNA clone IMAGE:3912555 5'
7495	17355	27556	1.25	1.0E-46	AB002297.1	EST_HUMAN	Human mRNA for KIAA0299 gene, partial cds
8231	19590	28359	4.3	1.0E-45	11418095	NT	Homo sapiens protein kinase C, alpha binding protein (PRKCABP), mRNA
8415	19697		5.39	1.0E-45	1158290	NT	Homo sapiens lymphocytic protein FLJ20454 (FLJ20454), mRNA
8421	19970		2.95	1.0E-45	11418177	NT	Homo sapiens Ras GTPase activating protein 1 (RANGAP1), mRNA
8630	18324	25207	3.17	1.0E-45	11418157	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1L subunit (CACNA1L), mRNA
8790	18599	25861	2.28	9.0E-46	5910283	NT	Male musculature ventral complex, 2, gene 5c (C25-5c), mRNA
7018	18585		6.71	9.0E-46	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21008
7368	17836	28077	7.89	9.0E-46	AI124694.1	EST_HUMAN	3522449.Spmc.NH1.MGC_77 Homo sapiens cDNA clone IMAGE:2822449 5'
2382	12270	22165	8.76	8.0E-46	AK53291.1	EST_HUMAN	162003.x1 NCL_COAP_Gas4 Homo sapiens cDNA clone IMAGE:2132199 3' similar to gpb.00314_fm2
2862	12270	22166	8.76	8.0E-46	AK53291.1	EST_HUMAN	162003.x1 NCL_COAP_Gas4 Homo sapiens cDNA clone IMAGE:2132199 3' similar to gpb.00314_fm2
6652	16572		3.67	8.0E-46	BE167244.1	EST_HUMAN	TUBULIN BETA-1, CYAN (TUBMAN);
4478	14372		6.54	7.0E-46	BE399165.1	EST_HUMAN	RC5-H10506-28020012-012 H10506 Homo sapiens cDNA
4701	14587		1.01	7.0E-46	BE064396.1	EST_HUMAN	891277292F1 NH1.MGC_20 Homo sapiens cDNA clone IMAGE:3616119 5'
5983	15562	25603	4.01	7.0E-46	8622709	NT	RC4-3T0310-110300105-110 BT0310 Homo sapiens cDNA
4912	15818	25943	1.35	7.0E-46	BF109445.1	EST_HUMAN	Homo sapiens lymphocytic protein FLJ10947 (FLJ10947), mRNA
8543	19144		1.35	7.0E-46	AL163246.2	NT	091828395F1 NH1.MGC_77 Homo sapiens cDNA clone IMAGE:3042735 5'
						EST_HUMAN	Homo sapiens chromosome 21 segment HS210048
						EST_HUMAN	wn31808.x1 NCL_COAP_UH4 Homo sapiens cDNA clone IMAGE:2457576 3' similar to contains MER19.12
2726	12588	22483	5.83	6.0E-46	AB844391.1	EST_HUMAN	MER19 repetitive element;
2726	12588	22484	5.83	6.0E-46	AB844391.1	EST_HUMAN	wn31808.x1 NCL_COAP_UH4 Homo sapiens cDNA clone IMAGE:2457576 3' similar to contains MER19.12
						EST_HUMAN	MER19 repetitive element;
						EST_HUMAN	ts8910.x1 NCL_COAP_Kid6 Homo sapiens cDNA clone IMAGE:2232895 3' similar to TR-060383 OB0383
5727	19534	25737	8.05	6.0E-46	AK33448.1	EST_HUMAN	SA.GENE..

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8684	17878		3.03	6.0E-48	BE78497.1	EST_HUMAN	001478497.1 NH1_MGC_68 Homo sapiens cDNA clone IMAGE:380865 5'
187	10169		0.41	5.0E-49	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21 C010
3484	13400	23265	1.12	5.0E-48	BE577184.1	EST_HUMAN	7681001.X1 Lupsak_dorsal_neo_ganglion Homo sapiens cDNA clone IMAGE:3279408 3'
3464	13400	23266	1.12	5.0E-48	BE577194.1	EST_HUMAN	7681001.X1 Lupsak_dorsal_neo_ganglion Homo sapiens cDNA clone IMAGE:3279408 3'
6030	15042	28074	1.79	5.0E-48	BF590442.1	EST_HUMAN	na33907.X1 NCI CGAP_K031 Homo sapiens cDNA clone IMAGE:3268757 3' similar to TR 073232
6144	16017	28155	3.32	5.0E-48	BF347228.1	EST_HUMAN	002502.HOMOLOG OF RAT KIDNEY-SPECIFIC
625	10522		1.81	4.0E-46	AA601143.1	EST_HUMAN	nc04408.s1 NCI CGAP_S511 Homo sapiens cDNA clone IMAGE:1104620 3' similar to gb-X55741_mn1
1876	11578	21448	3.57	4.0E-46	AW70544.1	EST_HUMAN	FBULN-1, ISOFORM 1 PRECURSOR (HUMAN);
1876	11578	21447	3.57	4.0E-46	AW70544.1	EST_HUMAN	H89603.X1 NCI CGAP_Lu04 Homo sapiens cDNA clone IMAGE:3008938 3' similar to gb-X14008_mn1
4320	14217	23066	1.07	4.0E-46	AB014622.1	NT	LYSO27.ME C PRECURSOR (HUMAN) contains element MER37 repetitive element;
4320	14217	23066	1.07	4.0E-46	AB014622.1	NT	Human endogenous retrovirus RTV1.32
5358	15298	25082	1.84	4.0E-48	N33852.1	NT	Homo sapiens mRNA for KIAA0652 protein, partial cds
5358	15298	25082	1.84	4.0E-48	N33852.1	NT	Homo sapiens mRNA for KIAA0652 protein, partial cds
8600	18221	23271	1.31	4.0E-46	AF502389.1	NT	Human Ig gamma-3 heavy-chain gene V region, partial cds
4294	14162	23975	0.8	3.0E-46	450378	NT	Human Ig gamma-3 heavy-chain gene V region, partial cds
4986	14522	24343	1.13	3.0E-46	Z73860.1	NT	Homo sapiens DNA for Human P2X4, complete cds
4986	14522	24343	1.13	3.0E-46	Z73860.1	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 3 (MAP4K3), mRNA
4986	14522	24344	1.13	3.0E-46	Z73860.1	NT	H. sapiens Ig lambda light chain variable region gene (7c.11.2) germline; Ig-Light-Lambda, V Lambda
7081	16659	27151	8.3	3.0E-46	AB831462.1	EST_HUMAN	H.sapiens Ig lambda light chain variable region gene (7c.11.2) germline; Ig-Light-Lambda, V Lambda
8856	18668	28955	2.83	3.0E-48	D31766.1	NT	THR repetitive element;
819	10747	20584	5.81	2.0E-48	AA48046.1	EST_HUMAN	Human mRNA for KIAA0061 gene, partial cds
1542	11447		1.32	2.0E-48	AA678246.1	EST_HUMAN	nc06069.s1 NCI CGAP_C03 Homo sapiens cDNA clone IMAGE:890408 3' similar to contains THRB2 THR repetitive element;
1623	11827	21386	2.43	2.0E-48	U78027.1	NT	257871.s1 Source: fetal_liver, spleen, INHLS_S1 Homo sapiens cDNA clone IMAGE:2451896 3'
							Homo sapiens Bruton's tyrosine kinase (BTK), L44-like ribosomal protein (L44), and F17P3 genes, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Mean (Top) HI BLAST E Value	Top HI Accession No.	Top Hit Database Source	Top HI Descriptor
4890	14779	24855	1.15	2.0E-48	AA369286.1	EST_HUMAN	z69402.1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:726950 5' similar to SW-RSP-1_MOUSE
6418	16280	28442	6.78	2.0E-48	9910699.1	NT	OM1730 RSP-1 PROTEIN ;
6703	16893		1.17	2.0E-48	BE068915.1	EST_HUMAN	Mus musculus sperm tail associated protein (Stap), mRNA
8571	18439		1.87	2.0E-48	7857233	NT	Homo sapiens small acidic protein (IMAGE:45052), mRNA
9157	19629		1.75	2.0E-48	BF028854.1	EST_HUMAN	Homo sapiens small acidic protein (IMAGE:45052), mRNA
9409	19629		1.44	2.0E-48	H48389.1	EST_HUMAN	OM176525PFI NHT_MGC_53 Homo sapiens cDNA clone IMAGE:3097328 5'
9728	19515	25135	3.81	2.0E-48	AW777214.1	EST_HUMAN	y432803.1 Soares fetal liver spleen 1NRL3 Homo sapiens cDNA clone IMAGE:206677 5'
1213	11121	20970	5.19	1.0E-48	490294	EST_HUMAN	hg78403.1 NCL_CGAP_Lig4 Homo sapiens cDNA clone IMAGE:2765769 3'
2236	12121	22023	4.6	1.0E-48	AW785916.1	EST_HUMAN	Homo sapiens cell division cycle 10 (homologous to CDC10 of S. cerevisiae) (CDC10) mRNA
2351	12231	22128	2.59	1.0E-48	H97330.1	EST_HUMAN	EST1390025 IMAGE resequencing, VAGP Homo sapiens cDNA
3211	13735	22936	2.81	1.0E-48	AA631912.1	EST_HUMAN	EST1480925 WATM1 Homo sapiens cDNA clone 48095
4772	14650		2.64	1.0E-48	AB023197.1	NT	np78402.s1 NCL_CGAP_Pf2 Homo sapiens cDNA clone IMAGE:1132365 similar to gb-X78717 H sephena
5065	15414	25477	4.18	1.0E-48	BF104707.1	EST_HUMAN	Homo sapiens mRNA for KIAA0680 protein, partial cds
5030	19449	25439	5.00	1.0E-48	8923762	NT	7922001.x1 NCL_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3944705 3'
5636	19449	25540	5.00	1.0E-48	8923762	NT	Homo sapiens centaurin-alpha 2 protein (HSA272180), mRNA
8258	15414	25477	4.26	1.0E-48	BF104707.1	EST_HUMAN	Homo sapiens centaurin-alpha 2 protein (HSA272180), mRNA
9168	18923	25348	1.43	1.0E-48	BF551102.1	EST_HUMAN	7923001.x1 NCL_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3943705 3'
9180	18923	25349	1.43	1.0E-48	BF551102.1	EST_HUMAN	60207236F1 NCL_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4215368 5'
9823	19397		1.51	1.0E-48	AW715371.1	EST_HUMAN	60207236F1 NCL_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4215368 5'
749	10079		4.51	9.0E-47	AL27135.1	NT	AY715371 DCS Homo sapiens cDNA clone DCSA353 5'
							Homo sapiens Xq pseudocentromeric region, segment 112
4848	14729	24512	2.51	9.0E-47	AW770625.1	EST_HUMAN	HP6043.x1 NCL_CGAP_Lig4 Homo sapiens cDNA clone IMAGE:300834 3' similar to TR-015703 075703
9662	19071	25001	1.84	9.0E-47	Y147966	NT	HYPOHETICL 12.4 KD PROTEIN ;
1766	11065	21539	14.02	8.0E-47	Y18536.1	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
1766	11065	21540	14.02	8.0E-47	Y18536.1	NT	Homo sapiens HJAC gene, exon 5, individual 18923
							Homo sapiens HJAC gene, exon 5, individual 18923
2054	12549	22439	1.74	8.0E-47	5453955	NT	Homo sapiens protein phosphatase 2, regulatory subunit B (B66), epsilon isoform (PPP4RBE) mRNA
2989	12617	22712	1.72	8.0E-47	AL229043.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 33
2901	12376	22266	3.05	6.0E-47	AL163346.2	NT	Homo sapiens chromosome 21 segment HS21C04d
7344	17212	27411	6.27	6.0E-47	AB09159.1	EST_HUMAN	tz98042.x1 NCL_CGAP_Kid1 Homo sapiens cDNA clone IMAGE:226666 3'
8053	15688	25890	5.27	5.0E-47	11422972	NT	Homo sapiens CD337 (cell division cycle 37, S. cerevisiae, homolog) (CD337), mRNA
8174	18082		3.91	5.0E-47	N78590.1	EST_HUMAN	EST007598 Fetal brain, Stragene (cell#63206) Homo sapiens cDNA clone HFB0707

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit BLAST Value)	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1379	11284	21140	3.41	4.0E-47	4557556	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA
6958	16816	27008	2.06	4.0E-47	BE616183.1	EST_HUMAN	601290458F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3622437 5'
6958	16816	27009	2.06	4.0E-47	BE616483.1	EST_HUMAN	601290458F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3622437 5'
8905	18713		4.84	4.0E-47	AW151509.1	EST_HUMAN	064822 VIRAL INTEGRATION SITE PROTEIN INT-6 [1]
521	10474	20287	1.76	3.0E-47	BE507894.1	EST_HUMAN	601487638F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3609721 5'
531	10474	20288	1.75	3.0E-47	BE507894.1	EST_HUMAN	601487638F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3609721 5'
801	10730	20371	5.17	3.0E-47	BE7183.1	EST_HUMAN	Y54804.41 Scara multiple sclerosis 2/NHASP Homo sapiens cDNA clone IMAGE:3609721 5'
9301	10595	20703	6.9	3.0E-47	AL163284.2	NT	064822 VIRAL INTEGRATION SITE PROTEIN INT-6 [1]
1984	11877	21770	1.5	3.0E-47	AB07898.1	NT	Homo sapiens chromosome 21 segment H521C084
3855	13796		4.99	3.0E-47	U03161.1	NT	Homo sapiens nuclear dual-specific phosphatase (SDF) mRNA, partial cds
4265	14764	23941	0.97	3.0E-47	NT2258.1	NT	Human T-cell receptor alpha-chain mRNA from JM cell line, complete cds
5659	15571	25956	4.26	3.0E-47	AW163600.1	EST_HUMAN	U14F-BM4-ctd-4-07-0-UL1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3603205 5'
5659	15571	25967	4.26	3.0E-47	AW163600.1	EST_HUMAN	U14F-BM4-ctd-4-07-0-UL1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3603205 5'
5953	15558		1.89	3.0E-47	A122413.1	EST_HUMAN	gH4-007.41 Scara multiple sclerosis 2/NHASP Homo sapiens cDNA clone IMAGE:1643716 3'
142	10118	19596	4.27	2.0E-47	4508319	NT	Homo sapiens myosin phosphatase, target subunit 2 (MYP2), mRNA
952	10878	20723	2.18	2.0E-47	AL163209.2	NT	Homo sapiens chromosome 21 segment H521C089
952	10878	20723	2.18	2.0E-47	AL163209.2	NT	Homo sapiens chromosome 21 segment H521C089
1548	11493		1.22	2.0E-47	7682109	NT	Homo sapiens KIA0439 mRNA, partial cds
1575	11479	21388	1.22	2.0E-47	AA12414.1	EST_HUMAN	Homo sapiens KIA0439 gene product (KIA0439), mRNA
1654	11557	21420	4.44	2.0E-47	AF090388.1	NT	Homo sapiens KIA0439 gene product (KIA0439), mRNA
2185	12072	21974	2.3	2.0E-47	AF090388.1	NT	Homo sapiens KIA0439 gene product (KIA0439), mRNA
4251	14150	23924	1.86	2.0E-47	4504989	EST_HUMAN	Homo sapiens myosin phosphatase, target subunit 2 (MYP2), mRNA
4287	14186	23967	1.75	2.0E-47	AA163602.1	EST_HUMAN	Homo sapiens myosin phosphatase, target subunit 2 (MYP2), mRNA
4287	14186	23968	1.75	2.0E-47	AA163602.1	EST_HUMAN	Homo sapiens myosin phosphatase, target subunit 2 (MYP2), mRNA
4405	14300	24084	2.06	2.0E-47	5174848	NT	Homo sapiens myosin phosphatase, target subunit 2 (MYP2), mRNA
4707	14593	24584	1.1	2.0E-47	AW165166.1	EST_HUMAN	Homo sapiens myosin phosphatase, target subunit 2 (MYP2), mRNA
5835	15546	25637	1.6	2.0E-47	BE78475.1	EST_HUMAN	60146332F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:3607487 5'
5835	15546	25638	1.6	2.0E-47	BE78475.1	EST_HUMAN	60146332F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:3607487 5'
6332	19464		1.33	2.0E-47	U03731.1	NT	Homo sapiens 5-hydroxytryptamine 1D receptor pseudogene with an A1 repeat insertion
6943	16520	26716	2.1	2.0E-47	D37675.1	NT	Homo sapiens DNA for myosin precursor protein, complete cds
6943	16520	26717	2.1	2.0E-47	D37675.1	NT	Homo sapiens DNA for myosin precursor protein, complete cds
7060	16637	27127	1.77	2.0E-47	AF017171.1	NT	Homo sapiens SPH-binding factor mRNA, partial cds
9070	10116	19536	5.77	2.0E-47	4508318	NT	Homo sapiens myosin phosphatase, target subunit 2 (MYP2), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5216	19658	24586	1.98	2.0E-47	RA2423.1	EST_HUMAN	yf2a08.1 Scores Infant brain 1MB Homo sapiens cDNA clone IMAGE:28668 3' similar to contains ORF repetitive element
5257	19659		1.32	2.0E-47	AL183209.2	NT	Homo sapiens chromosome 21 segment HS21009
1353	11398	21142	4.5	1.0E-47	AJ333429.1	EST_HUMAN	qp5803.x1 Scores_fall_lung_NH-L19W Homo sapiens cDNA clone IMAGE:1931'90 3'
3745	13692	23443	0.79	1.0E-47	BE280477.1	EST_HUMAN	0011155321F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138693 5'
3745	13692	23444	0.79	1.0E-47	BE280477.1	EST_HUMAN	0011155321F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138693 5'
5008	14882	24648	2.59	1.0E-47	AW613006.1	EST_HUMAN	RC3-ST0197-130400-077-R02 ST0197 Homo sapiens cDNA
							af19003.x1 Barsted axon IPI RB6 Homo sapiens cDNA clone IMAGE:2355589 3' similar to gb:M22965
6194	15564	20590	7.98	1.0E-47	AB80386.1	EST_HUMAN	RAS-RELATED PROTEIN RAP-1A (HUMAN);
7528	17778	28017	1.75	1.0E-47	L3017.5.1	NT	Homo sapiens cdkm chemo dephosphorylase class 1 (ADP) gene, 5' region
1595	11660	21358	2.34	9.0E-48	AF223391.1	NT	Homo sapiens cdkm chemo dephosphorylase class 1 (ADP) gene, 5' region
3505	13425	23228	0.83	9.0E-48	BF359047.1	EST_HUMAN	CM2-MT0100-310760-290-06 MT0100 Homo sapiens cDNA
8460	18333	25856	3.22	9.0E-48	BE333813.1	EST_HUMAN	RC3-ST0197-130400-077-R02 ST0197 Homo sapiens cDNA
1230	11138		1.32	8.0E-48	4801900	NT	Homo sapiens cdkm chemo dephosphorylase class 1 (ADP) gene, 5' region
1231	11138		1.31	8.0E-48	4801900	NT	Homo sapiens cdkm chemo dephosphorylase class 1 (ADP) gene, 5' region
3056	13023	22818	3.62	8.0E-48	AW178477.1	EST_HUMAN	h45103.x1 NCI_GOMP_L1m12 Homo sapiens cDNA clone IMAGE:3001133 3' similar to gb:264707
3060	13023	22819	3.02	8.0E-48	AW178477.1	EST_HUMAN	h45103.x1 NCI_GOMP_L1m12 Homo sapiens cDNA clone IMAGE:3001133 3' similar to gb:264707
482	10426		1.37	7.0E-48	AB033055.1	NT	h45103.x1 NCI_GOMP_L1m12 Homo sapiens cDNA clone IMAGE:3001133 3' similar to gb:264707
483	10426		1.37	7.0E-48	AB033055.1	NT	h45103.x1 NCI_GOMP_L1m12 Homo sapiens cDNA clone IMAGE:3001133 3' similar to gb:264707
1462	11387	21250	1.12	7.0E-48	6912719	NT	Homo sapiens mRNA for KDA1209 protein, partial cds
1620	11624	21362	3.49	7.0E-48	5790039	NT	Homo sapiens mRNA for KDA1209 protein, partial cds
6947	15552	26976	22.88	7.0E-48	11416831	NT	Homo sapiens basic-like kinase 1 (TLK1), mRNA
7275	17162	27348	1.82	6.0E-48	AF020816.1	NT	Homo sapiens SET domain and member transposase fusion gene (SETMAR) mRNA
7600	17370	27677	1.9	6.0E-48	11427429	NT	Homo sapiens putative oncogene protein mRNA, partial cds
7687	17438	27654	3.38	6.0E-48	AA180980.1	EST_HUMAN	Homo sapiens hypochlorite protein FLJ11099 (TL-111056), mRNA
3269	15037	22386	1.39	5.0E-48	4828891	NT	h45103.x1 NCI_GOMP_L1m12 Homo sapiens cDNA clone IMAGE:3001133 3' similar to gb:264707
8325	18202	28451	3.95	4.0E-48	AA020420.1	EST_HUMAN	Homo sapiens phosphodiesterase 1A, calmodulin-dependent (PDE1A) mRNA
1363	11289	21124	0.92	3.0E-48	AV650964.1	EST_HUMAN	h45103.x1 NCI_GOMP_P128 Homo sapiens cDNA clone IMAGE:2264154 3'
1633	11828	21711	18.97	3.0E-48	4885170	NT	AV650964.1 CGK Homo sapiens cDNA clone GKCORE12 5'
1933	11828	21711	18.97	3.0E-48	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
							Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3579	13463	23284	0.88	3.0E-48	AI0664631.1	EST_HUMAN	h1b412x1 INQ_CGAP_GUT Homo sapiens cDNA clone IMAGE:297255 5' similar to SW-DOR2_HUMAN
5552	15607	25582	2.35	3.0E-48	BE049471.1	EST_HUMAN	P9555 DOWN SYNDROME BT0001 BT0001 REGION PROTEIN B ;
6859	16768		2.86	3.0E-48	AA656930.1	EST_HUMAN	m30565.s1 INQ_CGAP_P122 Homo sapiens cDNA clone IMAGE:1219137 3' similar to contains P1RS.b1
8248	18128	28376	7.08	3.0E-48	BF54170.1	EST_HUMAN	UHHBW1-ar-b-10-041st INQ_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3082267 3'
35	10027	18627	1.18	2.0E-48	AA631940.1	EST_HUMAN	PTRS repetitive element ;
4431	14326	24114	1.35	2.0E-48	BE246085.1	EST_HUMAN	TCBAP13942 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project-TOBA Homo sapiens cDNA clone TCBAP13942
5553	15469	25540	72.29	2.0E-48	AA613171.1	EST_HUMAN	nt18001.s1 INQ_CGAP_P161 Homo sapiens cDNA clone IMAGE:1101072 3'
5553	15469	25540	72.29	2.0E-48	AA613171.1	EST_HUMAN	nt18001.s1 INQ_CGAP_P161 Homo sapiens cDNA clone IMAGE:1101072 3'
6140	16301	26464	4.29	2.0E-48	AB040934.1	NT	Homo sapiens mRNA for KIAA1501 protein, partial cds
6140	16301	26464	4.29	2.0E-48	AB040934.1	NT	Homo sapiens mRNA for KIAA1501 protein, partial cds
6447	16308	28473	2.9	2.0E-48	11496238	NT	Homo sapiens v-rel avian reticuloendotheliosis viral oncogene homolog A (nuclear factor of kappa light polypeptide gene enhancer in B-cells 3 (p50) (NFKB1)) mRNA
6564	16743	26936	2.39	2.0E-48	AV743451.1	EST_HUMAN	AV743451.CB Homo sapiens cDNA clone CBCCGG10 5'
8164	15082	24826	2.45	2.0E-48	AA465007.1	EST_HUMAN	z6003.r1 Soares ovary tumor N6HOT Homo sapiens cDNA clone IMAGE:310162 5'
8511	19679	29070	1.03	2.0E-48	BE777154.1	EST_HUMAN	60130502.H1.NH1.MGC_39 Homo sapiens cDNA clone IMAGE:3889782 5'
80	10037	19844	0.85	1.0E-48	7705934	NT	Homo sapiens epiphyseal resistance-associated overexpressed protein LOC511747, mRNA
855	10782	20632	6.93	1.0E-48	4502168	NT	Homo sapiens amyloid beta (A4) precursor protein (presenilin-1, Alzheimer disease) (APP), mRNA
1274	11182	21032	3.39	1.0E-48	5932023	NT	Homo sapiens RNA binding motif protein 6 (RBM6) mRNA
1876	11772	21648	44.65	1.0E-48	AL163002.2	NT	Homo sapiens chromosome 21, segment H31G102
3449	13340	23107	1.29	1.0E-48	AL163246.2	NT	Homo sapiens chromosome 21, segment H31G1046
8082	14682	24728	1.1	1.0E-48	MT0076.1	NT	Homo sapiens chromosome 4 (4-1), complete retinal segment
6333	16167	26325	2.21	1.0E-48	MT0076.1	NT	Homo sapiens chromosome 4 (4-1), complete retinal segment
7327	17259	27686	5.72	1.0E-48	AB030371.1	NT	Homo sapiens mRNA for KIAA1245 protein, partial cds
7327	17259	27686	5.72	1.0E-48	BF304683.1	EST_HUMAN	nt180035P1.NH1.MGC_17 Homo sapiens cDNA clone IMAGE:4122119 5'
7934	17784	28023	5.08	1.0E-48	11429008	NT	Homo sapiens B cell factor protein (SLP-65), mRNA
7934	17784	28023	5.08	1.0E-48	AF119117.1	NT	Homo sapiens B cell factor protein (SLP-65), mRNA
8559	18802	29066	1.73	1.0E-48	AF119117.1	NT	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds
8559	18802	29066	1.73	1.0E-48	AF119117.1	NT	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds
9145	19606		1.86	1.0E-48	U02785.1	EST_HUMAN	1506 Homo telina cDNA randomly primed subsidiary Homo sapiens cDNA
5552	15601	25702	2.95	8.0E-48	10048417	NT	Mus musculus T-box 20 (Tbx20), mRNA

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Table 4

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6562	16901	29703	2.58	8.0E-46	10048417	NT	Mus musculus 1.6kb, 20 (Thc20) mRNA
6563	16902	29704	2.58	8.0E-46	U20830.1	NT	Human Inositol 1,4,5 trisphosphate receptor type 1 mRNA, partial cds
6567	10708	26500	3.16	8.0E-46	U20830.1	NT	Human Inositol 1,4,5 trisphosphate receptor type 1 mRNA, partial cds
134	10338	20157	1.47	7.0E-46	5725560	NT	Human sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMCA) mRNA
134	10338	20157	1.47	7.0E-46	5725560	NT	Human sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMCA) mRNA
388	10335	20157	1.74	7.0E-46	5725560	NT	Human sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMCA) mRNA
388	10335	20157	1.74	7.0E-46	5725560	NT	Human sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMCA) mRNA
388	10335	20157	1.98	7.0E-46	5725560	NT	Human sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMCA) mRNA
388	10335	20158	1.98	7.0E-46	5725560	NT	Human sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMCA) mRNA
1202	11112	20538	4.08	7.0E-46	AL163284.2	NT	Human sapiens chromosome 21 segment HS21C084
4850	14443	24227	0.58	7.0E-46	030811	SWISSPROT	HYPOPHOSPHATE PROTEIN D3H4G024.3
5361	16271	28100	1.63	7.0E-46	A080719.1	EST_HUMAN	Wf28004.1 Soares_NFL_1 GBC S1 Homo sapiens cDNA clone IMAGE 2390603 3' similar to TR-049423
5367	15277	25107	1.34	7.0E-46	AL112653.1	EST_HUMAN	049423 RBSC16.15
160	10162	19978	11.77	6.0E-46	AW731740.1	EST_HUMAN	DKF262030B.1 31762 (synonym: hmal2) Homo sapiens cDNA clone DKF26203B.3 3'
6000	14827	28738	2.52	6.0E-46	AW45218.1	EST_HUMAN	Wf28004.1 Soares_NFL_1 GBC S1 Homo sapiens cDNA clone IMAGE2800564 3' similar to bcx17200 40S
8620	14728	24022	2.86	6.0E-46	AA36899.1	EST_HUMAN	REDSOMAL PROTEIN 84-(HUMAN), gb1206932 Mouse LRrg9 protein mRNA from a repetitive element, complete (MOUSE)
8620	14728	24023	2.86	6.0E-46	AA36899.1	EST_HUMAN	UHH933-alc-o-05-OUJ.1 NCI CGAP Sub3 Homo sapiens cDNA clone IMAGE30680.48 3'
8607	14760	24023	2.86	6.0E-46	AA36899.1	EST_HUMAN	EST177628 Pancreas tumor III Homo sapiens cDNA 5' end
8607	14760	24023	2.86	6.0E-46	AA36899.1	EST_HUMAN	EST177628 Pancreas tumor III Homo sapiens cDNA 5' end
6509	14828	24042	3.43	5.0E-46	AL163210.2	NT	250604.1 3 Soares_flyc_liver_NFLS_S1 Homo sapiens cDNA clone IMAGE461654 3'
655	10628	20462	3.37	5.0E-46	AL163210.2	NT	Human sapiens chromosome 21 segment HS21C070
655	10628	20463	3.37	5.0E-46	AL163210.2	NT	Human sapiens chromosome 21 segment HS21C070
1763	11653	21924	1.94	5.0E-46	AA17121.1	EST_HUMAN	z220-07.11 Stratagene neuroepithelium (#537251) Homo sapiens cDNA clone IMAGE610680 5' similar to TR-G333228 G333228 RYTL-H1 PROTEIN, contains LTR7.13 LTR7.1 LTR7 repetitive element;
2721	12983	22477	5.18	5.0E-46	U17114.1	NT	Homo sapiens putative tumor suppressor S113 (S113) mRNA, complete cds
3235	13195	22567	5.13	5.0E-46	11430356	NT	Homo sapiens similar to fibronectin protein S27 (mellagalin/tatulin-1) (H. sapiens) (LOC633392), mRNA
514	10496	20266	37.46	4.0E-46	AW15633.1	EST_HUMAN	X08041.x1 NCI CGAP_U4 Homo sapiens cDNA clone IMAGE2075993 3' similar to WP-B03300.2B
5376	15710	20266	2.43	4.0E-46	AA210768.1	EST_HUMAN	CE007033
5456	15060	20268	0.93	4.0E-46	AF240786.1	NT	Z59005.1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE_902577.5
546	15060	20268	0.93	4.0E-46	X08068.1	NT	Human sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
546	15060	20268	0.93	4.0E-46	X08068.1	NT	H. sapiens mRNA for acyl-CoA carboxylase

Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (BLAST) Hit Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
2611	12479	24694	2.01	3.0E-46	AA016191.1	EST_HUMAN	26211605.1 1 Soares retina K20-4HR Homo sapiens cDNA, clone IMAGE-300584, 5' similar to contains 1 (18 L)
4959	18748	24694	2.08	3.0E-46	AB06899.1	NT	negative element;
6386	16248	28409	0.6	3.0E-49	AB99479.1	EST_HUMAN	Human type II collagen (COL4A3) gene, exon 40
8621	18437	28769	2.3	3.0E-49	AA337961.1	EST_HUMAN	EST125912 WATM1 Homo sapiens cDNA, clone Z89.12
6443	10882	28769	2.06	2.0E-46	BE165890.1	EST_HUMAN	EST142572 Endometrial tumor Homo sapiens cDNA, 5' end
3155	13170	22914	2.86	2.0E-49	BE165890.1	EST_HUMAN	MR3-H10407-100200-115-g01 H10407 Homo sapiens cDNA
3155	13170	22914	1.4	2.0E-46	N626446.1	EST_HUMAN	523d00r.1 Soares melanocyte 282bH1 Homo sapiens cDNA, complete cds
3155	13170	22914	0.93	2.0E-49	AF0269564.1	NT	Homo sapiens RNA binding protein 1 (RBM1) gene, complete cds
4683	14879	24373	1.12	2.0E-46	AF167357.1	EST_HUMAN	g858802.1 Soares, 'anesthetized', fibroblasts, 28bH1GF Homo sapiens cDNA, clone IMAGE:1692403 3' similar to
4704	14880	24381	1.25	2.0E-49	BF511846.1	EST_HUMAN	g858802.1 Soares, 'anesthetized', fibroblasts, 28bH1GF Homo sapiens cDNA, clone IMAGE:1692403 3' similar to
8040	15943	28776	1.47	2.0E-49	AF177938.1	EST_HUMAN	g858802.1 Soares, 'anesthetized', fibroblasts, 28bH1GF Homo sapiens cDNA, clone IMAGE:1692403 3' similar to
6717	16897	28776	1.97	2.0E-49	M69033.1	EST_HUMAN	g858802.1 Soares, 'anesthetized', fibroblasts, 28bH1GF Homo sapiens cDNA, clone IMAGE:1692403 3' similar to
9467	18599	28776	1.53	2.0E-49	AF163844.1	NT	g858802.1 Soares, 'anesthetized', fibroblasts, 28bH1GF Homo sapiens cDNA, clone IMAGE:1692403 3' similar to
881	17089	21531	3.05	1.0E-49	BF038327.1	EST_HUMAN	g858802.1 Soares, 'anesthetized', fibroblasts, 28bH1GF Homo sapiens cDNA, clone IMAGE:1692403 3' similar to
1760	11659	21531	2.98	1.0E-49	BE295216.1	EST_HUMAN	g858802.1 Soares, 'anesthetized', fibroblasts, 28bH1GF Homo sapiens cDNA, clone IMAGE:1692403 3' similar to
5259	15201	25011	4.97	1.0E-49	BF110097.1	EST_HUMAN	g858802.1 Soares, 'anesthetized', fibroblasts, 28bH1GF Homo sapiens cDNA, clone IMAGE:1692403 3' similar to
6297	16151	26305	2.93	1.0E-49	BE338110.1	EST_HUMAN	g858802.1 Soares, 'anesthetized', fibroblasts, 28bH1GF Homo sapiens cDNA, clone IMAGE:1692403 3' similar to
6297	16151	26305	2.93	1.0E-49	BE338110.1	EST_HUMAN	g858802.1 Soares, 'anesthetized', fibroblasts, 28bH1GF Homo sapiens cDNA, clone IMAGE:1692403 3' similar to
6322	16165	26346	2.17	1.0E-49	N25884.1	EST_HUMAN	g858802.1 Soares, 'anesthetized', fibroblasts, 28bH1GF Homo sapiens cDNA, clone IMAGE:1692403 3' similar to
6322	16165	26347	2.17	1.0E-49	N25884.1	EST_HUMAN	g858802.1 Soares, 'anesthetized', fibroblasts, 28bH1GF Homo sapiens cDNA, clone IMAGE:1692403 3' similar to
6709	16890	26777	1.39	1.0E-49	11321650.1	EST_HUMAN	g858802.1 Soares, 'anesthetized', fibroblasts, 28bH1GF Homo sapiens cDNA, clone IMAGE:1692403 3' similar to
6709	16890	26778	1.26	1.0E-49	11321650.1	EST_HUMAN	g858802.1 Soares, 'anesthetized', fibroblasts, 28bH1GF Homo sapiens cDNA, clone IMAGE:1692403 3' similar to
7200	17077	27862	1.22	1.0E-49	BE440394.1	EST_HUMAN	g858802.1 Soares, 'anesthetized', fibroblasts, 28bH1GF Homo sapiens cDNA, clone IMAGE:1692403 3' similar to
7830	17980	27924	1.21	1.0E-49	AL045129.2	EST_HUMAN	g858802.1 Soares, 'anesthetized', fibroblasts, 28bH1GF Homo sapiens cDNA, clone IMAGE:1692403 3' similar to
8630	18406	28769	3.88	1.0E-49	11442395.1	EST_HUMAN	g858802.1 Soares, 'anesthetized', fibroblasts, 28bH1GF Homo sapiens cDNA, clone IMAGE:1692403 3' similar to
8018	18813	28769	1.73	1.0E-49	BE165943.1	EST_HUMAN	g858802.1 Soares, 'anesthetized', fibroblasts, 28bH1GF Homo sapiens cDNA, clone IMAGE:1692403 3' similar to
9387	19035	28769	1.06	1.0E-49	11418322.1	EST_HUMAN	g858802.1 Soares, 'anesthetized', fibroblasts, 28bH1GF Homo sapiens cDNA, clone IMAGE:1692403 3' similar to
4923	14902	19061	1.98	9.0E-50	AF101475.1	NT	g858802.1 Soares, 'anesthetized', fibroblasts, 28bH1GF Homo sapiens cDNA, clone IMAGE:1692403 3' similar to
163	10198	19061	2.69	8.0E-50	AL1193202.2	NT	g858802.1 Soares, 'anesthetized', fibroblasts, 28bH1GF Homo sapiens cDNA, clone IMAGE:1692403 3' similar to
163	10198	19061	2.69	8.0E-50	X695097.2	NT	g858802.1 Soares, 'anesthetized', fibroblasts, 28bH1GF Homo sapiens cDNA, clone IMAGE:1692403 3' similar to
7024	19385	20460	1.86	1.0E-49	11418322.1	EST_HUMAN	g858802.1 Soares, 'anesthetized', fibroblasts, 28bH1GF Homo sapiens cDNA, clone IMAGE:1692403 3' similar to

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
702	10395	20461	1.26	8.0E-50	X95097.2	NT	Homo sapiens mRNA for VIP receptor 2
1016	10394		1.21	8.0E-50	AF009573.1	NT	Homo sapiens homophilic 1,2-diacylglycerase gene, complete cds
1727	11928	21467	2.51	8.0E-50	4501800	NT	Homo sapiens actinin, alpha 1 (ACTN1) mRNA
2432	12309	22204	1.36	8.0E-50	7708304	NT	Homo sapiens p47 (LOC31674), mRNA
2432	12309	22205	1.36	8.0E-50	7708304	NT	Homo sapiens p47 (LOC31674), mRNA
2666	12331	22421	1.69	8.0E-50	4820563	NT	Homo sapiens capping protein (actin filament) muscle 2, beta (CAPZB), mRNA
8711	18528	29811	2.1	8.0E-50	A463467.1	EST_HUMAN	GUT/ATHIONE S-TRANSFERASE TESTIS/BRAN (HUMAN);
633	10393	20349	0.96	7.0E-50	BE009591.1	EST_HUMAN	U01810708:280400-211-c88 B70703 Homo sapiens cDNA
8139	18027	20273	0.92	7.0E-50	A4072157.1	EST_HUMAN	w055911.1 NCL CGAP_U12 Homo sapiens cDNA clone IMAGE:2439009.3'
8791	16980		4.47	8.0E-50	BE040476.1	EST_HUMAN	h039044.1 NCL CGAP_U11 Homo sapiens cDNA clone IMAGE:303811.3 similar to contains MER20L3
8791	16980		4.47	8.0E-50	BE040476.1	EST_HUMAN	MER20, negative element;
8791	16978	28326	3.17	8.0E-50	A4312079.1	EST_HUMAN	EST182775.1 Juncal T cells V1 Homo sapiens cDNA, 5' end
8791	16978	28327	3.17	8.0E-50	A4312079.1	EST_HUMAN	EST182775.1 Juncal T cells V1 Homo sapiens cDNA, 5' end
1752	11682	21522	0.85	3.0E-50	BF332938.1	EST_HUMAN	CH3-B70793-300505:398-055 B70792 Homo sapiens cDNA
1752	11682	21522	0.85	3.0E-50	BF332938.1	EST_HUMAN	CH3-B70793-300505:398-055 B70792 Homo sapiens cDNA
1752	11682	21523	0.86	3.0E-50	BF332938.1	EST_HUMAN	CH3-B70793-300505:398-055 B70792 Homo sapiens cDNA
7255	17132		5.94	5.0E-50	A4557883.1	EST_HUMAN	h04510.1 NCL CGAP_P41 Homo sapiens cDNA clone IMAGE:1040653 similar to contains PTH6.9 PTH5
8691	18706	20086	1.85	5.0E-50	A4403093.1	EST_HUMAN	282901.1 Scores, beta, NHT Homo sapiens cDNA clone IMAGE:726989.5 similar to TR-G135769
8691	18706	20086	1.85	5.0E-50	A4403093.1	EST_HUMAN	G135769 GAC-POL POLYPROTEIN.1;
8691	10824		1.29	4.0E-50	A601143.1	EST_HUMAN	nc04608.1 NCL CGAP_S51 Homo sapiens cDNA clone IMAGE:1104520.3 similar to gpX5374_1.m1
1880	11791		2.45	3.0E-50	N18045.1	NT	PIBLIN-1, ISOPHORA A PRECURSOR (HUMAN);
3259	13182	22981	1.14	3.0E-50	AA746142.1	EST_HUMAN	Human endogenous retrovirus RTV142
3692	13006	23992	4.6	3.0E-50	AW755254.1	EST_HUMAN	CKMT45 Human cardiac muscle expression library Homo sapiens cDNA clone IMAGE:1322627.3'
6056	16039	23780	1.85	3.0E-50	11421514	NT	Cardomyopathy associated gene 5
6056	16039	23780	1.85	3.0E-50	11421514	NT	Homo sapiens similar to beta domain, immunoglobulin domain (Ig), short basic domain, secreted, (sense) 3A (H. sapiens) (LOC83232), mRNA
6505	16564	23540	4.01	3.0E-50	AF233493.2	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-OSP*1a mRNA, complete cds
6505	16564	23541	4.01	3.0E-50	AF233493.2	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-OSP*1a mRNA, complete cds
7549	17499	27721	1.17	3.0E-50	AB046818.1	NT	Homo sapiens mRNA for KMA11598 protein, peritill crts
8790	17005	28163	5.94	3.0E-50	AJ245621.1	NT	Homo sapiens CTL2 gene

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Max Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
761	10691		4.91	2.0E-50	AF050066.1	NT	Homo sapiens MHC class I region
1063	10979	20823	4.6	2.0E-50	455752	NT	Homo sapiens midline 1 [Optic/RBB syndrome (MID1)] mRNA
1425	11330	21197	18.02	2.0E-50	AF138303.1	NT	Homo sapiens decorin D mRNA
6524	16802	26965	6.27	2.0E-50	X06565.1	NT	Human HAPHA44 gene for alpha-tubulin, isoform 1-3
6524	16802	26965	6.27	2.0E-50	X06565.1	NT	Human HAPHA44 gene for alpha-tubulin, isoform 1-3
7656	17539	27761	1.53	2.0E-50	5910239	NT	Mus musculus keratin complex 2, gene 6g (K12-6g), mRNA
7656	17539	27761	1.53	2.0E-50	5910239	NT	Mus musculus keratin complex 2, gene 6g (K12-6g), mRNA
235	10204	20018	1	1.0E-50	BE007090.1	EST_HUMAN	Human HAPHA44 gene for alpha-tubulin, isoform 1-3
235	10204	20018	1	1.0E-50	BE007090.1	EST_HUMAN	Human HAPHA44 gene for alpha-tubulin, isoform 1-3
454	10368	20215	2.1	1.0E-50	AL163209.2	NT	Human HAPHA44 gene for alpha-tubulin, isoform 1-3
234	12161		8.98	1.0E-50	AJ271753.1	NT	Homo sapiens chromosome 21 segment H521C009
7375	17244	27450	1.22	9.0E-51	A4404378.1	EST_HUMAN	Homo sapiens Xq pseudautosomal region, segment 1/2
4467	14361	24151	4.99	8.0E-51	A4610842.1	EST_HUMAN	Human HAPHA44 gene for alpha-tubulin, isoform 1-3
6510	16969	26546	2.34	8.0E-51	11139387	NT	Heterogeneous nucleolar protein (HNP) mRNA
7418	17557		1.36	8.0E-51	AL138590.1	EST_HUMAN	Homo sapiens PDZ-73 protein (PDZ-73) mRNA
3245	13168	22667	1.36	7.0E-51	AW936219.1	EST_HUMAN	Homo sapiens PDZ-73 protein (PDZ-73) mRNA
3317	13288	23042	0.83	7.0E-51	AW774720.1	EST_HUMAN	Homo sapiens PDZ-73 protein (PDZ-73) mRNA
4076	13578	23757	1.26	7.0E-51	AL070623.1	EST_HUMAN	Homo sapiens PDZ-73 protein (PDZ-73) mRNA
4076	13578	23757	1.26	7.0E-51	AL070623.1	EST_HUMAN	Homo sapiens PDZ-73 protein (PDZ-73) mRNA
4254	14153	23827	2.38	7.0E-51	AW259033.1	EST_HUMAN	Homo sapiens PDZ-73 protein (PDZ-73) mRNA
1656	11631	21714	5.3	6.0E-51	7857269	NT	Homo sapiens KIAA0929 protein (KIAA0929) mRNA
3428	13345	23150	12.02	8.0E-51	7857269	NT	Homo sapiens KIAA0929 protein (KIAA0929) mRNA
4212	14110	23867	0.76	6.0E-51	9910553	NT	Homo sapiens scd4 carrier family 2 (facilitated glucose transporter), member 9 (SLC22A9), mRNA
4212	14110	23868	0.76	6.0E-51	9910553	NT	Homo sapiens scd4 carrier family 2 (facilitated glucose transporter), member 9 (SLC22A9), mRNA
5545	15568	26561	2.28	6.0E-51	X01788.1	NT	Human Hsp40/chaperone (Hsp40) gene, exon 3
5550	15568	26561	6.08	6.0E-51	AF070083.1	NT	Homo sapiens mitogen-activated protein kinase kinase 1 (MKKK1) gene, exon 4
5550	15568	26567	6.08	6.0E-51	AF070083.1	NT	Homo sapiens mitogen-activated protein kinase kinase 1 (MKKK1) gene, exon 4
6168	15116	24559	2.16	6.0E-51	11420863	NT	Homo sapiens centrad cell adhesion molecule (LOC81148), mRNA
7583	17434	27549	2.28	6.0E-51	7851539	NT	Homo sapiens B9 protein (B9), mRNA
8580	18448	28716	1.72	6.0E-51	11525289	NT	Homo sapiens interleukin 17 receptor (IL17R), mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Meet Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
774	10704	20543	10.92	5.0E-51	AL16303.2	NT	Homo sapiens chromosome 21 segment HS21C003
766	10715	20557	1.47	5.0E-51	4507900	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TAM1) mRNA
975	12682	20746	1.37	5.0E-51	AL13320.1	NT	Novel human gene mapping to chromosome X
1580	11464	21354	0.84	5.0E-51	5031960	NT	Homo sapiens 25S proteasome-associated padf homolog (POHF) mRNA
2548	12422	22311	11.48	5.0E-51	AJ007558.1	NT	Homo sapiens mRNA for nucleoporin 155
3953	13774	23565	1.08	5.0E-51	AJ007558.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
3953	13774	23567	1.08	5.0E-51	AJ007558.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
5004	14679	24643	2.34	5.0E-51	AB037632.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
5901	18465	26739	3.72	5.0E-51	5003136	NT	Homo sapiens RNA binding motif protein 3 (RBM3) mRNA
130	10704	19026	0.92	3.0E-51	AJ587349.1	EST_HUMAN	h61609.x1 NCL CGAP. Part Homo sapiens cDNA clone IMAGE:2224720 3' similar to gb:M26328
1159	11073	20917	4.16	3.0E-51	AJ587348.1	EST_HUMAN	h61609.x1 NCL CGAP. Part Homo sapiens cDNA clone IMAGE:2224720 3' similar to gb:M26328
4232	14130	23906	2.13	3.0E-51	AL159142.1	NT	KERATIN, TYPE I CYTOSKELETAL 16 (HUMAN); Novel human gene mapping to chromosome 22
6474	16333	25600	1.73	3.0E-51	R145914.1	EST_HUMAN	ye47208.1 Sources infant brain (NIB Homo sapiens cDNA clone IMAGE:53233 5' similar to gb:M141123, c064
7131	17008		5.97	3.0E-51	M20063.1	NT	RETROVIRUS-RELATED POLYPROTEIN (HUMAN) contains LTR repetitive element;
9075	18233		1.55	3.0E-51	AF003528.1	NT	Human hBRIP C3 protein mRNA
362	10318	20139	1.81	2.0E-51	4507798	NT	Homo sapiens X-linked inhibitor of endodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
673	10307	20424	1.08	2.0E-51	BE391063.1	EST_HUMAN	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A) mRNA
673	10307	20425	1.08	2.0E-51	BE391063.1	EST_HUMAN	h712699.x1 UHR_1MGC_41 Homo sapiens cDNA clone IMAGE:3607463 5'
1682	11554	21431	2.24	2.0E-51	AJ233362.1	EST_HUMAN	270465.1 Stages N12 neuronal precursor 937200 Homo sapiens cDNA clone IMAGE:064480 5' similar to TR-G33526 G33526 RT VLA-H PROTEIN. Contains LTR/LTR repetitive element;
3672	13556	23378	2.21	2.0E-51	AJ492415.1	EST_HUMAN	h27903.x1 NCL CGAP. Part Homo sapiens cDNA clone IMAGE:213132 3'
4362	14268	24071	1.02	2.0E-51	AIW13726.1	EST_HUMAN	UHH-8H-adj-02-00-Uat NCL CGAP. Subd Homo sapiens cDNA clone IMAGE:2716851 3'
6962	15573	25670	2.96	2.0E-51	BE720215.1	EST_HUMAN	0174/04467.1 UHR_1MGC_67 Homo sapiens cDNA clone IMAGE:3973583 5'
7047	16924	27114	1.81	2.0E-51	BE601699.1	EST_HUMAN	0176/0767.1 UHR_1MGC_21 Homo sapiens cDNA clone IMAGE:3989813 5'
7047	16924	27115	1.61	2.0E-51	BE601699.1	EST_HUMAN	0176/0767.1 UHR_1MGC_21 Homo sapiens cDNA clone IMAGE:3989813 5'
7478	17348	27652	1.98	2.0E-51	AI917078.1	EST_HUMAN	h74607.x1 NCL CGAP. G08 Homo sapiens cDNA clone IMAGE:2206980 3' similar to SW:TRKC_HUMAN
7539	17590	27650	5.25	2.0E-51	BE165980.1	EST_HUMAN	Q16288 NT.3 GROWTH FACTOR RECEPTOR PRECURSOR ;
							MP3-HT0487-150200-115-401 HT0487 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7862	17612	28054	1.71	2.0E-51	AV68274.1	EST_HUMAN	AV68274.1 K143 Homo sapiens cDNA clone K143AF06 5'
8540	15259	25084	8.03	2.0E-51	AI732851.1	EST_HUMAN	cd3409.36 NCL CGAP K143 Homo sapiens cDNA clone IMAGE:1325609 3' similar to SW:NM1_MOUSE P34306 GLUTAMATE [MIMD] RECEPTOR SUBUNIT EPSILON 1 PRECURSOR ;
8540	15259	25085	8.03	2.0E-51	AI732851.1	EST_HUMAN	cd3409.36 NCL CGAP K143 Homo sapiens cDNA clone IMAGE:1325609 3' similar to SW:NM1_MOUSE P34306 GLUTAMATE [MIMD] RECEPTOR SUBUNIT EPSILON 1 PRECURSOR ;
9538	19227	25240	1.33	2.0E-51	11419169	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (t(11q24) [Drosophila] homolog), translocated to, 4 (MLL1), mRNA
109	10090	19905	4.4	1.0E-51	450323	NT	Homo sapiens autalytic translation initiation factor 4A, isoform 1 (EIF4A1) mRNA
1478	11383	227	22.7	1.0E-51	AV742248.1	EST_HUMAN	AV742248 CB Homo sapiens cDNA clone CBFBCC12 5'
4309	14206	23369	0.96	1.0E-51	4756071	NT	Homo sapiens small inducible cytokine subfamily A (Cys-Cys), member 15 (SCYA15) mRNA
4309	14206	23369	0.96	1.0E-51	4756071	NT	Homo sapiens small inducible cytokine subfamily A (Cys-Cys), member 15 (SCYA15) mRNA
8310	15231	25036	3.12	1.0E-51	T18882.1	EST_HUMAN	b120581 Testis 1 Homo sapiens cDNA clone b12058
8539	19771		3.37	1.0E-51	AV706590.1	EST_HUMAN	AV706590 M13 Homo sapiens cDNA clone MDC3B92 5'
9454	19056		3.38	9.0E-52	AA777621.1	EST_HUMAN	cd3409.36 NCL CGAP K143 Homo sapiens cDNA clone IMAGE:1325609 3' similar to contains THR 13 THR repetitive element ;
146	10120	19939	7.31	8.0E-52	AA729574.1	EST_HUMAN	mw21002.51 NCL CGAP K143 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR 13 THR repetitive element ;
1481	11368	21249	1.33	8.0E-52	X54900.1	NT	H sapiens mRNA for laminin-5, alpha3b chain
1633	11537	21307	2.05	8.0E-52	11989028	NT	Homo sapiens hypothetical protein FLJ13555 similar to N-myc downstream regulated 3 (FLJ13555), mRNA
1633	11537	21308	2.05	8.0E-52	11989028	NT	Homo sapiens hypothetical protein FLJ13555 similar to N-myc downstream regulated 3 (FLJ13555), mRNA
3913	11537	21397	0.44	8.0E-52	11989028	NT	Homo sapiens hypothetical protein FLJ13555 similar to N-myc downstream regulated 3 (FLJ13555), mRNA
3913	11537	21398	0.44	8.0E-52	11989028	NT	Homo sapiens hypothetical protein FLJ13555 similar to N-myc downstream regulated 3 (FLJ13555), mRNA
7211	17088	27278	1.48	7.0E-52	W56471.1	EST_HUMAN	329306.r1 Scoville, parathyroid, tumor, NRP4 Homo sapiens cDNA clone IMAGE:32676 6' similar to contains AU repetitive element ;
1170	11082		0.86	6.0E-52	BE072405.1	EST_HUMAN	QY317637-271739-049-047 B10537 Homo sapiens cDNA
1688	11670	21430	2.25	0.0E-52	AF106907.1	NT	Homo sapiens S104 gene, partial cds; P51 and hypothetical protein genes, complete cds, and S171 gene, partial cds
8540	18412	28976	2.23	0.0E-52	BE048172.1	EST_HUMAN	tz6R04.1 NCL CGAP K143 Homo sapiens cDNA clone IMAGE:2391671 5' similar to SW:PGM_MOUSE 005793 BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN PRECURSOR ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal Value	Most Similar Top Hit EST E	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4340	14237	24021	2.07	5.0E-52	Z78868.1	NT	H.sapiens flow-sorted chromosome 8 HincIII fragment, SCSB18H7
1053	11543	21402	0.93	4.0E-52	AF227318.1	NT	Homo sapiens SHC-containing protein SHG3L1 mRNA, complete cds
1748	11618	21516	8.88	4.0E-52	AF78843	NT	Homo sapiens nucleoporin 155D (NUP155) mRNA
3850	13761	23554	0.32	4.0E-52	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
6696	16566	26760	1.24	4.0E-52	BE622032.1	EST_HUMAN	601440057F1 NIH MG-72 Homo sapiens cDNA clone IMAGE3919536 5'
6595	16543	27035	7.25	4.0E-52	11417035	NT	Homo sapiens hydroxyacid (17-beta) dehydrogenase 4 (HSD17B4), mRNA
5291	18992		4.25	4.0E-52	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
6778	19293		5.08	4.0E-52	AB002036.1	NT	Homo sapiens DNA for Human P204, complete cds
4022	13008		9.88	3.0E-52	11437042	NT	Homo sapiens hypothetical protein FLJ10675 (FLJ10675), mRNA
859	10461	20266	1.35	2.0E-52	U10376.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
520	10461	20300	1.35	2.0E-52	U10376.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
2450	12227	22226	1.75	2.0E-52	SE207575.1	EST_HUMAN	6895407.X1 NIH MG-93 Homo sapiens cDNA clone IMAGE:3039421 5' similar to gp-X(846) M. musculus
2708	12568		20.33	2.0E-52	SE07575.1	EST_HUMAN	mRNA for Zfp-1 Zinc finger protein (MOLISE)
4022	14782	24557	2.74	2.0E-52	AL137188.3	EST_HUMAN	602649710F1 NIH MG-83 Homo sapiens cDNA clone IMAGE:4248891 5'
5497	15476	25479	2.74	2.0E-52	AW540941.1	EST_HUMAN	Novel human gene mapping to chromosome 20, similar to membrane transporters
8541	15747	23600	1.48	2.0E-52	1141868	NT	U3-C70214-231359-63-E12 CT0214 Homo sapiens cDNA
7028	16805		8.38	2.0E-52	AF14780.1	NT	Homo sapiens interleukin 21 receptor (IL21R), mRNA
							Macaca mulatta beta-tubulin mRNA, complete cds
							Homo sapiens NADH dehydrogenase (ubiquinone) Fe-S protein 5 (ND5) (NADH-coenzyme Q reductase) (NDU5) mRNA
7458	17207		1.88	2.0E-52	4756789	NT	Homo sapiens SET domain and nuclear transportase fusion gene (SETMAR) mRNA
7625	17675	27818	4.53	2.0E-52	5730039	NT	Homo sapiens SET domain and nuclear transportase fusion gene (SETMAR) mRNA
7625	17675	27819	4.53	2.0E-52	5730039	NT	Homo sapiens SET domain and nuclear transportase fusion gene (SETMAR) mRNA
8536	18408	26871	5.33	2.0E-52	AB31482.1	EST_HUMAN	W4804.X1 NC1 CGAP_Lun19 Homo sapiens cDNA clone IMAGE:2406190 3' similar to contains THR12 THR repetitive element;
							w4804.X1 NC1 CGAP_Lun19 Homo sapiens cDNA clone IMAGE:2406190 3' similar to contains THR12 THR repetitive element;
8536	18408	26872	5.33	2.0E-52	AB31482.1	EST_HUMAN	W4804.X1 NC1 CGAP_Lun19 Homo sapiens cDNA clone IMAGE:2406190 3' similar to contains THR12 THR repetitive element;
8547	18419	26898	3.08	2.0E-52	AV171537.1	EST_HUMAN	AV171537.DC8 Homo sapiens cDNA clone DC8AE03 5'
8650	18548		2.08	2.0E-52	W17260.1	EST_HUMAN	AD891212.1 Soares, Jidali, Hsueh, NHHH18W Homo sapiens cDNA clone IMAGE:344068 5'
8891	18701		3.22	2.0E-52	11417800	NT	Homo sapiens LIM domain kinase 2 (LMK2), mRNA
							W4804.X1 NC1 CGAP_Lun19 Homo sapiens cDNA clone IMAGE:2406190 3' similar to contains THR12 THR repetitive element;
9101	18755	24854	8.86	2.0E-52	AW230297.1	EST_HUMAN	W4804.X1 NC1 CGAP_Lun19 Homo sapiens cDNA clone IMAGE:2406190 3' similar to contains THR12 THR repetitive element;
9466	19112		4.37	2.0E-52	AB009885.1	EST_HUMAN	W4804.X1 NC1 CGAP_Lun19 Homo sapiens cDNA clone IMAGE:2406190 3' similar to contains THR12 THR repetitive element;
522	10464	20276	1.38	1.0E-52	AB634446.1	EST_HUMAN	Q16889 CARBOXYLESTERASE 1; 275H12.51 Soares, Jidali, Hsueh, NHHH18W Homo sapiens cDNA clone IMAGE:344068 5'

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Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1349	11265	21111	8.25	1.0E-52	4504026	NT	Homo sapiens glutamate-oxaloacetate transaminase (glutamate synthase) (GLUT1) mRNA
2489	12394		1.2	1.0E-52	4502238	NT	Homo sapiens aspartate aminotransferase 2 (A2SD), transcript variant 1, mRNA
3021	12649	22741	1.41	1.0E-52	S61070.1	NT	Human P-glycoprotein (MDR1) gene, exon 4
5270	15192	24087	3.59	1.0E-52	N23426.1	NT	Human PMS2 related (HNPMS2) gene, complete cds
5551	15737	25676	2.11	1.0E-52	U38964.1	NT	Human aldolase C gene for fructose-1,6-bisphosphate aldolase
5394	16266	26417	3.19	1.0E-52	X07292.1	NT	Homo sapiens chromosome 21 segment HS21C027
6321	16710		1.84	1.0E-52	AL18327.2	NT	Homo sapiens chromosome 21 segment HS21C027
8023	17673		1.81	1.0E-52	U48366.1	NT	Homo sapiens chromosome 21 segment HS21C027
8147	18035	28283	2.04	1.0E-52	U48366.1	NT	Homo sapiens chromosome 21 segment HS21C027
8270	18094		2.04	1.0E-52	U48366.1	NT	Homo sapiens chromosome 21 segment HS21C027
8721	18635	29420	1.03	9.0E-53	AF01446.1	NT	Homo sapiens protein kinase C, delta type 2 (PSKDB2) mRNA
3723	18635	29420	1.03	9.0E-53	AF01446.1	NT	Homo sapiens protein kinase C, delta type 2 (PSKDB2) mRNA
4293	14191	23575	1.01	9.0E-53	AF01446.1	NT	Homo sapiens protein kinase C, delta type 2 (PSKDB2) mRNA
4666	14811	24511	0.93	9.0E-53	766173	NT	Homo sapiens protein kinase C, delta type 2 (PSKDB2) mRNA
6938	19018		2.06	7.0E-53	BF238465.1	EST_HUMAN	Human sapiens protein kinase C, delta type 2 (PSKDB2) mRNA
9752	19632		2.98	7.0E-53	AA42182.1	EST_HUMAN	Human sapiens protein kinase C, delta type 2 (PSKDB2) mRNA
4000	13915	23690	2.2	5.0E-53	4759543	NT	Homo sapiens heterogenous nuclear ribonucleoprotein C (C1/C2) (HNRPC) mRNA
9380	19048		1.72	5.0E-53	AW181593.1	EST_HUMAN	Human sapiens heterogenous nuclear ribonucleoprotein C (C1/C2) (HNRPC) mRNA
43	10031	18634	1.92	4.0E-53	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
43	10031	18634	1.92	4.0E-53	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
4715	14001	24387	1.09	4.0E-53	7705414	NT	Homo sapiens hook1 protein (HOOK1), mRNA
8545	18417	26865	3.33	4.0E-53	BF128701.1	EST_HUMAN	Human sapiens hook1 protein (HOOK1), mRNA
8545	18417	26866	3.33	4.0E-53	BF128701.1	EST_HUMAN	Human sapiens hook1 protein (HOOK1), mRNA
2025	12493	22384	2.59	3.0E-53	AB026886.1	NT	Homo sapiens DNA, DLEC1 to ORC1L4 gene region, section 1/2 (DLEC1, ORC1L4, complete cds)
3670	13854	23171	1.29	3.0E-53	AW090336.1	EST_HUMAN	Human sapiens DNA, DLEC1 to ORC1L4 gene region, section 1/2 (DLEC1, ORC1L4, complete cds)
4480	14390	24167	1.18	3.0E-53	AW090336.1	EST_HUMAN	Human sapiens DNA, DLEC1 to ORC1L4 gene region, section 1/2 (DLEC1, ORC1L4, complete cds)
4333	14716	24498	0.85	3.0E-53	BE009344.1	EST_HUMAN	Human sapiens DNA, DLEC1 to ORC1L4 gene region, section 1/2 (DLEC1, ORC1L4, complete cds)
6833	16712	23905	9.86	3.0E-53	S17943.1	NT	GIF-growth inhibitory factor (human, brain, Genomic, 2015 nt)
7238	17115		4.25	2.0E-53	AA306556.1	EST_HUMAN	Human sapiens FGR-R1 oncogene partner (FOP), mRNA
460	10394		4.25	2.0E-53	AA306556.1	EST_HUMAN	Human sapiens FGR-R1 oncogene partner (FOP), mRNA
2279	12163	22050	2.98	2.0E-53	U78027.1	NT	Human sapiens Bcl-2-like protein (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44), and FIP3 (FIP3) genes, complete cds

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Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Mean Similar (Top Hit BLAST E Value)	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2450	12295		10.54	2.0E-53	4502310	NT	Homo sapiens ATPase, H ⁺ transporting, lysosomal (vacuolar proton pump) 31kD; Vacuolar protein-ATPase, subunit E; V-ATPase, subunit E (ATP9E), mRNA
2654	12259	22446	6.03	2.0E-53	4757915	NT	Homo sapiens core-binding factor, runt domain, alpha subunit 2; translocated to, 1; cyclin D-related (CBFA2T1) mRNA
2654	12259	22447	6.03	2.0E-53	4757915	NT	Homo sapiens core-binding factor, runt domain, alpha subunit 2; translocated to, 1; cyclin D-related (CBFA2T1) mRNA
3207	13131	22353	1.18	2.0E-53	AF038222.1	NT	Homo sapiens dihydropyrimidine receptor alpha 2 subunit (CA2N2D-1) gene, exon 6
3370	13577	23553	2.06	2.0E-53	V61873.1	NT	Human Kruettel-related DNA-binding protein (TF34) gene, partial cds
4350	14286	24068	1.07	2.0E-53	4505602	NT	Homo sapiens SKAP55 homologous (SKAP-HOM) mRNA
5051	14611	24735	1.12	2.0E-53	AL163281.2	NT	Homo sapiens chromosome 21 segment H321C081
5091	14691	24735	1.12	2.0E-53	AL163281.2	NT	Homo sapiens chromosome 21 segment H321C081
5331	15251	25056	3.11	2.0E-53	BF334740.1	EST_HUMAN	P4H-210396-70900-001-203 C10355 Homo sapiens cDNA
5331	15251	25057	3.11	2.0E-53	BF334740.1	EST_HUMAN	P4H-210396-70900-001-203 C10355 Homo sapiens cDNA
7413	17260		5.6	2.0E-53	AW245675.1	EST_HUMAN	2622965 5' Homo sapiens NH1_MGC_7 Homo sapiens cDNA, clone IMAGE 2622965 5'
1426	11334	21200	0.5	1.0E-53	AJ271755.1	NT	Homo sapiens Xq pseudobacterial segment, segment 22
3354	13283	23053	1	1.0E-53	AB026855.1	NT	Homo sapiens DNA, DLEC1 to ORC1L4 gene region, section 1/2 (DLEC1, ORC1L3, ORC1L4 genes, CH44-NN1028) 16900-543-402 NH1028 Homo sapiens cDNA
8021	15225	23055	1.42	1.0E-53	BF334201.1	EST_HUMAN	H1 sapiens mRNA for hRNP-core protein A1
7283	17125	27321	5.14	1.0E-53	X74535.1	NT	Homo sapiens T cell lymphoma invasion and metastasis 1 (TAM1) mRNA
8152	15019	24787	0.8	9.0E-54	4507500	NT	Homo sapiens T cell lymphoma invasion and metastasis 1 (TAM1) mRNA
8152	15019	24788	0.8	9.0E-54	4507500	NT	Homo sapiens T cell lymphoma invasion and metastasis 1 (TAM1) mRNA
5244	14430	24430	4.71	9.0E-54	4506789	NT	Homo sapiens T cell lymphoma invasion and metastasis 1 (TAM1) mRNA
200	10172	19688	3.09	8.0E-54	BE338785.1	EST_HUMAN	6012726031 NH1_MGC_20 Homo sapiens cDNA, clone IMAGE3614031 5'
1794	11652	21668	1.33	8.0E-54	4504610	NT	Homo sapiens insulin-like growth factor 2 receptor (IGF2R) mRNA
4625	14617	24307	1.25	8.0E-54	4507843	NT	Homo sapiens ubiquitin specific protease 13 (ubiquitinase 1-3) (USP13) mRNA
4625	14617	24308	1.25	8.0E-54	4507843	NT	Homo sapiens ubiquitin specific protease 13 (ubiquitinase 1-3) (USP13) mRNA
5030	14617	24307	1.08	8.0E-54	4507843	NT	Homo sapiens ubiquitin specific protease 13 (ubiquitinase 1-3) (USP13) mRNA
5030	14617	24308	1.08	8.0E-54	4507843	NT	Homo sapiens ubiquitin specific protease 13 (ubiquitinase 1-3) (USP13) mRNA
5914	15529	25612	20.81	8.0E-54	6005700	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC), member 6 (ABCA6), mRNA
3719	10593	20180	1.26	7.0E-54	AA812537.1	EST_HUMAN	aBc12.1 Score, testis, NH1 Homo sapiens cDNA, clone 1377046 3' similar to contains MER30.13 MER30 repetitive element
1789	11657	21653	1.54	7.0E-54	V16945.1	NT	Homo sapiens mRNA for monocyte chemotactic protein-2
2155	12045	21845	4.81	7.0E-54	N27177.1	EST_HUMAN	yy68412.51 Score, placenta, 62cWeeks, ZNHRP82GW Homo sapiens cDNA, clone IMAGE 257559 3' similar to contains LTR7 b3 LTR7 repetitive element;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Meet Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7831	17681	27926	2.23	7.0E-54	11417222	NT	Homo sapiens similar to nuclear factor related to kappa B binding protein (H. sapiens) [LOC8182], mRNA
8611	18478		6.24	7.0E-54	AI00189.1	EST_HUMAN	g97g03.x1 Scores: final heart, NHH-H19W Homo sapiens cDNA clone IMAGE:1705204 3' similar to contains ORF 1 ORF repetitive element;
22	10009	19802	1.54	6.0E-54	AB003018.1	NT	Homo sapiens cDNA for MCB, exon 4, 5 and partial cds
1833	11720	21605	0.87	6.0E-54	450052	NT	Homo sapiens lymphocyte antigen 75 (LY75) mRNA, and translated products
1833	11720	21606	0.87	6.0E-54	450052	NT	Homo sapiens lymphocyte antigen 75 (LY75) mRNA, and translated products
3246	13169	22968	0.84	6.0E-54	8622148	NT	Homo sapiens hypothetical protein DKFZp434035 (DKFZp434035), mRNA
3623	13632	23612	2.4	6.0E-54	4302872	NT	Homo sapiens chloride channel 6 (CLCN6) mRNA
4359	14255	24240	1.24	6.0E-54	AV7547.6	EST_HUMAN	AV7547.6 TP Homo sapiens cDNA clone TPCMAIG10 5'
4774	14658		1.71	6.0E-54	Y09416.1	NT	H sapiens abc pseudogene, p65 isoform
4820	14659		1.3	6.0E-54	Y09416.1	NT	H sapiens abc pseudogene, p65 isoform
8750	17650	28143	1.77	6.0E-54	AB163597.1	EST_HUMAN	RC3-ST0197-151059-011408 ST0197 Homo sapiens cDNA
2104	11663	21863	2.25	5.0E-54	PI1623	SWISSPROT	ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2)
176	10147		108.86	4.0E-54	AF110103.1	NT	Tupai belangeri beta-actin mRNA, partial cds
940	10865	20712	41.94	4.0E-54	AA308784.1	EST_HUMAN	EST117769.hkafat T-cells VI Homo sapiens cDNA 5' and similar to glyceraldehyde-3-phosphate dehydrogenase
1764	11663	21636	3.24	4.0E-54	D38521.1	NT	Human mRNA for KIAA0077 gene, partial cds
1764	11663	21637	3.24	4.0E-54	D38521.1	NT	Human mRNA for KIAA0077 gene, partial cds
3198	13093		1.17	4.0E-54	AA309083.1	EST_HUMAN	w32841 L1 Scores: MEL_T_GSC S1 Homo sapiens cDNA clone IMAGE:239298 3' similar to TR:002711
86	100721	19886	5.11	3.0E-54	AA310467.1	EST_HUMAN	Q02711 PRO-POLYUTERASE POLYPROTEIN;
2522	12268	22287	0.93	3.0E-54	AA110393.1	EST_HUMAN	EST18531 Cdkn coxsoma (CCK) cell from Homo sapiens cDNA 5' and
2593	13154		0.86	3.0E-54	AA309197.1	EST_HUMAN	DKFZp434037.91 T1 634 (synonym: HES2) Homo sapiens cDNA clone DKFZp434037.91 5'
2593	13154		0.86	3.0E-54	AA309197.1	EST_HUMAN	DKFZp434037.91 T1 634 (synonym: HES2) Homo sapiens cDNA clone DKFZp434037.91 5'
5398	15512	25580	1.48	3.0E-54	AA404091.1	EST_HUMAN	Homo sapiens BAK non-receptor tyrosine kinase (BAK) mRNA
6373	16258	26384	1.98	3.0E-54	AA404091.1	EST_HUMAN	Homo sapiens BAK non-receptor tyrosine kinase (BAK) mRNA
6373	16258	26384	1.98	3.0E-54	AA404091.1	EST_HUMAN	Homo sapiens BAK non-receptor tyrosine kinase (BAK) mRNA
8438	18369	28565	4.17	3.0E-54	BF345600.1	EST_HUMAN	6020164081 NCI CCAP Brn67 Homo sapiens cDNA clone IMAGE:4158121 5'
8675	16663	28847	3.34	3.0E-54	AA383382.1	EST_HUMAN	2701271 Scores: Jellis, NIH Homo sapiens cDNA clone IMAGE:72727 5' similar to TR:G101316
9166	18632	25353	2.86	3.0E-54	AA394959.1	EST_HUMAN	G194915 ANDROGEN-DEPENDENT EXPRESSED PROTEIN ;
9242	19714		7	3.0E-54	AA1748665.1	EST_HUMAN	RC1-BT0313-151190-011409 BT0313 Homo sapiens cDNA
628	10583	20374	6.26	2.0E-54		NT	Homo sapiens Uter, cell lectin-like receptor subfamily G, member 1 (KLRG1), mRNA
1342	11248	21105	1.84	2.0E-54	4507164	NT	Homo sapiens nuclear antigen SP100 (SP100) mRNA

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Probe SEQ ID NO.	Exon NO.	ORF SEQ ID NO.	Expression Signal	Mean Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1620	11434	21230	1.6	2.0E-54	AA65008.1	EST_HUMAN	nt8400.s1 NOL CGAG Fp8 Homo sapiens cDNA clone IMAGE:1204600 similar to contains element L1 repetitive element;
2463	12367	22261	1.3	2.0E-54	AAW3175.1	EST_HUMAN	ad29203.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783764 5' similar to
2656	12328	22261	1.32	2.0E-54	AL16320.2	NT	SWI_CUL1_HUMAN Q13616 CULLIN HOMOLOG 1;
2865	12763	22287	1.85	2.0E-54	AW057624.1	EST_HUMAN	Homo sapiens chromosome 21 segment H821C010 ; WY6012.x1 Soares_NSF_F8_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2453227 3' similar to
3501	13418		4.06	2.0E-54	AA52925.1	EST_HUMAN	TRQ0284.Q02084 PHOSPHOLIPASE C NEIGHBORING ;
4110	14010		2.03	2.0E-54	AB02842	NT	H4509.s1 NOL CGAG Fp8 Homo sapiens cDNA clone IMAGE:365448 similar to gb:X63777 90S
4343	14240		1.13	2.0E-54	AL16320.2	NT	RIBOSOMAL PROTEIN L23 (HUMAN);
4780	14664	24450	1.45	2.0E-54	7709446	NT	Homo sapiens chromosome 21 segment H821C001
5166	15023	24760	0.84	2.0E-54	AF033823.1	NT	Homo sapiens dihydroxydicarboxylate receptor alpha 2 subunit (CACNA2D1) gene, exon 7
5363	15283	25116	3.75	2.0E-54	AF033823.1	NT	Homo sapiens small inducible cyclin subfamily A (Opa-Opa) member 14 (SOYA14) mRNA
5440	15359	25417	1.34	2.0E-54	BE047864.1	EST_HUMAN	25831.v1 NOL CGAG Fp8c6 Homo sapiens cDNA clone IMAGE:2261348 5'
5521	15439	25503	3.95	2.0E-54	11128657	NT	Homo sapiens KIAA1001 gene product (KIAA1001) mRNA
5573	15488	25564	18.15	2.0E-54	AB046811.1	NT	Homo sapiens mRNA for KIAA1551 protein, partial cds
5573	15488	25566	18.15	2.0E-54	AB046811.1	NT	Homo sapiens mRNA for KIAA1551 protein, partial cds
6227	16093	26243	8.14	2.0E-54	1142844	NT	Homo sapiens insulin-like growth factor 1 (IGF1) mRNA
7521	17463	27017	3.02	2.0E-54	AB041025.1	NT	Homo sapiens mRNA for brain tyrosine receptor, complete cds
7748	17689	27821	1.26	2.0E-54	11429127	NT	Homo sapiens Janus kinase 2 (a protein tyrosine kinase) (JAK2), mRNA
8603	1870		2.97	2.0E-54	785145	NT	Homo sapiens perlecan (basal laminar) homolog 1 containing BRCT domain (PES1), mRNA
9653	18244	28216	1.46	2.0E-54	8567387	NT	Homo sapiens period (circadian) homolog 2 (PER2), mRNA
4363	14269		1.07	1.0E-54	3F316418.1	EST_HUMAN	001662001.1 NH_MGC_19 Homo sapiens cDNA clone IMAGE:4128855 5'
9852	19346		2.26	1.0E-54	AB077441.1	EST_HUMAN	001662001.1 NH_MGC_19 Homo sapiens cDNA clone IMAGE:4128855 5'
1294	11201		14.96	8.0E-55	Y07629.2	NT	gamma-glutamyl transaminase mRNA, 5' end
1297	11204		2.32	8.0E-55	Y07629.2	NT	Homo sapiens RPS30 gene for RING finger protein
8530	18402		2.76	8.0E-55	AAW409714.1	EST_HUMAN	Homo sapiens RPS30 gene for RING finger protein
1065	10581	20826	1.16	7.0E-55	RO3446.1	EST_HUMAN	002021.1 NH_MGC_17 Homo sapiens cDNA clone IMAGE:2560607 5'
7297	17173	27973	1.26	7.0E-55	AA869581.1	EST_HUMAN	Y0504.1 Sources field liver cytosol: 1NFLS Homo sapiens cDNA clone IMAGE:127698 5' similar to
7315	17191	27983	1.56	7.0E-55	AA195069.1	EST_HUMAN	SP-C801 BOVIN P10897 OXYTOCIN- 002841.1 Sources field liver cytosol: 1NFT Homo sapiens cDNA clone IMAGE:147200 3'
							al2841.1 Sources field liver cytosol: 1NFT Homo sapiens cDNA clone IMAGE:101576 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Mean Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8541	18413	28679	12.75	7.0E-55	AI061056.1	EST_HUMAN	lc2509.x1 NCL CGAP_UH Homo sapiens cDNA clone IMAGE:2210248 3'
8541	18413	28680	12.75	7.0E-55	AI061056.1	EST_HUMAN	lc2509.x1 NCL CGAP_UH Homo sapiens cDNA clone IMAGE:2210248 3'
9823	19948		4.3	7.0E-45	U52936.1	EST_HUMAN	ym5760.7 T Scores infant trant NMIS Homo sapiens cDNA clone IMAGE:52444 5'
8803	18617	28608	1.98	6.0E-55	AB040834.1	NT	Homo sapiens mRNA for KIAA16501 protein, partial cds
1732	11633	21600	1.12	5.0E-55	AA704971.1	EST_HUMAN	29B500.1 Sources, fetal_liver, spleen, 1NFLS_S1 Homo sapiens cDNA clone IMAGE:462817 3'
1732	11633	21601	1.12	5.0E-55	AA704971.1	EST_HUMAN	29B500.1 Sources, fetal_liver, spleen, 1NFLS_S1 Homo sapiens cDNA clone IMAGE:462817 3'
5941	15648	25659	1.82	6.0E-55	4502240	NT	Homo sapiens arylsulfoxidase E (chlorodioxidase) punctata 1 (ARSE), mRNA
5941	15648	25670	1.82	6.0E-55	4502240	NT	Homo sapiens arylsulfoxidase E (chlorodioxidase) punctata 1 (ARSE), mRNA
7229	17103	27258	2.08	6.0E-55	4505302	NT	Homo sapiens protein tyrosine phosphatase, receptor type, alpha polypeptide (PTPRA) mRNA
7770	17520	27881	1.98	5.0E-55	AB014511.1	NT	Homo sapiens mRNA for KIAA0811 protein, partial cds
7770	17520	27882	1.98	5.0E-55	AB014511.1	NT	Homo sapiens mRNA for KIAA0811 protein, partial cds
7869	17719	27965	1.19	5.0E-55	8453765	NT	Homo sapiens mRNA for KIAA0811 protein, partial cds
9283	12658		2.13	5.0E-55	11417072	NT	Homo sapiens mRNA for KIAA0811 protein, partial cds
401	12658	19843	1.38	4.0E-55	AI067094.1	EST_HUMAN	Homo sapiens peccadillo (zebrin) homolog 1, containing BRG1 domain (PES1), mRNA
858	10891	20409	33.85	4.0E-55	4632973	NT	EST370964 IMAGE message, MAGE Homo sapiens cDNA
1422	11328	21183	1.98	4.0E-55	7865713	NT	Homo sapiens RNA binding motif protein, Y chromosome, family 1, member A1 (RBMYA1A1) mRNA
1422	11328	21184	1.98	4.0E-55	7865713	NT	Homo sapiens predicted catalytic protein (CS3786), mRNA
					7865713	NT	Homo sapiens predicted catalytic protein (CS3786), mRNA
1488	11402		1.28	4.0E-55	BF094141.1	EST_HUMAN	782910.x1 Sources, NSF_F4_QW_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:390043 3' similar to contains L1 IS L1 repeat element
1979	11672	21783	1.83	4.0E-55	4506183	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type 2 (PSMA2), mRNA
1979	11672	21784	1.83	4.0E-55	4506183	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type 2 (PSMA2), mRNA
2059	11600	21624	7.73	4.0E-55	4503314	NT	Homo sapiens diacylglycerol kinase, gamma (GAKO) (DGK) mRNA
2059	11600	21625	7.73	4.0E-55	4503314	NT	Homo sapiens diacylglycerol kinase, gamma (GAKO) (DGK) mRNA
2382	12148	22048	1.26	4.0E-55	4507754	NT	Homo sapiens ubiquitin-conjugating enzyme E2, variant 1 (UBE2V1) mRNA
2545	12419		1.04	4.0E-59	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
3242	13168	22964	1.98	4.0E-55	AI163300.2	NT	Homo sapiens chromosome 21 segment H821C100
6857	18736		6.44	4.0E-55	AI163210.2	NT	Homo sapiens chromosome 21 segment H821C010
8859	18429		4.48	4.0E-55	W28165.1	EST_HUMAN	4345 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
9200	18883		2.38	4.0E-55	BF303941.1	EST_HUMAN	90T188676P2 NHF_MGC_17 Homo sapiens cDNA clone IMAGE:4120388 5'
9138	18894		2.76	3.0E-55	BE178518.1	EST_HUMAN	PH1-H10603-090300-001-g08 HT0603 Homo sapiens cDNA
9868	19396		1.95	3.0E-55	AL153284.2	NT	Homo sapiens chromosome 21 segment H821C094
373	10327	20100	2.3	2.0E-55	X67147.1	NT	Human endogenous retroviral DNA (4-1), complete retroiral segment
539	10480		0.98	2.0E-55	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroiral segment
633	10570	20383	3.08	2.0E-55	4507259	NT	Homo sapiens syntaxin-binding protein 1 (STXB1) mRNA, and translated products

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2626	12656	22656	0.79	2.0E-55	4007796	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A) mRNA
4695	14551	24542	2.97	2.0E-55	BE16936.1	EST_HUMAN	CM1-HYT08/RE-150900-357/203 HT0876 Homo sapiens cDNA
7394	17160	28448	4.3	2.0E-55	A002636.1	EST_HUMAN	enr0604.s1 Stralingeria schizo brain S11 Homo sapiens cDNA clone IMAGE:1684185.3 similar to contains THR32 THR repetitive element;
8319	18195	28448	2.2	2.0E-55	AU19344.1	EST_HUMAN	AU119344 HEMBA1 Homo sapiens cDNA clone HEMBA1055933.5
91	10076	19891	1.6	1.0E-55	4500660	NT	Homo sapiens mannose-6-phosphate receptor (cation dependent) (M6PR) mRNA
182	10164	19930	11.9	1.0E-55	U09823.1	NT	Oryctolagus cuniculus New Zealand white elongation factor 1 alpha (Rabefla2) mRNA, complete cds
1132	11045	20988	3.55	1.0E-55	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
1907	11992	21980	0.95	1.0E-55	BE277891.1	EST_HUMAN	801120116F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2867027.5
1907	11992	21981	0.85	1.0E-55	BE277891.1	EST_HUMAN	801120116F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2867027.5
2271	12161	23271	2.3	1.0E-55	5869174	NT	Homo sapiens SIVA3 (SMA3) mRNA
2280	12651	23271	1.63	1.0E-55	A000920.1	NT	Homo sapiens heps-specific factor Transcript Y1 (TTY1) mRNA, partial cds
2470	12545	22238	33.18	1.0E-55	X13111.1	NT	Homo mRNA for HL4-11E, a MHC class I molecule (major histocompatibility complex)
2507	12581	22271	4.71	1.0E-55	AB007852.2	NT	Homo sapiens mRNA for KIAA0496 protein, partial cds
2607	12581	22272	4.71	1.0E-55	AB007852.2	NT	Homo sapiens mRNA for KIAA0496 protein, partial cds
2658	12439	22331	1.35	1.0E-55	L54057.1	NT	Homo sapiens CLP mRNA, partial cds
3353	13282	23062	1.16	1.0E-55	W2189.1	EST_HUMAN	4323 Human retina cDNA randomly primed, sublibrary Homo sapiens cDNA
3607	13517	23062	3.47	1.0E-55	AL163210.2	NT	Homo sapiens chromosome 21 segment H321C087
4197	14607	23578	1.04	1.0E-55	AL163210.2	NT	Homo sapiens chromosome 21 segment H321C010
4721	14607	24392	0.98	1.0E-55	AB1937103.1	NT	Homo sapiens DSCR35 mRNA, complete cds
4721	14607	24393	0.98	1.0E-55	AB037103.1	NT	Homo sapiens DSCR35 mRNA, complete cds
5081	14697	24727	1.19	1.0E-55	8623125	NT	Homo sapiens hypothetical protein FL20126 (FL20126), mRNA
5784	15700	26809	5.76	1.0E-55	11433046	NT	Homo sapiens head domain and RLD 2 (HERC2), mRNA
5784	15700	26910	5.76	1.0E-55	11433046	NT	Homo sapiens head domain and RLD 2 (HERC2), mRNA
6294	16163	29463	4.74	1.0E-55	AL163210.2	NT	Homo sapiens chromosome 21 segment H321C010
8284	18163	29408	4.74	1.0E-55	AL163210.2	NT	Homo sapiens chromosome 21 segment H321C010
8745	17894	28138	2.98	1.0E-55	U09501.2	NT	Human infant brain unknown product mRNA, complete cds
8650	18671	28950	2.04	1.0E-55	10507821	NT	Homo sapiens DNA-binding protein (LOC559242), complete cds
6358	15221	23583	1.81	9.0E-59	BE376074.1	EST_HUMAN	Y03203.1 Score adult brain N265B95Y Homo sapiens cDNA clone IMAGE:3609592.5
2703	12657	22457	5.18	7.0E-59	AU19934.1	EST_HUMAN	Y03203.1 Score adult brain N265B95Y Homo sapiens cDNA clone IMAGE:179044.5 similar to contains THR repetitive element;
5504	15593	23539	1.84	7.0E-59	AW351213.1	EST_HUMAN	RC1-CT0252-231059-013-507 CT0252 Homo sapiens cDNA

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6604	16363	26536	1.84	7.0E-56	AW361213.1	EST_HUMAN	RC1-CT0252-231069-013-b07 CT0252 Homo sapiens cDNA
1666	11668	21434	2.26	5.0E-56	AW597112.1	EST_HUMAN	RC3-BN0053-170200-011-b01 BN0053 Homo sapiens cDNA
7940	17790		1.31	5.0E-56	W218183.1	EST_HUMAN	4365 Human retina cDNA randomly primed auxiliary Homo sapiens cDNA
5375	19701	24902	2.68	5.0E-56	H55099.1	EST_HUMAN	CHR220038 Chromosome 22 exon Homo sapiens cDNA clone C22_55 5'
25	10012	19805	6.15	4.0E-56	AF141349.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
2076	12441	18806	6.15	4.0E-56	AF141349.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
2076	12441	22431	4.11	4.0E-56	4507728	NT	Homo sapiens tubulin, beta polypeptide (TUBB) mRNA
2076	12441	22432	4.11	4.0E-56	4507728	NT	Homo sapiens tubulin, beta polypeptide (TUBB) mRNA
2781	10457	20268	3.05	4.0E-56	AF043328.1	NT	Homo sapiens X-linked aniridia ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
5768	15694	25602	6.28	4.0E-56	AF217508.1	NT	Homo sapiens uncharacterized bone marrow protein BM031 mRNA, complete cds
5768	15694	28603	6.28	4.0E-56	AF217508.1	NT	Homo sapiens uncharacterized bone marrow protein BM031 mRNA, complete cds
7599	17849	28600	1.23	4.0E-56	AF043349.1	NT	Homo sapiens lymphocyte-specific protein 1 (LSP1) gene, LSP1-7 allele, partial cds
8295	18174	28417	8.75	4.0E-56	AF489098.1	EST_HUMAN	hw5512x1 NCL CGAP Bn023 Homo sapiens cDNA clone IMAGE:2163046 3'
8295	18174	28418	8.75	4.0E-56	AF489098.1	EST_HUMAN	hw5512x1 NCL CGAP Bn023 Homo sapiens cDNA clone IMAGE:2163046 3'
1316	11225	21081	9.85	3.0E-56	8924023	NT	Homo sapiens bryostatin protein PRO1304 (PRO1304), mRNA
2103	11922	21852	2.7	3.0E-56	6912607	NT	Homo sapiens progesterone (C21, TC21), cDNA
3086	13013	22804	1.58	3.0E-56	AA325826.1	EST_HUMAN	EST26850 Cerebellum II Homo sapiens cDNA, 5' and 3'
3086	13013	22805	1.58	3.0E-56	AA325826.1	EST_HUMAN	EST26850 Cerebellum II Homo sapiens cDNA, 5' and 3'
3701	13674		1.39	3.0E-56	AF055068.1	NT	Homo sapiens MFC class 1, 1p31
4327	14224	24006	4.05	3.0E-56	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C088
4470	14364	24154	2.14	3.0E-56	5932389	NT	Homo sapiens superfamily viral-like activity 2 (S_cerevisiae homolog) like (SKIVL2), mRNA
5468	15405	25467	1.57	3.0E-56	4759163	NT	Homo sapiens sparcetactonectin, ovov and kazal-like domains proteoglycan (testican) (SPOCK) mRNA
5468	15405	25468	1.57	3.0E-56	4759163	NT	Homo sapiens sparcetactonectin, ovov and kazal-like domains proteoglycan (testican) (SPOCK) mRNA
6106	16003	26141	6.34	3.0E-56	11421724	NT	Homo sapiens glycocalyx-associated membrane protein 2 (LAMP2), mRNA
7117	16984	27185	5.74	3.0E-56	11418704	NT	Homo sapiens bone nitrilotriacetic protein 2 (BNP5), mRNA
7387	17837	28678	1.52	3.0E-56	11434598	NT	Homo sapiens KIA0317 gene product (KIA0317), mRNA
8124	18012	28259	10.72	3.0E-56	AB042566.1	NT	Homo sapiens KIA0317, similar to rat myomesin, complete cds
8632	18467	28711	3.89	3.0E-56	5902013	NT	Homo sapiens nuclear pore complex interacting protein (NPIP), mRNA
8632	18467	28712	3.89	3.0E-56	5902013	NT	Homo sapiens nuclear pore complex interacting protein (NPIP), mRNA
9240	18955	29315	2.3	3.0E-56	11434978	NT	Homo sapiens caveolin 3 (CAV3), mRNA
9240	18955	29316	2.3	3.0E-56	11434978	NT	Homo sapiens caveolin 3 (CAV3), mRNA

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
613	10455		2.84	2.0E-50	AA196818.1	EST_HUMAN	2952506.11 Statalagene neuroepithelium (9937231) Homo sapiens cDNA clone IMAGE:546203 3'
716	12675	20476	1.19	2.0E-50	BE094386.1	EST_HUMAN	RC4-BT0310-110300-015-110 BT0310 Homo sapiens cDNA
716	12675	20476	1.19	2.0E-50	BE094386.1	EST_HUMAN	RC4-BT0310-110300-015-110 BT0310 Homo sapiens cDNA
2334	12215	22113	1.02	2.0E-50	M203951.1	NT	Human GMP phosphodiesterase alpha subunit (GSPR-A) mRNA, complete cds
2334	12215	22114	1.02	2.0E-50	M203951.1	NT	Human GMP phosphodiesterase alpha subunit (GSPR-A) mRNA, complete cds
2959	12885	22884	0.93	2.0E-50	AB027835.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
3459	13405	23210	1.08	2.0E-50	AF703184.1	EST_HUMAN	AV703184 ADB Homo sapiens cDNA clone ADBCFG10 5'
964	10687		1.44	1.0E-50	AF100930.1	NT	Muscle fasciolaris protein tyrosine phosphatase (PRL-1) mRNA, complete cds
3622	13396	23321	1.70	1.0E-50	AW186833.1	EST_HUMAN	1023511.1 x1 NCL CGAP_G05 Homo sapiens cDNA clone IMAGE:2045452 3'
3622	13396	23322	1.70	1.0E-50	AW186833.1	EST_HUMAN	1023511.1 x1 NCL CGAP_G05 Homo sapiens cDNA clone IMAGE:2045452 3'
4603	14338	24065	1.32	1.0E-50	AB001022.1	EST_HUMAN	RC2-BT0168-220999-001-E02 GT0163 Homo sapiens cDNA
7790	17630	27863	1.86	1.0E-50	AW45987.1	EST_HUMAN	QV0-OT0038-070300-152-043 OT0033 Homo sapiens cDNA
609	10545		1.97	9.0E-57	AW186833.1	EST_HUMAN	Homo sapiens EPHA4 (EPHA4) mRNA
4109	14509	23785	1.17	9.0E-57	4755279	NT	Homo sapiens hypodermal protein FLJ20371 (FLJ20371) mRNA
4109	14509	23787	1.17	9.0E-57	4755279	NT	Homo sapiens hypodermal protein FLJ20371 (FLJ20371) mRNA
131	9969	19700	1.55	8.0E-57	6023349	NT	QV4-5T0234-18109-037-R05-3T0234 Homo sapiens cDNA
284	10258	20679	2.91	8.0E-57	AW167405.1	EST_HUMAN	Y64510.1 x1 NCL CGAP_Em43 Homo sapiens cDNA clone IMAGE:2760251 3' similar to gh-L05875
895	10792	20542	5.76	8.0E-57	AW126499.1	EST_HUMAN	NTF5P80N-GAMMA RECEPTOR BETA CHAIN PRECURSOR (HUMAN),
1174	11673	21561	1.93	8.0E-57	AA406109.1	EST_HUMAN	2515112.1 Soares_Tsukaguchi NIT Homo sapiens cDNA clone IMAGE:397151 5'
3333	13255	23060	1.02	8.0E-57	4755279	NT	Homo sapiens EPHA4 (EPHA4) mRNA
3335	13255	23061	1.02	8.0E-57	4755279	NT	Homo sapiens EPHA4 (EPHA4) mRNA
5107	14675	24750	0.99	8.0E-57	AA871001.1	EST_HUMAN	g97062.51 Soares_VHL_T_GBC-ST Homo sapiens cDNA clone IMAGE:166189 3'
5207	19524	25054	0.96	8.0E-57	11418185	NT	Homo sapiens isozyme 2, mitochondrial (ACO2) mRNA
5888	15794	26915	11.76	8.0E-57	AB023177.1	NT	Homo sapiens mRNA for KIAA0900 protein, partial cds
5888	15794	26916	11.76	8.0E-57	AB023177.1	NT	Homo sapiens mRNA for KIAA0900 protein, partial cds
6557	16415	26584	67.76	8.0E-57	AB003044.1	NT	Homo sapiens mRNA for KIAA0837 protein, partial cds
6557	16415	26586	67.76	8.0E-57	AB003044.1	NT	Homo sapiens mRNA for KIAA0837 protein, partial cds
8771	19999	19790	3.32	8.0E-57	6923349	NT	Homo sapiens hypodermal protein FLJ20371 (FLJ20371) mRNA
9498	19097		1.27	8.0E-57	7019528	NT	Homo sapiens monocarboxylate transporter 3 (SLC16A3), mRNA
9607	19188	26251	2.02	8.0E-57	11546732	NT	Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA
9622	19188	26251	1.99	8.0E-57	11546732	NT	Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA
2592	12492	22353	2.02	7.0E-57	7057602	NT	Homo sapiens smg GDS-ASSOCIATED PROTEIN (SNAP), mRNA
2592	12492	22354	2.02	7.0E-57	7057602	NT	Homo sapiens smg GDS-ASSOCIATED PROTEIN (SNAP), mRNA

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Probe SEQ ID NO.	Even SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Disease Source	Top Hit Descriptor
3312	1318	22937	0.92	7.0E-57	7242168	NT	Homo sapiens N1E7 (N1E7), mRNA
3312	1318	22938	0.92	7.0E-57	7242168	NT	Homo sapiens N1E7 (N1E7), mRNA
3333	1317	22936	0.46	7.0E-57	0605979	NT	Homo sapiens Dnaip1b2, isoform 8 (KLFS8), mRNA
3501	1313	23300	2.17	7.0E-57	AF0128272.1	NT	Homo sapiens Dnaip1b2, isoform 4, kinase 230 (PK4230) mRNA, complete cds
3501	1313	23301	2.17	7.0E-57	AF0128272.1	NT	Homo sapiens Dnaip1b2, isoform 4, kinase 230 (PK4230) mRNA, complete cds
9384	1355	23591	2.98	7.0E-57	AJ271193.1	NT	Homo sapiens Xp pseudoclassical region, segment 12
3984	1308	23393	1.23	4.0E-57	AB026888.1	NT	Homo sapiens cDNA, DLEC1 to ORC1L4 gene region, section 1/2 (DLEC1, ORC1L3, ORC1L4 genes, complete cds)
4935	1473	24381	0.90	4.0E-57	BE76349.1	EST_HUMAN	901471228P1 NH_1002_57 Homo sapiens cDNA clone IMAGE:387419.5
787	10718	20558	0.78	3.0E-57	4907790	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein), Argentinian syndrome (UBC3A), mRNA
1306	11215	21151	11.84	3.0E-57	AA230297.1	EST_HUMAN	nc13807.1 NC1_OGAP_P11 Homo sapiens cDNA clone IMAGE:1008307 similar to SW-RS10_HUMAN
2842	12222	22118	2.83	3.0E-57	AA348335.1	EST_HUMAN	FA6783_405 HIBOSOMAL PROTEIN S10 : 1
2842	12222	22118	2.83	3.0E-57	AA348335.1	EST_HUMAN	EST164770 HIBOSOMAL Homo sapiens cDNA, 5' end
2670	12935	22425	1.62	3.0E-57	BE766622.1	EST_HUMAN	783810.1 NC1_OGAP_GLI1 Homo sapiens cDNA clone IMAGE:329644.3 similar to WP:Y47H6C.2 CE20003 :
2670	12935	22428	1.62	3.0E-57	BE766622.1	EST_HUMAN	783810.1 NC1_OGAP_GLI1 Homo sapiens cDNA clone IMAGE:329644.3 similar to WP:Y47H6C.2 CE20003 :
3514	13304	23230	1.15	3.0E-57	AF523708.1	NT	Homo sapiens cell line tsA201a cHc24a Ion current inducer protein (ICh) gene, complete cds
9038	13353		115.04	3.0E-57	AW183364.1	EST_HUMAN	RC3_C10254-1103600 c270 c270 CT0254 Homo sapiens cDNA
5723	12530	25733	3.34	3.0E-57	BE769537.1	EST_HUMAN	90158968P1 NH_1002_7 Homo sapiens cDNA clone IMAGE:3944302.5
6738	16615	22605	3.86	3.0E-57	BE769537.1	EST_HUMAN	4206 Homo telina cDNA randomly primed sublibrary Homo sapiens cDNA
6751	16630	26917	1.56	3.0E-57	BE769537.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ11656 (FLJ11656), mRNA
6751	16630	26918	1.56	3.0E-57	BE769537.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ11656 (FLJ11656), mRNA
7142	17017	27412	4.95	3.0E-57	AL117659.1	EST_HUMAN	AL117659 HEMX1 Homo sapiens cDNA clone HEMX1A101910.5
8279	18169	28240	20.31	3.0E-57	AW23871.1	EST_HUMAN	2320478 Splice NH_1002_7 Homo sapiens cDNA clone IMAGE:2820473.5
5247	17121	24907	2.12	3.0E-57	AW178575.1	EST_HUMAN	cd4541.11 Scores, fetal_lung_NHL-1B.W Homo sapiens cDNA
9608	18520		5.15	3.0E-57	AW178575.1	EST_HUMAN	ROD110112-090569-001-C06 HT0112 Homo sapiens cDNA
2066	12963	22453	1.16	2.0E-57	AAB45419.1	EST_HUMAN	ad02802.5t Scores, perilymphoid_tumor_NB-FA Homo sapiens cDNA clone IMAGE:30549.5
3352	13309		2.51	2.0E-57	AL162304.2	NT	contains AU repetitive element/contains element MER22 repetitive element :
3504	13421	23223	0.84	2.0E-57	RR07702.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C004
3504	13421	23224	0.84	2.0E-57	RR07702.1	EST_HUMAN	ye08401.1t Scores, fetal_liver_spleen_TNFS Homo sapiens cDNA clone IMAGE:128506.5
4403	14303	24066	0.86	2.0E-57	AL162383.2	NT	ye08401.1t Scores, fetal_liver_spleen_TNFS Homo sapiens cDNA clone IMAGE:128506.5
4409	14303	24066	0.86	2.0E-57	AL162383.2	NT	Homo sapiens chromosome 21 segment HS21C083

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Probe SEQ ID NO:	Exon ID NO:	ORF SEQ ID NO:	Expression Signal	Mean Similar EST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5478	15398		1.43	2.0E-57	AA016131.1	EST_HUMAN	z331r51r51 Scores refina N23-CHR Homo sapiens cDNA clone IMAGE:300584 5' similar to contains L1,13 L1 repetitive element
5676	15885		28.14	2.0E-57	BF115266.1	EST_HUMAN	7h8004.x1 NCL CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3370868 3' similar to contains TAR.1t MER22 repetitive element
7695	17515	27084	1.29	2.0E-57	AF045452.1	NT	Homo sapiens cell-line K51 transcriptional regulatory protein p54 mRNA, complete cds
7695	17515	27742	1.71	2.0E-57	AF057722.1	NT	Homo sapiens 17-beta-hydroxysteroid dehydrogenase IV (HSD17B4) gene, exons 3 and 4
8592	18460	28729	2.22	2.0E-57	11424084	NT	Homo sapiens hypothetical protein FLJ20041 (FLJ20041), mRNA
8592	18460	28730	2.22	2.0E-57	11424084	NT	Homo sapiens hypothetical protein FLJ20041 (FLJ20041), mRNA
2184	12271	21073	1.12	1.0E-57	AW533203.1	EST_HUMAN	UHF-BNO-akt-p-97-0JUI1 NH_MGC_50 Homo sapiens cDNA clone IMAGE:3076848 5'
7045	18822		2.08	1.0E-57	BE043081.1	EST_HUMAN	HYPOPHYSICAL 9.3 KD PROTEIN
9401	19055		3.47	1.0E-57	AW470791.1	EST_HUMAN	h83300.x1 NCL CGAP_K5412 Homo sapiens cDNA clone IMAGE:2875498 3' similar to contains THR b3 THR repetitive element
9563	19223	23238	1.43	9.0E-58	BE395061.1	EST_HUMAN	UHF-BNO-akt-p-97-0JUI1 NH_MGC_44 Homo sapiens cDNA clone IMAGE:3831000 5'
574	10572		1.41	8.0E-58	BE688716.1	EST_HUMAN	601339458F1 NH_MGC_65 Homo sapiens cDNA clone IMAGE:3850211 5'
638	10575	20389	2.02	8.0E-58	AT798376.1	EST_HUMAN	k34907.x1 NCL CGAP_Ov28 Homo sapiens cDNA clone IMAGE:2220181 3' similar to TRC016475 O16475 UNNAMED HERVH PROTEIN
638	10575	20390	2.02	8.0E-58	AT798376.1	EST_HUMAN	k34907.x1 NCL CGAP_Ov28 Homo sapiens cDNA clone IMAGE:2220181 3' similar to TRC016475 O16475 UNNAMED HERVH PROTEIN
1813	11710	21580	2.23	8.0E-58	11434621	NT	Homo sapiens putative protein Ovarian/parietal (POM12), mRNA
1813	11710	21580	2.23	8.0E-58	11434621	NT	Homo sapiens putative protein Ovarian/parietal (POM12), mRNA
2845	12872		2.83	8.0E-58	17705132	NT	Homo sapiens DRHG protein (LOC51324), mRNA
8231	18112		5.61	7.0E-58	5174542	NT	Homo sapiens MADS box transcription enhancer factor 2, polypeptide B (myocyte enhancer factor 2B) (MEF2B), mRNA
8300	18179	28733	3.25	7.0E-58	AW804109.1	EST_HUMAN	UHF-BNO-akt-p-97-0JUI1 NH_MGC_50 Homo sapiens cDNA clone IMAGE:3076887 5'
8300	18179	28736	3.25	7.0E-58	AW804109.1	EST_HUMAN	UHF-BNO-akt-p-97-0JUI1 NH_MGC_50 Homo sapiens cDNA clone IMAGE:3076887 5'
2207	12894	21087	2.9	6.0E-58	BE395061.1	EST_HUMAN	UHF-BNO-akt-p-97-0JUI1 NH_MGC_44 Homo sapiens cDNA clone IMAGE:3851000 5'
2324	12265	21053	2.86	6.0E-58	AT130089.1	EST_HUMAN	AT130089 NT2933 Homo sapiens cDNA clone NT293301283 5'
2871	12769	22592	1.19	6.0E-58	BE242190.1	EST_HUMAN	TOAAPIE1219 Putative acute myelogenous leukemia cell (FAB M1) Bcr/tau-HGSC project=ICAA Homo sapiens cDNA clone TOAAPIE1219
2871	12769	22593	1.19	6.0E-58	BE242190.1	EST_HUMAN	TOAAPIE1219 Putative acute myelogenous leukemia cell (FAB M1) Bcr/tau-HGSC project=ICAA Homo sapiens cDNA clone TOAAPIE1219
7609	17769	28000	1.3	6.0E-58	11434746	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type 2 (PTPN21), mRNA
8492	18709		1.8	6.0E-58	11820291	NT	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
297	10261	20081	2.9	5.0E-58	4507334	NT	Homo sapiens synapomannin 1 (SYN1), mRNA
683	10026	20451	5.97	5.0E-58	BE76384.1	EST_HUMAN	RC4-NT0037-160000-016-005 NT0037 Homo sapiens cDNA
1176	11088	20832	4.47	5.0E-58	AW167948.1	EST_HUMAN	C83-UM0043-240000-127-407 UM0043 Homo sapiens cDNA
1176	11088	20833	4.47	5.0E-58	AW167948.1	EST_HUMAN	C83-UM0043-240000-127-407 UM0043 Homo sapiens cDNA
1177	11088	20832	2.99	5.0E-58	AW167948.1	EST_HUMAN	C83-UM0043-240000-127-407 UM0043 Homo sapiens cDNA
1177	11088	20833	2.99	5.0E-58	AW167948.1	EST_HUMAN	C83-UM0043-240000-127-407 UM0043 Homo sapiens cDNA
2261	12022	23022	3.58	5.0E-58	AA988183.1	EST_HUMAN	096207.s1 NOL CGAP L65 Homo sapiens cDNA clone IMAGE1603908.3
2261	12022	23023	2.21	5.0E-58	AA988183.1	EST_HUMAN	096207.s1 NOL CGAP L65 Homo sapiens cDNA clone IMAGE1603908.3
5485	13078	25764	5.98	5.0E-58	U32072.1	EST_HUMAN	yr51607.r1 Sacchar infant brain N1B Homo sapiens cDNA clone IMAGE52071.5
5745	13078	25764	5.98	5.0E-58	U32072.1	EST_HUMAN	yr51607.r1 Sacchar infant brain N1B Homo sapiens cDNA clone IMAGE52071.5
5894	13600	23024	1.45	5.0E-58	11421330	NT	Homo sapiens spinal protein, Xenopus laevis-like (APXL), mRNA
6547	16527	20721	6.77	5.0E-58	8622893	NT	Homo sapiens histidylated protein FLJ10925 (FL10925), mRNA
7629	17679	21723	1.86	5.0E-58	AL163216.2	NT	Homo sapiens chromosome 21 segment HS27C918
8275	19650		3.20	5.0E-58	1152263	NT	Homo sapiens cat eye syndrome oncogene region, candidate 1 (CEOR1), mRNA
8676	19622		2.49	5.0E-58	11416177	NT	Homo sapiens Rho GTPase activating protein 1 (RANGAP1), mRNA
369	10325	20147	17.97	4.0E-58	4502302	NT	Homo sapiens ATP synthase, H ⁺ transporting, mitochondrial F1 complex, O subunit (atgonyon sensitivity conferring protein) (ATP5O), mRNA
1779	10709	20548	1.56	4.0E-58	4506634	NT	Homo sapiens intercalin 10 receptor, beta (IL10RB), mRNA
1462	11357	21221	1.24	4.0E-58	4503646	NT	Homo sapiens coagulation factor IX (plasma thromboplastin component, Christmas disease, hemophilia B) (F9), mRNA
2831	12405	23297	0.97	4.0E-58	AF265055.1	NT	Homo sapiens ubiquitin-conjugating BR-domain enzyme APOLLON mRNA, complete cds
2980	12461	23251	2.7	4.0E-58	U93257.1	NT	Human beta-primo-sapin (BPM22) gene, exon 3
3283	13204	23004	1.1	4.0E-58	U61470.1	NT	Human mRNA, X4 terminal portion
3680	13594	23390	2.11	4.0E-58	5031600	NT	Homo sapiens EGF-like repeat and disordered-like domains 3 (EDL3), mRNA
8651	16515	26786	7.84	4.0E-58	11424059	NT	Homo sapiens E1B-550-alpha-associated protein 3 (E1BAP3), mRNA
332	10291		1.17	3.0E-58	R17879.1	EST_HUMAN	yr106202.1 Sacchar infant brain N1B Homo sapiens cDNA clone IMAGE31088.5
1367	11273	21123	2.34	3.0E-58	4759881	NT	Homo sapiens peptide YY (PPY), mRNA
3141	13056	22884	2.91	3.0E-58	BF59848.1	EST_HUMAN	602165769F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE4309843.5
3141	13066	22865	2.91	3.0E-58	BF59848.1	EST_HUMAN	602165769F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE4309843.5
6002	15907	26331	1.39	3.0E-58	AV112877.1	EST_HUMAN	AV1712877 DCA Homo sapiens cDNA clone DCA25094.5
925	10950	20698	8.16	2.0E-58	AF08624.1	NT	Homo sapiens epsilon-adenylate synthase 2 (ALAS2) gene, complete cds
1298	11175		12.06	2.0E-58	BE76832.1	EST_HUMAN	db08007.v1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE282373.5 similar to gp-X06891.60S
5298	19441	24960	4.42	2.0E-58	BE507186.1	EST_HUMAN	RIBOSOMAL PROTEIN L5 (HUMAN), gp-X81987 M.musculus mRNA for TAX-responsive element binding protein (MOUSE)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Mean Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5288	19441	25010	4.42	2.0E-58	BE507186.1	EST_HUMAN	0014996951 NF1L_MGC_70 Homo sapiens cDNA clone IMAGE:3001911 5'
5721	15628	25731	1.74	2.0E-58	AI124874.1	EST_HUMAN	am756202.x1 Jdfrin frontal cortex Homo sapiens cDNA clone IMAGE:1630874 3' similar to WP-ZK328.1 CE95068 UBRIQUITIN CONJUGATING ENZYME1, RECOVERIN SUBFAMILY OF EF-HAND CALCIUM BINDING PROTEIN:
6246	16112	26063	2.76	2.0E-58	AF134835.1	NT	Homo sapiens endocytic receptor Endo180 (ENDO180) mRNA, complete cds
6246	16112	26064	2.76	2.0E-58	AF134835.1	NT	Homo sapiens endocytic receptor Endo180 (ENDO180) mRNA, complete cds
8123	18011	28268	10.78	2.0E-58	BF307745.1	EST_HUMAN	001808012F1 NHL_MGC_17 Homo sapiens cDNA clone IMAGE:4131851 5'
8332	18209	28456	2.26	2.0E-58	AW572641.1	EST_HUMAN	hm25060.x1 NCI CGAP Thy1 Homo sapiens cDNA clone IMAGE:3013871 3'
705	10638	20463	0.33	1.0E-58	V05134.1	NT	Human complement component C5 mRNA, 3' end
1052	10090	20911	5.45	1.0E-58	6274549	NT	Homo sapiens NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8 (22kD, B22) (NDU1B9), mRNA
1305	11212	21087	2.17	1.0E-58	AW567182.1	EST_HUMAN	EST1396252 IMAGE sequences, IMAGE3 Homo sapiens cDNA
1305	11212	21088	2.17	1.0E-58	AW567182.1	EST_HUMAN	EST1396252 IMAGE sequences, IMAGE3 Homo sapiens cDNA
1375	11281	21136	1.07	1.0E-58	AJ238093.1	EST_HUMAN	Homo sapiens partial AF-4 gene, exons 2 to 7 and Alu repeat elements
1641	11548	21406	2.02	1.0E-58	BE106132.1	EST_HUMAN	001083011 NCI CGAP GGS Homo sapiens cDNA clone IMAGE:3198835 3'
2771	13283	23527	0.95	1.0E-58	47591493	NT	Homo sapiens steroid and androgen receptor binding transcription factor 2 (SREBF-2) mRNA
3483	13408	23215	0.88	1.0E-58	4758081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
3483	13408	23215	0.88	1.0E-58	4758081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
3650	13573	23360	0.84	1.0E-58	4507628	NT	Homo sapiens translation protein 1 (during initiation to proteins replacement) (TNP1) mRNA
4627	14515	24366	0.85	1.0E-58	V05083.1	NT	Human phenolase converting enzyme (NEC2) gene, exon 4
4855	14775	24553	4.96	1.0E-58	AI141053.1	EST_HUMAN	0043001.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:2358836 3'
7148	17023	27217	6.7	1.0E-58	4505314	EST_HUMAN	Homo sapiens myosin (M-protein) 2 (105kD) (MYO2), mRNA
8955	18760	21921	3.48	1.0E-58	X63392.1	NT	H. sapiens immunoglobulin kappa light chain variable region L14
2162	12069	21971	27.47	8.0E-58	4507378	NT	Homo sapiens TATA box binding protein (TBP) mRNA
6765	16638	26826	1.2	8.0E-58	AW191693.1	EST_HUMAN	001455031F1 NCI CGAP Kd11 Homo sapiens cDNA clone IMAGE:2384171 3'
1771	12680	22807	1.03	6.0E-58	BF03537.1	EST_HUMAN	wh50006.x1 NF1L_MGC_66 Homo sapiens cDNA clone IMAGE:3662086 5'
3085	13015	22807	6.21	5.0E-58	AI007494.1	EST_HUMAN	wf1861.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358836 3'
4550	14451	24237	5.85	5.0E-58	X63497.1	NT	H. sapiens cDNA for ZNF60-like ERV9 long terminal repeat
6173	15130	24580	7.46	5.0E-58	AW162904.1	EST_HUMAN	ad66007.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781228 3' similar to contains element TAR1 repetitive element:
7596	17447	27962	1.71	5.0E-58	AW762899.1	EST_HUMAN	AV762899 Homo sapiens cDNA clone MDS0612 5'
8278	18158	28396	2.8	5.0E-58	11434008	NT	Homo sapiens hypothetical protein (LOC87143), mRNA
776	10706	20546	2.42	4.0E-58	D90006.1	NT	Homo sapiens mRNA for KIAA0184 gene, partial cds
4685	14571	24366	1.2	4.0E-58	4509758	NT	Homo sapiens tyrosine receptor 3 (RYR3) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4685	14671	24369	1.2	4.0E-59	4500759	NT	Homo sapiens tyrosine receptor 2 (RYR2) mRNA
8366	19186		2.16	4.0E-59	AF09720.1	NT	Homo sapiens 17-beta-hydroxysteroid dehydrogenase IV (HSD17B4) gene, promoter region and exon 1
9	9695		5.96	3.0E-59	AW96624.1	EST_HUMAN	EST171582 IMAGE; transcriptase, MAGI Homo sapiens cDNA
21	10191	20002	4.12	3.0E-59	7802247	NT	Homo sapiens KIAA0680 gene product (KIAA0680), mRNA
1682	11184	21455	9.87	3.0E-59	4508900	NT	Homo sapiens plasminogen activator, tissue (PLAT) mRNA
1682	11184	21456	9.87	3.0E-59	4508903	NT	Homo sapiens plasminogen activator, tissue (PLAT) mRNA
2062	11672	21860	7.68	3.0E-59	AB020935.1	NT	Homo sapiens mRNA for KIAA1112 protein, partial cds
2062	11672	21867	7.68	3.0E-59	AB020935.1	NT	Homo sapiens mRNA for KIAA1112 protein, partial cds
3090	13017	22811	3.71	3.0E-59	4502014	NT	Homo sapiens A kinase (PKA) anchor protein 1 (AKAP1), mRNA
3090	13017	22812	3.71	3.0E-59	4502014	NT	Homo sapiens A kinase (PKA) anchor protein 1 (AKAP1), mRNA
3763	13668	23446	1.17	3.0E-59	4508044	NT	Homo sapiens zona pellucida glycoprotein 2 (sperm receptor) (ZP2) mRNA
4683	14669	24368	1.07	3.0E-59	4759232	NT	Homo sapiens T-cell-specific, YC-related protein on Y (XKRY) mRNA
4754	14619	24405	1.95	3.0E-59	7427622	NT	Homo sapiens protein tyrosine phosphatase, receptor type, 1 (PTPR) mRNA
5721	14670	28788	2.03	3.0E-59	8924072	NT	Homo sapiens lymphohelial protein PRO1741 (PRO1741), mRNA
6363	16216	30377	1.92	3.0E-59	5454137	NT	Homo sapiens nuclear receptor co-repressor 1 (NCOB1), mRNA
6626	16569	28087	1.25	3.0E-59	X12565.1	NT	Homo mRNA for the proto-oncogene
8620	16569	28087	1.25	3.0E-59	X12565.1	NT	Homo mRNA for the proto-oncogene
8633	16574	28088	1.64	3.0E-59	11417868	NT	Homo sapiens gamma-glutamyl transferase-like activity 1 (GGTL1), mRNA
9474	19101		3.9	3.0E-59	11417868	NT	Homo sapiens gamma-glutamyl transferase-like activity 1 (GGTL1), mRNA
7555	17066		5.01	2.0E-59	AJ309774.1	EST_HUMAN	EST 186053 Juxal T-cells T-Homo sapiens cDNA 5 and
8003	17853		2.97	2.0E-59	AF305954.1	EST_HUMAN	RCU-NT0056-100700-092-307 NT0058 Homo sapiens cDNA
8305	18069	28341	1.84	2.0E-59	AW470698.1	EST_HUMAN	H07042.1 NH1_MGC_17 Homo sapiens cDNA clone IMAGE:2661654 5'
8305	18069	28342	1.84	2.0E-59	AW470698.1	EST_HUMAN	H07042.1 NH1_MGC_17 Homo sapiens cDNA clone IMAGE:2661654 5'
8235	18863	26359	5.14	2.0E-59	AB31809.1	EST_HUMAN	w83612.x1 NO1_GGAP_K411 Homo sapiens cDNA clone IMAGE:200182 3' similar to TRC06542
9765	19611	24697	2.75	2.0E-59	LT1645.1	NT	Q8542 RTVL-H PROTEIN, contains LTR7.1 LTR7 repetitive element;
157	10131		3.48	1.0E-59	BC29641.1	EST_HUMAN	Homo sapiens alpha-tubulin mRNA, complete cds
						EST_HUMAN	0011707071 NH1_MGC_17 Homo sapiens cDNA
						EST_HUMAN	003611.1 NO1_GGAP_G081 Homo sapiens cDNA clone IMAGE:3031627 5'
						EST_HUMAN	Q19357 MER3 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE. ;
						EST_HUMAN	003611.1 NO1_GGAP_G081 Homo sapiens cDNA clone IMAGE:3031627 5'
						EST_HUMAN	Homo sapiens mRNA for transcription factor
						EST_HUMAN	Homo sapiens zinc finger protein 275 (ZNF275), mRNA
						NT	Homo sapiens mRNA for transcription factor
						NT	Homo sapiens small nuclear ribonucleoprotein D3 polypeptide (180D)(SNRPD3) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top 5) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2125	12013	21911	2.7	8.0E-60	5174656	NT	Homo sapiens differentiation-related gene 1 (nucleo-specific induction protein) (RTF) mRNA
2125	12013	21912	2.7	8.0E-60	5174650	NT	Homo sapiens differentiation-related gene 1 (nucleo-specific induction protein) (RTF) mRNA
5940	15553	25645	1.41	8.0E-60	A802004.1	NT	Homo sapiens mRNA for KIAA1051 protein, partial cds
6544	16524	26718	2.65	8.0E-60	U17933.1	NT	Human mRNA for Integrin alpha-2 subunit
7174	17051	27240	2.26	8.0E-60	11428649	NT	Homo sapiens 5'-antigen, refseq and pncial claud (arrestin) (SAG) mRNA
7451	17260	27465	1.98	8.0E-60	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
8207	18091	28344	5.38	8.0E-60	AL16304.2	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
8207	18091	28345	5.38	8.0E-60	AL16304.2	NT	Homo sapiens chromosome 21 segment HS21C004
737	10569	20504	6.99	7.0E-60	AF555968.1	NT	Homo sapiens chromosome 21 segment HS21C004
738	10569	20504	32.94	7.0E-60	AF555968.1	NT	Homo sapiens UHC class 1 region
768	10727	20567	1.15	7.0E-60	469434	NT	Homo sapiens interleukin 10 receptor, beta (IL10RB) mRNA
2031	11571	21863	1.59	7.0E-60	AF077183.1	NT	Homo sapiens cullin 4A (CUL4A) mRNA, complete cds
4088	13888	23765	2.93	7.0E-60	455548	NT	Homo sapiens ornithine decarboxylase 1 (ODC1) mRNA
7412	17779	27468	3.28	7.0E-60	H68041.1	EST_HUMAN	Y12941.1 Scores full liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:205087 5' similar to contains 1TFS, repetitive element.
8871	16556	23843	1.96	7.0E-60	H68041.1	EST_HUMAN	Y12941.1 Scores full liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:205087 5' similar to contains 1TFS, repetitive element.
8814	16792		7.13	8.0E-60	H42458.1	EST_HUMAN	M78406.1 Scores full liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:201953 5' similar to contains ORF, repetitive element.
78	10052	19878	1.94	5.0E-60	AB070971.1	EST_HUMAN	W52507.X1 Scores NFL T_GSC_31 Homo sapiens cDNA clone IMAGE:2356212 3'
78	10052	19879	1.94	5.0E-60	AB070971.1	EST_HUMAN	W52507.X1 Scores NFL T_GSC_31 Homo sapiens cDNA clone IMAGE:2356212 3'
2188	12075	21979	0.83	4.0E-60	AW503208.1	EST_HUMAN	UHF-BND-akt-g-97-5JUL71 NIH MGCG 50 Homo sapiens cDNA clone IMAGE:3078948 5'
2188	12075	21980	0.83	4.0E-60	AW503208.1	EST_HUMAN	UHF-BND-akt-g-97-5JUL71 NIH MGCG 50 Homo sapiens cDNA clone IMAGE:3078948 5'
2642	12869		1.12	4.0E-60	AA326067.1	EST_HUMAN	EST11488 Unius Homo sapiens cDNA 5' and similar to similar to retrovirus-related pol
1815	11712	21591	1.45	3.0E-60	BE526011.1	EST_HUMAN	001339446P1 NIH MGCG 74 Homo sapiens cDNA clone IMAGE:3900395 5'
1815	11712	21592	1.45	3.0E-60	BE526011.1	EST_HUMAN	001339446P1 NIH MGCG 74 Homo sapiens cDNA clone IMAGE:3900395 5'
1826	11723		2.22	3.0E-60	6031180	EST_HUMAN	Homo sapiens profilin (PH) mRNA
4354	14250	24035	2.08	3.0E-60	AJ271795.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
5463	15383	25433	2.08	3.0E-60	AW630106.1	EST_HUMAN	RC3L1.0023-200109-012-01 LT10023 Homo sapiens cDNA
6153	15111	24875	1.31	3.0E-60	AF762814.1	EST_HUMAN	deOHN1.Y6 NC1 CGAP K68 Homo sapiens cDNA clone IMAGE:1534003 5' similar to SWJUDP_MOUSE
6896	16775	28968	5.4	3.0E-60	5174644	NT	P8264 URDINE PHOSPHORYLASE 1
6896	16775	28969	5.4	3.0E-60	5174644	NT	Homo sapiens proline dehydrogenase (proline oxidase) (PRODH) mRNA

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Probe SEQ ID NO.	Even SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
							cd59409.1 Swiss: NHHURA_S1 Homo sapiens cDNA clone IMAGE:1903397 3' similar to SW FORM MOUSE CD59409 FORNMI; SW FORM MOUSE CD59409 FORNMI; Homo sapiens Jurkat T-cells cytoplasmic (poline esterase) (PREDI) mRNA (010422271) NH_100260 Homo sapiens cDNA clone IMAGE:3930680 5'
28	3015	18910	1.79	2.0E-60	AF002858.1	NT	Homo sapiens salivary carrier (SLC25A18) mRNA, complete cds, nuclear gene for mitochondrial product
1405	11710	21711	2.88	2.0E-60	AF002858.1	NT	H. sapiens 4700A protein kinase related to rat ERK2
1687	11583	21420	1.28	2.0E-60	M24843.1	NT	Human for protein mRNA, 8' end
3839	13760	23543	0.78	2.0E-60	M24843.1	NT	Homo sapiens chromosome 21 unknown mRNA
8510	18516	26841	1.57	2.0E-60	AF021916.1	NT	Homo sapiens pro-alpha 2(I) collagen (COL1A2) gene, complete cds
6063	15703	24681	2.44	2.0E-60	AF021916.1	NT	Homo sapiens corticotropin releasing hormone receptor 2 (CRHR2) mRNA
6063	15703	24681	2.44	2.0E-60	4530344.1	NT	Homo sapiens corticotropin releasing hormone receptor 2 (CRHR2) mRNA
6222	16088	26728	3.22	2.0E-60	AA311159.1	EST_HUMAN	EST181949 Jurkat T-cells V-Homo sapiens cDNA 5' and similar to similar to prothymosin, alpha
6222	16088	26728	3.22	2.0E-60	AA311159.1	EST_HUMAN	EST181949 Jurkat T-cells V-Homo sapiens cDNA 5' and similar to similar to prothymosin, alpha
7145	17022	27218	3.86	2.0E-60	L38003.1	NT	Human pre-3 cell stimulating factor homologue (SPD15) mRNA, complete cds
7732	17582	27808	1.85	2.0E-60	11891695.1	NT	Homo sapiens sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 8A (SEMA6A), mRNA
7732	17582	27807	1.86	2.0E-60	11891695.1	NT	Homo sapiens sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 8A (SEMA6A), mRNA
6506	17293	27807	2.86	2.0E-60	111418192.1	NT	Homo sapiens non-histone chromosome protein 2 (S. cerevisiae) like 1 (NHP2L1), mRNA
9539	19743	26731	1.31	2.0E-60	AF008767.1	NT	Homo sapiens somatostatin receptor subtype 3 (SSTR3) gene, 5' flanking region and partial cds
9539	19743	26731	1.31	2.0E-60	AF008767.1	NT	Homo sapiens somatostatin receptor subtype 3 (SSTR3) gene, 5' flanking region and partial cds
6658	16220	25169	1.47	2.0E-60	AB011389.1	NT	Homo sapiens similar to HSPC022 protein (H. sapiens) (LOC358504), mRNA
9957	19420	25169	1.47	2.0E-60	AB011389.1	NT	Homo sapiens similar to HSPC022 protein (H. sapiens) (LOC358504), mRNA
511	10453	20284	1.86	1.0E-60	BE178586.1	EST_HUMAN	Homo sapiens calcium channel, voltage-dependent, alpha 11 subunit (CACNA11), mRNA
3827	13768	23789	1.12	1.0E-60	AF143389.1	EST_HUMAN	PWG1170005-270200-301-e06 HT0005 Homo sapiens cDNA
4874	14754	24533	1.1	1.0E-60	AF163285.2	NT	AU143389 Y78A1 Homo sapiens cDNA clone IMAGE:1001854 5'
7056	16863		2.9	1.0E-60	AA24041.1	EST_HUMAN	ncf412.1 NCL CGAP_F11 Homo sapiens cDNA clone IMAGE:1001782 similar to contains L1.it L1 repetitive element ;
7101	16878	27770	1.88	1.0E-60	AFV754081.1	EST_HUMAN	AV754081 TP Homo sapiens cDNA clone TFGAED08 5'
1083	10586	20840	1.39	8.0E-61	AF118344.1	EST_HUMAN	AU118344 HEMBA1 Homo sapiens cDNA clone HEMBA1005583 5'
2055	12502	22365	1.39	8.0E-61	AW005478.1	EST_HUMAN	wf5b510.1 NCL CGAP_C03 Homo sapiens cDNA clone IMAGE:2505556 3'
2635	12502	22366	1.39	8.0E-61	AW005478.1	EST_HUMAN	wf5b510.1 NCL CGAP_C03 Homo sapiens cDNA clone IMAGE:2505556 3'
2635	12502	22366	1.39	8.0E-61	AW005478.1	EST_HUMAN	wf5b510.1 NCL CGAP_C03 Homo sapiens cDNA clone IMAGE:2505556 3'
2821	12848		1.74	8.0E-61	X57147.1	NT	Homo sapiens retrovirus p1.E.1 (ERV6)

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
122	10096	19618	0.84	7.0E-61	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
123	10096	19618	0.84	7.0E-61	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
123	10096	19618	0.86	7.0E-61	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
123	10096	19618	0.86	7.0E-61	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
265	10230	20045	2	6.0E-61	BE06810.1	EST_HUMAN	601300938F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635460 5'
794	10723	20964	1.69	6.0E-61	BE06810.1	EST_HUMAN	Homo sapiens NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635460 5'
1299	11006	21090	10.26	6.0E-61	AF116860.1	NT	Homo sapiens PR02014 mRNA, complete cds
1612	11518	21376	0.95	6.0E-61	BE267400.1	EST_HUMAN	601109238F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350145 5'
1626	11532	21382	2.12	6.0E-61	AA06033.1	EST_HUMAN	m96909.1 NCL CGAP_Lar1 Homo sapiens cDNA clone IMAGE:3350145 5'
3266	13189	22387	8.19	6.0E-61	AF190690.1	EST_HUMAN	601109238F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350145 5'
6741	15593	24584	2.92	6.0E-61	G782498.1	NT	Human subcutaneous adipose tissue (abdominal) poly(A ⁺) RNA, 3' UTR
6344	16207	26570	1.93	6.0E-61	AF02408.1	NT	Human subcutaneous adipose tissue (abdominal) poly(A ⁺) RNA, 3' UTR
8482	16351	26571	2.03	6.0E-61	AF02408.1	NT	Human subcutaneous adipose tissue (abdominal) poly(A ⁺) RNA, 3' UTR
8471	10723	20964	1.49	6.0E-61	BE06810.1	EST_HUMAN	601300938F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635460 5'
1655	11568	21421	1.78	6.0E-61	AF068008	NT	Homo sapiens protein phosphatase 1 regulatory subunit 10 (PPP1R10) mRNA
3000	12628	22720	1.92	6.0E-61	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
3141	13039	22835	0.84	6.0E-61	AB020821.1	NT	Homo sapiens mRNA for KIAA0825 protein, partial cds
3161	13086	22930	1.6	5.0E-61	4802169	NT	Homo sapiens amyloid beta (A4) precursor protein (prelase neurin), Alzheimer disease (APP), mRNA
3899	13009		1.88	5.0E-61	AJ29041.1	NT	Homo sapiens 5S1 to 5S28 contig between AML1 and CSRT1 on chromosome 21G22 segment 1/3
8213	16941		2.78	6.0E-61	AF731140.1	EST_HUMAN	AF731140 HT-Homo sapiens cDNA clone HTFARBD1 3'
4119	14019	23197	1.13	3.0E-61	SC36679.1	EST_HUMAN	601300938F1 NIH_MGC_24 Homo sapiens cDNA clone IMAGE:3631220 5'
490	10433	20246	1.5	2.0E-61	8622829	NT	Homo sapiens hypothetical protein FLJ11026 (FLJ11026), mRNA
1164	11104	20950	1.35	2.0E-61	BE168410.1	EST_HUMAN	QY34710513-060405-147-401 HT10513 Homo sapiens cDNA
1194	11104	20951	1.35	2.0E-61	BE168410.1	EST_HUMAN	QY34710513-060405-147-401 HT10513 Homo sapiens cDNA
1642	11546	21407	1.31	2.0E-61	NS0309.1	EST_HUMAN	QY34710513-060405-147-401 HT10513 Homo sapiens cDNA clone IMAGE:246403 3' similar to
2109	11998	21697	1.41	2.0E-61	4758003	NT	g125444.005 RIBOSOMAL PROTEIN L35A (HUMAN);
2604	12472		1.16	2.0E-61	N39397.1	EST_HUMAN	Homo sapiens calnexin (CLGN), mRNA
6611	15717	25946	1.7	2.0E-61	11428166	NT	Homo sapiens ATPase, H ⁺ transporting, lysosomal (vacuolar proton pump) non-catalytic accessory protein
121	17089	23779	1.33	2.0E-61	AF694317.1	EST_HUMAN	1A (1101160) (A17681A), mRNA
7707	17557	27763	1.62	2.0E-61	AF00256.1	EST_HUMAN	UHFH-BND-aid-f12-c-UL1 NH_MGC_30 Homo sapiens cDNA clone IMAGE:307671 5'
7885	17735	27979	3.09	2.0E-61	11421779	NT	Homo sapiens polymerase (RNA) III (DNA directed) (RNAP3) (RNC3), mRNA

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8258	18138		7.14	2.0E-61	11410729	NT	Homo sapiens fibronectin protein L44 (RPL4), mRNA
428	10373		0.85	1.0E-61	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
750	10586	20524	1.32	1.0E-61	54583829	NT	Homo sapiens origin recognition complex, subunit 2 (like (ORC2)), mRNA
1377	11283	21136	1.09	1.0E-61	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
1731	11632		0.97	1.0E-61	U93857.1	NT	Homo polymorphic translocatable repeat in X-linked retinitis pigmentosa (RP3) gene region
1814	11711	21690	4.47	1.0E-61	6005693	NT	Homo sapiens zona pellucida glycoprotein 3A (sparm receptor) (ZP3A), mRNA
2150	12035	21935	1.49	1.0E-61	AV182784.1	EST_HUMAN	XM1806.y1 NC1 CGAP L18 Homo sapiens cDNA clone IMAGE:2863389 5' similar to contains element
2804	12734	22533	1.97	1.0E-61	BE3366363.1	EST_HUMAN	MSR1 repetitive element
3330	13250	23055	0.88	1.0E-61	7692319	EST_HUMAN	801273513P1 NH MGCC 20 Homo sapiens cDNA clone IMAGE:3814867 5'
3571	13565	23372	1.47	1.0E-61	BE174455.1	EST_HUMAN	Homo sapiens KIA0069 gene product (KIA0069), mRNA
4339	14268	24019	0.95	1.0E-61	4759249	NT	QV21T0577:140300-077-508 H10577 Homo sapiens cDNA
4339	14268	24020	0.95	1.0E-61	4759249	NT	Homo sapiens TRAF family member-associated NFkB activator (TANK) mRNA
4751	14558	24423	7.83	1.0E-61	AV126818.1	EST_HUMAN	Homo sapiens TRAF family member-associated NFkB activator (TANK) mRNA
4751	14558	24423	7.83	1.0E-61	AV126818.1	EST_HUMAN	UI-HBWG-4H-L93-U1 of NC1 CGAP Sub8 Homo sapiens cDNA clone IMAGE:2733871 3'
4878	14768	24535	0.95	1.0E-61	AL163310.2	NT	UI-HBWG-4H-L93-U1 of NC1 CGAP Sub8 Homo sapiens cDNA clone IMAGE:2733871 3'
8124	15571	28107	7.19	1.0E-61	M30105.1	NT	Homo sapiens chromosome 21 segment HS21C010
8368	16133	28297	1.4	1.0E-61	8623130	NT	Homo P40 T cell and mast cell growth factor (P40) gene, complete cds
8368	16133	28298	1.4	1.0E-61	8623130	NT	Homo sapiens hypophyseal protein FL20128 (FL20128), mRNA
8728	16505	28500	3.38	1.0E-61	11034640	NT	Homo sapiens hypophyseal protein FL20128 (FL20128), mRNA
							Homo sapiens growth hormone releasing hormone (GHRH), mRNA
							Homo sapiens hemostasis, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D) genes, complete cds
8838	16717	28910	3.89	1.0E-61	AF224686.1	NT	NR0-5N007D-044003-070-501 BN0070 Homo sapiens cDNA
7348	17216	27840	2.79	1.0E-61	AV1999726.1	EST_HUMAN	Homo sapiens KIA00971 protein (KIA00971), mRNA
7703	17573	27840	0.28	1.0E-61	11428892	NT	Homo sapiens actin, alpha 4 (ACTN4), mRNA
8031	17923	28169	1.95	1.0E-61	11428578	NT	Homo sapiens gene for AIF-3, complete cds
9110	19631		1.26	1.0E-61	AB011399.1	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
9149	19620	28002	2.86	1.0E-61	11430469	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
9149	19620	28003	2.86	1.0E-61	11430469	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
9515	19128	28281	1.8	1.0E-61	M20009.1	NT	Human kappa-immunoglobulin germline pseudogene (Chr1) variable region (subgroup V kappa I)
9805	19317	28205	8.26	1.0E-61	11418127	NT	Homo sapiens GTP binding protein 1 (GTF2BP1), mRNA
							cd06111.51 NC1 CGAP, GGB1 Homo sapiens cDNA clone IMAGE:1354726 3' similar to SW-PC1_MLVRK
4451	14346	24138	0.79	8.0E-62	AA830420.1	EST_HUMAN	P31795 POL POL VPROTEN
9933	19417		1.96	8.0E-62	AA788861.1	EST_HUMAN	nc24901.51 NC1 CGAP, GGB1 Homo sapiens cDNA clone IMAGE:1301328 3'
10591	19007	20848	1.27	7.0E-62	AA714334.1	EST_HUMAN	AV714334 DDB Homo sapiens cDNA clone DDBMA35 5'

Table 4

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Single Exon Probes Expressed in Heart

Probe SEQ ID NC:	Exon SEQ ID NC:	ORF SEQ ID NC:	Expression Signal Value	Most Similar (Top Hit) BLAST E	Top HR Accession	Top Hit Database Source	Top Hit Description
4947	14824		2.03	4.0E-62	AJ243213.1	NT	Homo sapiens partial EHTA receptor gene, clones 2 to 5 mRNA
5959	15524	22506	1.66	4.0E-62	4506978	NT	Homo sapiens soluble carrier family 13 (cation-dependent dicarboxylate transporter), member 2 (SLC13A2) mRNA
5964	15709	25922	2.42	4.0E-62	11420564	NT	Homo sapiens diacylglycerol specific phospholipase A ₂ X chromosome (Diacylglycerol lipase related) (USP9X), mRNA
6254	16020	26723	1.88	4.0E-62	11421041	NT	Homo sapiens phosphatidyl prothymosin synthetase 2 (PP2S2), mRNA
6468	16397	28728	2.21	4.0E-62	7657057	NT	Homo sapiens cytochrome b oxidase subunit 2B, subunit 2 (cyt. b2SD) (EF2B2), mRNA
6468	16397	28729	2.21	4.0E-62	7657057	NT	Homo sapiens cytochrome b oxidase subunit 2B, subunit 2 (cyt. b2SD) (EF2B2), mRNA
7134	17011	32204	6.3	4.0E-62	A3303098.1	NT	Homo sapiens NRYK4 for KIAA1725 protein, partial cds
8377	15284	28068	2.43	4.0E-62	A3303098.1	NT	Homo sapiens NRYK4 for KIAA1725 protein, partial cds
8377	15284	28069	2.43	4.0E-62	Z78168.1	NT	H. sapiens flow-sorted chromosome 6 (HinfI) fragment, SCBA16C5
8153	15891	28162	2.43	4.0E-62	Z78168.1	NT	H. sapiens flow-sorted chromosome 6 (HinfI) fragment, SCBA16D3
8350	15978	28201	2.98	4.0E-62	11418060	NT	Homo sapiens putative nuclear protein (HRH1-F2122), mRNA
8743	16303	29201	1.39	4.0E-62	11418162	NT	Homo sapiens non-Hodgkin chromosome protein 2 (S. cerevisiae-like) 1 (NHP2L1), mRNA
8762	16302	28198	4.2	4.0E-62	11418322	NT	Homo sapiens cadherin EGF-LAG seven-pass type I transmembrane protein 2 (CELSR1), mRNA
8762	16302	28199	4.2	4.0E-62	11417862	NT	Homo sapiens cadherin binding protein 1 (KIAA0330), mRNA
8855	16235	28210	1.51	4.0E-62	11417862	NT	Homo sapiens caldesmon binding protein 1 (KIAA0330), mRNA
68	10331	18668	1.12	3.0E-62	4557794	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
3008	12336	22728	0.93	3.0E-62	ASIC00609.1	NT	Homo sapiens neurofilament 2 (bilateral acoustic neuroma) (NF2), mRNA
3008	12336	22729	0.96	3.0E-62	ASIC00609.1	NT	Homo sapiens neurofilament 2 (bilateral acoustic neuroma) (NF2), mRNA
3640	13354	23340	1.92	3.0E-62	X32888.1	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds
6969	16846	27038	4.35	3.0E-62	A632738.1	EST_HUMAN	Homo cyclophilin-related processed pseudogene
1211	12110	20069	1.15	2.0E-62	A16284.2	NT	THR repetitive element
7096	16973	27165	4.8	2.0E-62	BF329911.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C084
7096	16973	27169	4.8	2.0E-62	BF329911.1	EST_HUMAN	RCD-BN0284-300500-031-e05 BN0284 Homo sapiens cDNA
7946	16796		3.84	2.0E-62	A729469.1	NT	Homo sapiens neurofilament, beta A, neuronal (MANBA) gene, and diacylglucyl-conjugating enzyme E2D 3 (UBE2D) genes, complete cds
8936	18714		8.23	2.0E-62	AF230676.1	EST_HUMAN	GVA-E10257-681159-017-e03 B10257 Homo sapiens cDNA
1028	10646	20791	1.84	1.0E-62	AF24864.0	NT	Homo sapiens Intersectin 2 (SHD21B) mRNA, complete cds
1526	11451	21288	6.83	1.0E-62	L78810.1	NT	Homo sapiens ALPIYA P1 carrier protein (ANT-2) gene, complete cds
1758	12611	21528	1.02	1.0E-62	AAG52097.1	EST_HUMAN	#f0art1.17 Soares_NHMPU_S1 Homo sapiens cDNA clone IMAGE:1047464 5' similar to WIP-XG1H12.1 CE03463
2884	12811	22065	1.12	1.0E-62	A033044.1	EST_HUMAN	DKF25596F104.1 nt 556 (anonymous) tln422 Homo sapiens cDNA clone DKF25596F104.5'

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Extension Signal	Most Similar Protein BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
426	14321	24108	1.32	1.0E-02	8923201	NT	Homo sapiens hypothetical protein FLJ20212, mRNA
6236	15102	26251	2.17	1.0E-02	AAT22876.1	EST_HUMAN	z98910.s1 Soares, fetal heart, NHHH19W Homo sapiens cDNA clone IMAGE:409771 3'
6236	15102	26252	2.17	1.0E-02	AAT22876.1	EST_HUMAN	z98910.s1 Soares, fetal heart, NHHH19W Homo sapiens cDNA clone IMAGE:409771 3'
7239	17116	27310	1.53	1.0E-02	7602289	NT	Homo sapiens KIAA0765 gene product (KIA0765), mRNA
7239	17116	27311	1.53	1.0E-02	7602289	NT	Homo sapiens KIAA0765 gene product (KIA0765), mRNA
7262	17139	27331	1.81	1.0E-02	K1633.1	NT	H. sapiens lysosomal acid phosphatase gene (EG 3.1.3.2) Exon 9
7262	17139	27332	1.81	1.0E-02	K1633.1	NT	H. sapiens lysosomal acid phosphatase gene (EG 3.1.3.2) Exon 9
7512	17300	27507	2.81	1.0E-02	AA46570.1	EST_HUMAN	sa33068.s1 NC1 CGAP, GCB1 Homo sapiens cDNA clone IMAGE:81565 3'
9673	18561	28845	2.13	1.0E-02	Z76968.1	NT	H. sapiens low-sorbed chromosome 6 HindIII fragment, SCSpA1D8
9673	18169			1.94	11418322	NT	H. sapiens low-sorbed chromosome 6 HindIII fragment, SCSpA1D8
9613	18322	29206	2.3	1.0E-02	11430490	NT	Homo sapiens low density lipoprotein-related protein 2 (LDLR), mRNA
933	10244	20109	2.14	9.0E-03	AW619405.1	EST_HUMAN	OV4-ST0234-18195-037.665 S10234 Homo sapiens cDNA
2297	12179		1.51	9.0E-03	CH169.1	EST_HUMAN	CL18180 Human decalin cDNA (TF1899) Homo sapiens cDNA clone GEN-558C10 5'
3955	13953	23938	7.42	9.0E-03	AB02234.2	NT	Homo sapiens mRNA for KIA00350 protein, partial cds
3955	13953	23939	7.42	9.0E-03	AB02234.2	NT	Homo sapiens mRNA for KIA00350 protein, partial cds
5210	15098	25003	6.51	9.0E-03	U002248.2	NT	Homo sapiens scapula 2, microchondrial (AC02), mRNA
5254	15274	25104	1.31	9.0E-03	Y19365.1	NT	Homo sapiens mRNA for P16 protein
5252	15121	25281	4.38	9.0E-03	11428965	NT	Homo sapiens nucleosom 880 (NUP83), mRNA
5245	15724	25917	1.37	9.0E-03	11421160	NT	Homo sapiens Rsa association (RAC3/SA-5) contain family 2 (RASSF2), mRNA
2286	12178	22077	1.52	8.0E-03	4557334	NT	Homo sapiens monomine oxidase A (MOA), nuclear gene encoding mitochondrial protein, mRNA
2222	12203	22102	2.17	8.0E-03	031810	NT	Homo sapiens L2-Inducible 1 Cell Kinase (ICK), mRNA
3415	13332	23134	3.81	8.0E-03	AF196546.1	NT	Callitrix jacchus Dnae2 protein (Dnae2) mRNA, complete cds
3415	13332	23135	3.81	8.0E-03	AF196546.1	NT	Callitrix jacchus Dnae2 protein (Dnae2) mRNA, complete cds
4168	14098	23643	3.37	8.0E-03	AL103368.2	NT	Homo sapiens chromosome 21 segment HS21C0368
913	10837		1.78	7.0E-03	AB72137.1	EST_HUMAN	w945917.x1 NC1 CGAP, U22 Homo sapiens cDNA clone IMAGE:246906 3'
5274	15186		40.61	6.0E-03	AA420003.1	EST_HUMAN	hcs3802.1 NC1 CGAP, P11 Homo sapiens cDNA clone IMAGE:748947 similar to gb:Y00361 60S
3279	13206	23001	0.98	4.0E-03	AL163278.2	NT	RIBOSOMAL PROTEIN (HUMAN);
6879	15785	25005	2.86	4.0E-03	AW76372.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C078
5979	15785	25009	2.86	4.0E-03	AW76372.1	EST_HUMAN	OM3-370695-190100-072-408 BT0595 Homo sapiens cDNA
8474	18347	28611		4.0E-03	AW137060.1	EST_HUMAN	UHH-B1-abq-q-02-U1.s1 NC1 CGAP, Su33 Homo sapiens cDNA clone IMAGE:2712482 3'
8474	18347	28612		4.0E-03	AW137060.1	EST_HUMAN	UHH-B1-abq-q-02-U1.s1 NC1 CGAP, Su33 Homo sapiens cDNA clone IMAGE:2712482 3'
1593	11788	21660	1.97	3.0E-03	AB018260.1	NT	Homo sapiens mRNA for KIAA0717 protein, partial cds

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2763	12615	22806	1.34	3.0E-63	J00310.1	NT	Human Met-RNA, gene 1
2764	12617	20718	8.97	3.0E-63	6069693	NT	Human sapiens 30c Puroc protein 144 (V4-18) (ZNF144), mRNA
5596	16002	25926	27.68	3.0E-63	11242510	NT	Human sapiens 30c Puroc protein 144 (V4-18) (ZNF144), mRNA
7597	17483	27953	1.62	3.0E-63	U52976.1	EST_HUMAN	Human sapiens 30c Puroc protein 144 (V4-18) (ZNF144), mRNA
7597	17484	27954	1.52	3.0E-63	U52976.1	EST_HUMAN	Human sapiens 30c Puroc protein 144 (V4-18) (ZNF144), mRNA
184	10156	19972	1.11	2.0E-63	U07804.1	NT	Human DNA topoisomerase II α , partial cds
191	10163	19960	1.74	2.0E-63	4958228	NT	Human sapiens 30c Puroc protein 144 (V4-18) (ZNF144), mRNA
489	10432		1.39	2.0E-63	4557042	NT	Human sapiens 30c Puroc protein 144 (V4-18) (ZNF144), mRNA
809	10733	20583	5.26	2.0E-63	7957024	NT	Human sapiens 30c Puroc protein 144 (V4-18) (ZNF144), mRNA
1547	11462	21312	2.47	2.0E-63	A0030388.1	NT	Human sapiens 30c Puroc protein 144 (V4-18) (ZNF144), mRNA
1547	11462	21313	2.47	2.0E-63	A0030388.1	NT	Human sapiens 30c Puroc protein 144 (V4-18) (ZNF144), mRNA
3179	13044	22841	1.88	2.0E-63	4902166	NT	Human sapiens 30c Puroc protein 144 (V4-18) (ZNF144), mRNA
3248	13171	22570	1.78	2.0E-63	AF109718.1	NT	Human sapiens 30c Puroc protein 144 (V4-18) (ZNF144), mRNA
3881	13743	23353	1.86	2.0E-63	L38981.1	NT	Human sapiens 30c Puroc protein 144 (V4-18) (ZNF144), mRNA
4760	14846	24534	1.13	2.0E-63	AF11167.2	NT	Human sapiens 30c Puroc protein 144 (V4-18) (ZNF144), mRNA
5597	15902	25972	2.45	2.0E-63	BF373541.1	EST_HUMAN	Human sapiens 30c Puroc protein 144 (V4-18) (ZNF144), mRNA
5597	15902	25978	2.45	2.0E-63	BF373541.1	EST_HUMAN	Human sapiens 30c Puroc protein 144 (V4-18) (ZNF144), mRNA
0025	15929	26961	1.37	2.0E-63	U98049.1	NT	Human sapiens 30c Puroc protein 144 (V4-18) (ZNF144), mRNA
8208	15936	26703	1.41	2.0E-63	9910365	NT	Human sapiens 30c Puroc protein 144 (V4-18) (ZNF144), mRNA
8208	15936	26704	1.41	2.0E-63	9910365	NT	Human sapiens 30c Puroc protein 144 (V4-18) (ZNF144), mRNA
6064	16842	27084	3.8	2.0E-63	AL103210.2	NT	Human sapiens 30c Puroc protein 144 (V4-18) (ZNF144), mRNA
8120	18017	23935	12.54	2.0E-63	N78945.1	EST_HUMAN	Human sapiens 30c Puroc protein 144 (V4-18) (ZNF144), mRNA
8154	18042	23932	3.02	2.0E-63	AF109610.1	NT	Human sapiens 30c Puroc protein 144 (V4-18) (ZNF144), mRNA
8154	18042	23933	3.02	2.0E-63	AF109610.1	NT	Human sapiens 30c Puroc protein 144 (V4-18) (ZNF144), mRNA
9243	18623	25958	10.85	2.0E-63	111418185	NT	Human sapiens 30c Puroc protein 144 (V4-18) (ZNF144), mRNA
9684	19354	25180	1.39	2.0E-63	111418157	NT	Human sapiens 30c Puroc protein 144 (V4-18) (ZNF144), mRNA
4346	14145	23518	2.91	2.0E-63	F08495.1	EST_HUMAN	Human sapiens 30c Puroc protein 144 (V4-18) (ZNF144), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4246	14145	23919	2.91	1.0E-63	F08485.1	EST_HUMAN	HSC2/D111 normalized infant brain cDNA Homo sapiens cDNA clone c-22t11
5526	15443	26509	1.39	1.0E-63	AW82266.1	EST_HUMAN	QY0-5T0215.080100-083-b09 ST0215 Homo sapiens cDNA
6935	16813		2.3	1.0E-63	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
9879	19633		3.02	1.0E-63	AL18207.2	NT	Homo sapiens chromosome 21 segment HS21C007
6591	16471	26661	4.78	9.0E-64	AF193108.1	EST_HUMAN	hm50107.x1 NCI CGAP_K411 Homo sapiens cDNA clone IMAGE:2161526 3'
1030	10948		7.89	8.0E-64	BE8397.66.1	EST_HUMAN	801185523F1 NHL MGC_21 Homo sapiens cDNA clone IMAGE:319038 5'
5733	15641	25747	3.16	8.0E-64	BE8397.66.1	EST_HUMAN	801508938F1 NHL MGC_21 Homo sapiens cDNA clone IMAGE:3070356 5'
9111	18875		2.81	8.0E-64	11418177	NT	Homo sapiens Ram GTPase activating protein 1 (RANGAP1), mRNA
9059	18841		2.89	8.0E-64	T06851.1	EST_HUMAN	y49802.01 StrataGene lung (#637210) Homo sapiens cDNA clone IMAGE:79179 5'
3460	13402		0.99	7.0E-64	BE394321.1	EST_HUMAN	801311459F1 NHL MGC_44 Homo sapiens cDNA clone IMAGE:3333204 5'
4626	14513	24303	2.44	7.0E-64	4507490	NT	Homo sapiens thymal oligonucleotidase 1 (THOPT) mRNA
4625	14513	24304	2.44	7.0E-64	4507490	NT	Homo sapiens thymal oligonucleotidase 1 (THOPT) mRNA
7768	17618	27844	2.13	7.0E-64	Y07848.1	NT	Homo sapiens EWS, grc22, trc22 and bcr22 genes
1892	11594	21483	1.7	6.0E-64	AB051922.1	EST_HUMAN	w65107.x1 NCI CGAP_G03 Homo sapiens cDNA clone IMAGE:2009220 3' similar to gb-M15162 BETA-GLUCURONIDASE PRECURSOR (HUMAN)
4692	11594	21464	1.7	6.0E-64	AB051922.1	EST_HUMAN	w65107.x1 NCI CGAP_G03 Homo sapiens cDNA clone IMAGE:2009220 3' similar to gb-M15162 BETA-GLUCURONIDASE PRECURSOR (HUMAN)
3054	13011	22801	3.7	6.0E-64	AY028445.1	EST_HUMAN	w13903.x1 NCI CGAP_Bnc23 Homo sapiens cDNA clone IMAGE:3529438 3'
3054	13011	22802	3.7	6.0E-64	AY028445.1	EST_HUMAN	w13903.x1 NCI CGAP_Bnc23 Homo sapiens cDNA clone IMAGE:3529438 3'
5454	15375	25433	2.84	6.0E-64	U18333.1	NT	Homo sapiens MOP-1 gene and enhancer region
5454	15375	25434	2.84	6.0E-64	U18333.1	NT	Homo sapiens MOP-1 gene and enhancer region
6494	13384	25444	4.41	6.0E-64	U13975.1	NT	Homo sapiens protein kinase C beta1 type (PKCβ1) mRNA, complete cds
6253	16157	26312	2.88	6.0E-64	11525979	NT	Homo sapiens mesenchymal homeo box 1 (MEOX1), mRNA
6253	16157	26313	2.88	6.0E-64	11525979	NT	Homo sapiens mesenchymal homeo box 1 (MEOX1), mRNA
7376	17246	27451	7.8	6.0E-64	11425958	NT	Homo sapiens acyl-CoA synthetase (LCC59502), mRNA
7472	17332	27558	2.06	6.0E-64	AF247453.1	NT	Homo sapiens progressive ankylosis-like protein (ANK) mRNA, complete cds
7604	17455	27669	2.34	6.0E-64	S76476.1	NT	BHC Human, brain, mRNA, 2715 nt
8151	18039	28257	7.87	6.0E-64	11420187	NT	Homo sapiens stromal antigen 2 (STAG2), mRNA
8151	18039	28258	7.87	6.0E-64	11420187	NT	Homo sapiens stromal antigen 2 (STAG2), mRNA
9262	18667	26321	4.08	6.0E-64	11526108	NT	Homo sapiens interleukin 10 receptor, beta (LIGR8), mRNA
893	10732	20574	2.44	5.0E-64	AF231918.1	NT	Homo sapiens chromosome 21 unknown mRNA
803	10732	20575	2.44	5.0E-64	AF231918.1	NT	Homo sapiens phosphoglucomutase-related protein (PGMURP) gene, complete cds
1402	11307	21167	2.42	5.0E-64	U40833.1	NT	Homo sapiens phosphoglucomutase-related protein (PGMURP) gene, complete cds
1402	11307	21168	2.42	5.0E-64	U40833.1	NT	Homo sapiens phosphoglucomutase-related protein (PGMURP) gene, complete cds

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) JFE BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1883	11965	21457	1.87	5.0E-64	U89358.1	NT	Human (S) hnt protein homolog mRNA, complete cds
2766	11370	21235	2.66	5.0E-64	7662203	NT	Homo sapiens KIAA0618 gene product (KIAA0618), mRNA
2796	11370	21236	2.66	5.0E-64	7662203	NT	Homo sapiens KIAA0618 gene product (KIAA0618), mRNA
3676	13787	23576	5.61	5.0E-64	AF017433.1	NT	Homo sapiens putative transcription factor CR33 (CR33) mRNA, partial cds
8188	18074	28324	3.9	4.0E-64	AW18783.1	EST_HUMAN	RC3-ST0197-12200-015-403 ST0197 Homo sapiens cDNA
8188	18074	28325	3.9	4.0E-64	AW18783.1	EST_HUMAN	RC3-ST0197-12200-015-403 ST0197 Homo sapiens cDNA
2151	12039	21936	3.85	3.0E-64	C18995.1	EST_HUMAN	C18995 Human placenta cDNA (Tgfwara) Homo sapiens cDNA clone GEN569E07.9
3216	13140	22943	0.95	3.0E-64	BE79438.1	EST_HUMAN	6169955F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE3943577.5
3366	13313	23112	1.81	3.0E-64	AV11714.1	EST_HUMAN	AV11714 DCA Homo sapiens cDNA clone DCAAM001.5
3366	13313	23113	1.81	3.0E-64	AV11714.1	EST_HUMAN	AV11714 DCA Homo sapiens cDNA clone DCAAM001.5
5703	15611	25713	1.34	3.0E-64	23273.1	NT	H.sapiens isoform 1 gene for L-type calcium channel, exon 28
5911	18746	25942	3.39	3.0E-64	BF70900.1	EST_HUMAN	RC3-FN0019-28093-011-0511 FN0019 Homo sapiens cDNA
6933	16811	27005	1.81	3.0E-64	AF246933.1	NT	Homo sapiens polylactid protein GH130 (GOLGA2) mRNA, complete cds
6933	16811	27006	1.81	3.0E-64	AF246933.1	NT	Homo sapiens polylactid protein GH130 (GOLGA2) mRNA, complete cds
8846	18824	27018	1.3	3.0E-64	BE206521.1	EST_HUMAN	PROTEIN HOMOLOG 2 (HUMAN);
6946	18824	27017	1.3	3.0E-64	BE206521.1	EST_HUMAN	PROTEIN HOMOLOG 2 (HUMAN);
7422	17289	21487	1.26	3.0E-64	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
7422	17289	21488	1.26	3.0E-64	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
8585	18434	28703	1.76	3.0E-64	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
8585	18434	28704	1.76	3.0E-64	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
6936	18746	25943	4.59	3.0E-64	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
1072	10968	20831	0.94	2.0E-64	AA06940.1	EST_HUMAN	af0608.s1 Scarsa_testa_NHT Homo sapiens cDNA clone IMAGE1031151.3
1376	11282	21137	1.32	2.0E-64	4757701	NT	Homo sapiens eIF4E-like cap-binding protein (eIF4F) mRNA
2476	12354		1.78	2.0E-64	AB07600.1	EST_HUMAN	w087001.x1 NC1_GCAP_Kd011 Homo sapiens cDNA clone IMAGE2462281.3' similar to contains element
2484	12359	22552	3.03	2.0E-64	AL163246.2	NT	L1 repetitive element;
2484	12359	22553	3.03	2.0E-64	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
3101	13027	22823	2.96	2.0E-64	4504068	NT	Homo sapiens glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2) (GOT2)
3719	13631	23416	1.33	2.0E-64	AA1968146.1	EST_HUMAN	nuclear gene encoding mitochondrial protein, mRNA
3719	13631	23417	1.33	2.0E-64	AA1968146.1	EST_HUMAN	EST1370215 IMAGE reassurance, IMAGE Homo sapiens cDNA
5693	15696	25662	2.82	2.0E-64	AU124387.1	EST_HUMAN	EST1370215 IMAGE reassurance, IMAGE Homo sapiens cDNA
							AU124387 NT2RM2 Homo sapiens cDNA clone NT2RM2002113.5

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) E-VALUE	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5783	15689	25769	1.3	2.0E-64	AF113705.1	NT	Homo sapiens angiotensin 4 (ANG4) mRNA, partial cds
5905	15812	25938	4.97	2.0E-64	BF068537.1	EST_HUMAN	60212327471 NIH_MGC 56 Homo sapiens cDNA clone IMAGE4280395 5'
5976	15880	26004	1.31	2.0E-64	AF078387.1	EST_HUMAN	cc220903.x1 Score: 1641 Id:fa. N23HF8. 5w Homo sapiens cDNA clone IMAGE-1679717 3'
6024	15928	26000	3.86	2.0E-64	M77185.1	NT	H. sapiens dopamine receptor D5 pseudogene 1, partial cds
8144	18032	28634	2.95	2.0E-64	BF28114.1	EST_HUMAN	602042832F1 NC1_CGAP_Bm67 Homo sapiens cDNA clone IMAGE-4180559 5'
8405	18282	28534	6.4	2.0E-64	AB92911.1	EST_HUMAN	wa81805.x1 NC1_CGAP_UH1 Homo sapiens cDNA clone IMAGE-2452213 3'
8405	18282	28535	6.4	2.0E-64	AB92911.1	EST_HUMAN	wa81805.x1 NC1_CGAP_UH1 Homo sapiens cDNA clone IMAGE-2452213 3'
9182	18921	25947	1.73	2.0E-64	8567287	NT	Homo sapiens period (Drosophila) homolog 3 (PER3) mRNA
9877	19195		2.68	2.0E-64	AF56162.1	EST_HUMAN	CHR220101 Chromosome 22 even Homo sapiens cDNA clone C22_132 5'
255	10224	20039	1.74	1.0E-64	AF231918.1	NT	Homo sapiens chromosome 21 unknown mRNA
1740	11641	21508	5.88	1.0E-64	AB929416.1	EST_HUMAN	af69031.x1 Schneider fetal brain 00054 Homo sapiens cDNA clone IMAGE-2519138 3' similar to p81.14696. cd81 PROTHYMOSIN ALPHA (HUMAN)(contains element MSRY repetitive element ;
3466	13382	23188	5.01	1.0E-64	AF106770.1	NT	Homo sapiens transcription factor GCM1 enhancer 3, GCM1 protein, GCM protein, Tcd protein, HNF protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds. (Homo sapiens) human channel 4
3550	13452	23248	1.32	1.0E-64	AF728527.1	NT	Homo sapiens TRIM33 mRNA, partial cds
3558	13452	23249	1.32	1.0E-64	AF728527.1	NT	Homo sapiens TRIM33 mRNA, partial cds
9754	18004		1.62	1.0E-64	AL163346.2	NT	Homo sapiens chromosome 21 segment H821C046
2320	12115	22017	0.93	8.0E-65	AB82711.1	NT	Homo sapiens chromosome 21 segment H821C046
2320	12115	22017	0.93	8.0E-65	AB82711.1	NT	H. sapiens DNA for endogenous neuronal like element
8822	18335		15.1	9.0E-65	BF330676.1	EST_HUMAN	CI74410257-381999-017363 B10267 Homo sapiens cDNA
8799	18613	28903	10.83	8.0E-65	A929244.1	EST_HUMAN	AB08807.x1 Schneider fetal brain 00054 Homo sapiens cDNA clone IMAGE-2519005 3' similar to
7241	17891	27593	2.05	7.0E-65	BE081653.1	EST_HUMAN	SV-RL21_HUMAN P46776 60S RIBOSOMAL PROTEIN L21 ;
1040	10058	20801	1.52	6.0E-65	AV721888.1	EST_HUMAN	QV2810535-240405-162-522 B1 0355 Homo sapiens cDNA
1860	11776		8.32	6.0E-65	AA550929.1	EST_HUMAN	AF721898 HTB Homo sapiens cDNA clone HTB22068 5'
							AF06010.x1 NC1_CGAP_P111 Homo sapiens cDNA clone IMAGE-998379 similar to gb1K03002 60S RIBOSOMAL PROTEIN L32 (HUMAN).
7080	19857	27150	2.52	6.0E-65	AW05252.1	EST_HUMAN	xc07309.x1 NC1_CGAP_C621 Homo sapiens cDNA clone IMAGE-2993543 3' similar to TR_Q63306 Q63306
7209	17066	27275	4.25	6.0E-65	AA427878.1	EST_HUMAN	LONG INTERSPERSED REPETITIVE DNA CONTAINING 7 ORFs, contains L132.L1 repetitive element ;
7209	17066	27275	4.25	6.0E-65	AA427878.1	EST_HUMAN	zw55306.x1 Score: 1641 Id:fa. N23HF8. 5w Homo sapiens cDNA clone IMAGE-773747 3'
8247	18127	28575	6.18	6.0E-65	BE067616.1	EST_HUMAN	zw55306.x1 Score: 1641 Id:fa. N23HF8. 5w Homo sapiens cDNA clone IMAGE-773747 3'
8787	18602	28992	4.76	6.0E-65	AL169210.2	NT	601340465F1 NIH_MGC 58 Homo sapiens cDNA clone IMAGE-3682377 5'
							Homo sapiens chromosome 21 segment H821C010

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Probe SEQ ID NO	Exon SEQ ID NO	ORF SEQ ID NO	Expression Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
615	10351	20352	0.91	5.0E-05	AF064904.1	NT	Homo sapiens KEG3 protein mRNA, partial cds
1331	11239	21034	1.62	5.0E-05	7861951	NT	Homo sapiens KIAA0156 gene product (KIAA0156), mRNA
1331	11239	21035	1.62	5.0E-05	7861951	NT	Homo sapiens KIAA0156 gene product (KIAA0156), mRNA
2110	11999	21698	1.02	5.0E-05	AB033768.1	NT	Homo sapiens HPAD-cdky10 mRNA for papillary carcinoma, complete cds
3217	13141	22944	1.91	5.0E-05	4507848	NT	Homo sapiens ubiquitin specific protease 13 (ubiquitinase T-3) (USP13) mRNA
3217	13141	22945	1.91	5.0E-05	4507848	NT	Homo sapiens ubiquitin specific protease 13 (ubiquitinase T-3) (USP13) mRNA
186	10158	19675	1.09	4.0E-05	AL120419.1	EST_HUMAN	DKF45763G108.11 (synonym: hamy2) Homo sapiens cDNA clone DKF45763G108.6
726	10550	20491	1.56	4.0E-05	AI206498.1	EST_HUMAN	gm4801.x1 Soares, placenta, 2NCH-P869W Homo sapiens cDNA clone IMAGE:1891800.3
726	10550	20492	1.56	4.0E-05	AI206498.1	EST_HUMAN	gm4801.x1 Soares, placenta, 2NCH-P869W Homo sapiens cDNA clone IMAGE:1891800.3
1052	10378	20522	1.86	4.0E-05	4620735	NT	Homo sapiens fragile X mental retardation, autosomal homolog 1 (FXR1), mRNA
1070	11375	21240	8.26	4.0E-05	4509338	NT	Homo sapiens ribosomal protein L34 (RPL34) mRNA
2265	12171	22068	1.03	4.0E-05	BE221499.1	EST_HUMAN	h25594X1 NC1 CGAP, Mat15 Homo sapiens cDNA clone IMAGE:3171103.3
2265	12171	22069	1.03	4.0E-05	BE221499.1	EST_HUMAN	h25594X1 NC1 CGAP, Mat15 Homo sapiens cDNA clone IMAGE:3171103.3
5195	15035	24775	0.95	4.0E-05	3055269	NT	Homo sapiens low density lipoprotein receptor related protein-1 (LRP1), mRNA
5195	15035	24776	0.95	4.0E-05	3055269	NT	Homo sapiens low density lipoprotein receptor related protein-1 (LRP1), mRNA
5740	15948	25753	3.93	4.0E-05	AB033933.1	NT	Homo sapiens mRNA for KIAA1267 protein, partial cds
6285	16149	26304	2.28	4.0E-05	11545750	NT	Homo sapiens hypothetical protein FLJ22057 (FLJ22057), mRNA
8020	17920		2.17	4.0E-05	AL277546.2	NT	Homo sapiens WEE1 gene for protein kinase and partial ZNF143 gene for zinc finger transcription factor
9446	18330	28579	1.47	4.0E-05	AF119946.1	NT	Homo sapiens PRO474 mRNA, complete cds
9471	10978	20522	1.74	4.0E-05	4620735	NT	Homo sapiens fragile X mental retardation, autosomal homolog 1 (FXR1), mRNA
9975	19434	25152	1.58	4.0E-05	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
1212	12946		5.37	3.0E-05	U76922.1	NT	H. sapiens 10279 mRNA for zinc finger protein
1760	11679	21657	1.14	3.0E-05	U000982.1	EST_HUMAN	002303.s1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE: 038173.3 similar to contains element MGR1 repetitive element;
3239	13162	22982	1.39	3.0E-05	4504920	NT	Homo sapiens testis, NHT Homo sapiens cDNA clone IMAGE: 038173.3 similar to contains element MGR1 repetitive element;
3690	13574	23361	0.96	3.0E-05	AD00692.1	EST_HUMAN	002303.s1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE: 038173.3 similar to contains element MGR1 repetitive element;
4851	14444	24228	1.41	3.0E-05	6912395	NT	Homo sapiens rab6 GTPase activating protein (GAP and centrin-associated) (GAPCEN), mRNA
7785	17643	27676	1.43	3.0E-05	BE787965.1	EST_HUMAN	001470566F1 NHT, MO6 Homo sapiens cDNA clone IMAGE:3802405.5

Table 4

Probe SEQ. ID NC.	Even SEQ. ID NC.	ORF SEQ ID NC.	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6893	17677	28149	9.00	3.0E-65	AA430096.1	EST - HUMAN	wt5505r.11 Scores: testis, NHT Homo sapiens cDNA clone IMAGE:781042.5
3350	13277	23078	5.27	2.0E-65	BF602994.1	EST - HUMAN	wt159062r.1 NHT, MGC, 83 Homo sapiens cDNA clone IMAGE:426569.5
6698	16069		4.95	2.0E-65	BF53373.1	EST - HUMAN	wt193859r.1 NHT, MGC, 7 Homo sapiens cDNA clone IMAGE:353474.5
6233	16069	26247	23.12	2.0E-65	BF576922.1	EST - HUMAN	wt2734359r.1 NHT, MGC, 81 Homo sapiens cDNA clone IMAGE:628393.5
7133	17010	27202	1.27	2.0E-65	AK024463.1	EST - HUMAN	Homo sapiens mRNA for PU00658 protein, partial cds
7133	17010	27203	1.27	2.0E-65	AK024463.1	NT	Homo sapiens SWISN1 related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 3 (SMARCC3), mRNA
8048	17939	28186	2.85	2.0E-65	11419247	NT	wt15787.55 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end similar to endogenous retrovirus
0109	18874		4.15	2.0E-65	AA307904.1	EST - HUMAN	wt408333r.1 NHT, MGC, 57 Homo sapiens cDNA clone IMAGE:407169.5
9590	18904		2.37	2.0E-65	BF246986.1	EST - HUMAN	wt767638r.1 NHT, MGC, 20 Homo sapiens cDNA clone IMAGE:402801.5
65	10069		1.06	1.0E-65	BF125544.1	EST - HUMAN	Homo sapiens putative Rab5 GDP/GTP exchange factor homologue (RABEX5), mRNA
528	10470	20262	1.32	1.0E-65	7657492.1	EST - HUMAN	Homo sapiens mRNA for KIAA1513 protein, partial cds
1964	11688	21781	0.91	1.0E-65	AB040346.1	NT	wt24400r.1 NCT, CGAP, G08 Homo sapiens cDNA clone IMAGE:3203883.3
3326	13246	23052	0.89	1.0E-65	BE466981.1	EST - HUMAN	Homo sapiens glycican 4 (GPC4) mRNA
9971	13626	23069	2.13	1.0E-65	4594082.1	EST - HUMAN	Homo sapiens glycican 4 (GPC4) mRNA
9971	13626	23067	2.13	1.0E-65	4594082.1	EST - HUMAN	Homo sapiens glycican 4 (GPC4) mRNA
4112	1412	23786	2.37	1.0E-65	AW032940.1	EST - HUMAN	wt80909r.1 NCT, CGAP, Gas4 Homo sapiens cDNA clone IMAGE:2543152.3
4112	1412	23780	2.37	1.0E-65	AW032940.1	EST - HUMAN	wt80909r.1 NCT, CGAP, Gas4 Homo sapiens cDNA clone IMAGE:2543152.3
6802	16981	26710	1.88	1.0E-65	AW20481.1	EST - HUMAN	wt523026r.1402000452r.112 ST0268 Homo sapiens cDNA
6802	16981	26711	1.88	1.0E-65	AW20481.1	EST - HUMAN	wt523026r.1402000452r.112 ST0268 Homo sapiens cDNA
6842	16721	26714	2.38	1.0E-65	AU123456.1	EST - HUMAN	wt141295r.128 THYRO1 Homo sapiens cDNA clone THYRO100356.5
6842	16721	26715	2.38	1.0E-65	AU123456.1	EST - HUMAN	wt141295r.128 THYRO1 Homo sapiens cDNA clone THYRO100356.5
7132	17009	27201	1.76	1.0E-65	BF689707.1	EST - HUMAN	wt2162262r.1 NHT, MGC, 58 Homo sapiens cDNA clone IMAGE:628313.5
7215	17092	27282	1.62	1.0E-65	AW129040.1	EST - HUMAN	AUT029040 NT25972 Homo sapiens cDNA clone NT2P:2004714.5
7215	17092	27283	1.62	1.0E-65	AW129040.1	EST - HUMAN	AUT029040 NT25972 Homo sapiens cDNA clone NT2P:2004714.5
7222	17902	27283	2.83	1.0E-65	11431984r.1	EST - HUMAN	Homo sapiens insulin1.1,4,5-triphosphate receptor, type 1 (TIPR1), mRNA
7222	17902	27283	2.83	1.0E-65	11431984r.1	EST - HUMAN	Homo sapiens insulin1.1,4,5-triphosphate receptor, type 1 (TIPR1), mRNA
7456	17265	27469	6	1.0E-65	AI019716.1	EST - HUMAN	wt55602r.2 Scores: testis, NHT Homo sapiens cDNA clone IMAGE:7733469.3 similar to g5-M29383.2 ZINC FINGER PROTEIN 8 (ZFP818) contains MER19.11 MER19 complete element
7687	17537	27763	1.25	1.0E-65	AI019716.1	EST - HUMAN	wt55602r.2 Scores: testis, NHT Homo sapiens cDNA clone IMAGE:7733469.3 similar to g5-M29383.2 ZINC FINGER PROTEIN 8 (ZFP818) contains MER19.11 MER19 complete element
8042	17933	28181	2.23	1.0E-65	M28187.1	NT	AUT153793 NT2P933 Homo sapiens cDNA clone NT2P:2004016.3
8156	18046	28298	12.99	4.05966E-07		NT	Homo palatilis (factor 4 variation 1 (PF4var1) gene, complete cds
8473	18346	28610	2.18	1.0E-65	BF639707.1	EST - HUMAN	Homo sapiens ribosomal protein L7a (RPL7a) mRNA
8473	18346	28610	2.18	1.0E-65	BF639707.1	EST - HUMAN	Homo sapiens ribosomal protein L7a (RPL7a) mRNA

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8542	18414	28881	2.35	1.0E-66	AB21017.1	EST_HUMAN	187606.x1 NCL_CGAP_G08 Homo sapiens cDNA clone IMAGE:229770 3' similar to gb115832_mst1
9155	18605		2.27	1.0E-65	11418041	NT	PANCREATITIS ASSOCIATED PROTEIN 1 PRECURSOR (HUMAN);
9254	18603	26516	4.95	1.0E-65	11418322	NT	Homo sapiens TNF-inducible protein G31241 (G31241), mRNA
9695	19226		1.44	1.0E-65	11418249	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
65	10051	19864	1.51	9.0E-60	AL10311.1	NT	Homo sapiens sulfotransferase-related protein (SULTX3), mRNA
65	10051	19865	1.51	9.0E-60	AL10311.1	NT	Novel human gene mapping to chromosome 22
1332	11239	21095	2.49	9.0E-60	5031900	NT	Homo sapiens 26S proteasome-associated part1 homolog (POH1) mRNA
1468	11373		4.18	9.0E-60	M87266.1	NT	Homo sapiens 26S proteasome-associated part1 homolog (POH1) mRNA
3826	13738	23529	0.9	9.0E-60	M7293.1	NT	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
3826	13738	23530	0.9	9.0E-60	M7293.1	NT	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
4591	14470	24266	0.88	8.0E-60	AA24304.1	EST_HUMAN	260005.r1 Soares, NHKPL, S1 Homo sapiens cDNA clone IMAGE:767048 5'
8554	18543		1.73	7.0E-60	BE054410.1	EST_HUMAN	RC4187031-141109-011-105 B10311 Homo sapiens cDNA
4286	14168	23844	1.22	6.0E-60	AB24653.1	EST_HUMAN	WS7407.x1 NCL_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2449597 3' similar to WP.F15G9.4A
4286	14168	23845	1.22	6.0E-60	AB24653.1	EST_HUMAN	WS7407.x1 NCL_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2449597 3' similar to WP.F15G9.4A
4286	14168	23846	1.22	6.0E-60	AB24653.1	EST_HUMAN	WS7407.x1 NCL_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2449597 3' similar to WP.F15G9.4A
8490	18372	28535	7.07	6.0E-60	X51811.1	EST_HUMAN	Hsalpha mRNA for ribosomal protein L31
1344	11250	21107	2.25	5.0E-60	95084410.1	EST_HUMAN	RC4187031-141109-011-105 B10311 Homo sapiens cDNA
7357	17226	27424	12.51	5.0E-60	11420557	NT	Homo sapiens thyroid hormone receptor binding protein (AB3), mRNA
773	10703	20542	0.79	4.0E-60	6679919	NT	Mus musculus fragile X mental retardation syndrome 1 homolog (FMR1), mRNA
2236	12720	22022	1.94	4.0E-60	X59211.1	NT	H. sapiens DNA for endogenous retroviral like element
2426	12302		3.06	4.0E-60	AJ25394.1	NT	Homo sapiens gamma DNA upstream of <i>hscap</i> locus
4974	14650		5.15	4.0E-60	9635487	NT	Human endogenous retrovirus, complete genome
5407	15326	28376	3.35	4.0E-60	11428543	NT	Homo sapiens methylase tetrahydrofolate dehydrogenase (NAD+ dependent), methyltetrahydrofolate
5512	15430	28464	1.78	4.0E-60	AW965718.1	EST_HUMAN	cydohydroxase (MTHFD2), mRNA
6055	15106	24889	4.71	4.0E-60	AW965473.1	EST_HUMAN	QVH-DT0059-110050-007-g10 D10059 Homo sapiens cDNA
6232	16098	25246	6.89	4.0E-60	U78108.1	NT	EST377546 IMAGE: ressequencing, MAGI Homo sapiens cDNA
6708	16588	25776	6.38	4.0E-60	11421039	NT	Homo sapiens cAMP-regulated guanine nucleotide exchange factor 1 (GAMP-GEF1) mRNA, complete cds
							Homo sapiens hypothetical protein FLJ20116 (FLJ20116), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Top Hit (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8062	17943	28160	1.90	4.0E-06	BF507483.1	EST_HUMAN	UHH-BW1-arr-a-3-DU-L1 NCAP_SuB7 Homo sapiens cDNA clone IMAGE:3070747 3'
1408	11313	21176	24.92	3.0E-66	4902068	NT	Homo sapiens solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 5 (SLC25A5), nuclear gene encoding mitochondrial protein, mRNA
1408	11313	21176	24.92	3.0E-66	4902068	NT	Homo sapiens solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 5 (SLC25A5), nuclear gene encoding mitochondrial protein, mRNA
1939	11834	21717	0.84	3.0E-60	N65223.1	EST_HUMAN	y27/g12/r1 Soares, multiple, scdarsis, 2NHNSP Homo sapiens cDNA clone IMAGE:294323 5' similar to SW-H2B4_TGCA P35008 HISTONE H2B.1H2B.2. [2] PIR-B86012;
1939	11834	21718	0.84	3.0E-60	N65223.1	EST_HUMAN	y27/g12/r1 Soares, multiple, scdarsis, 2NHNSP Homo sapiens cDNA clone IMAGE:294323 5' similar to SW-H2B4_TGCA P35008 HISTONE H2B.1H2B.2. [2] PIR-B86012;
1939	11834	21719	0.84	3.0E-60	N65223.1	EST_HUMAN	y27/g12/r1 Soares, multiple, scdarsis, 2NHNSP Homo sapiens cDNA clone IMAGE:294323 5' similar to SW-H2B4_TGCA P35008 HISTONE H2B.1H2B.2. [2] PIR-B86012;
2075	12540	22430	5.97	3.0E-60	11141890	NT	Homo sapiens TGF-beta1-induced transcription factor 2 (TGIF2), mRNA
3079	13005	22797	2.41	3.0E-60	7692223	NT	Homo sapiens KIA00246 gene product (KIA00246), mRNA
5528	15446	25611	1.84	3.0E-60	11417948	NT	Homo sapiens NIPS/NAP, C. elegans, homolog 1 (NIPS/NAP1), mRNA
5528	15446	25612	1.84	3.0E-60	11417948	NT	Homo sapiens NIPS/NAP, C. elegans, homolog 1 (NIPS/NAP1), mRNA
8800	16614	26504	8.3	3.0E-60	5453949	NT	Homo sapiens protein phosphatase 2, regulatory subunit B (P50), alpha isoform (PPP2R5A) mRNA
46	10033	19637	1.02	2.0E-60	7057234	NT	Homo sapiens Mitochondrial-related kinase (MINK), mRNA
46	10033	19638	1.02	2.0E-60	7057234	NT	Homo sapiens Mitochondrial-related kinase (MINK), mRNA
410	9683	19774	0.93	2.0E-60	4905524	NT	Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORC5), mRNA, and translated products
410	9683	19775	0.93	2.0E-60	4905524	NT	Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORC5), mRNA, and translated products
1784	11682	21560	2.02	2.0E-60	AI163301.2	NT	Homo sapiens chromosome 21 segment H521C101
2044	12671	23569	0.95	2.0E-60	Y55866.1	NT	H sapiens pseudogenes for the low affinity IL-8 receptor
3075	13822	23887	0.95	2.0E-60	AF100389.1	NT	Homo sapiens sodium/calcium exchanger isoform NaCx8 (NCX1) mRNA, complete cds
4559	14446	24293	12.86	2.0E-60	AI153267.2	NT	Homo sapiens HLA-B gene for human leukocyte antigen B
4559	14446	24294	12.86	2.0E-60	AI153267.2	NT	Homo sapiens HLA-B gene for human leukocyte antigen B
7138	17171	27206	2.16	2.0E-60	N64640.1	EST_HUMAN	y556022.1 Soares, multiple, scdarsis, 2NHNSP Homo sapiens cDNA clone IMAGE:277626 5'
9475	19721	27206	2.22	2.0E-60	1141818	NT	Homo sapiens C2- and S-phase expressed 1 (C13E1), mRNA
2864	12762	22686	1.38	1.0E-60	AV177817.1	EST_HUMAN	AV177817 DCR Homo sapiens cDNA clone DGBAD007 5'
2864	12762	22686	1.38	1.0E-60	AV177817.1	EST_HUMAN	AV177817 DCR Homo sapiens cDNA clone DGBAD007 5'
4288	12762	22686	3.26	1.0E-60	AV177817.1	EST_HUMAN	AV177817 DCR Homo sapiens cDNA clone DGBAD007 5'
4288	12762	22686	3.26	1.0E-60	AV177817.1	EST_HUMAN	AV177817 DCR Homo sapiens cDNA clone DGBAD007 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) HT BLAST E Value	Top HT Accession No.	Top HT Database Source	Top HT Descriptor
5306	16227	26031	5.36	1.0E-66	BF070983.1	EST_HUMAN	R02163594F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4294161 5'
61-43	15901	26126	1.49	1.0E-66	BF329623.1	EST_HUMAN	R05-580169-010900-034-Q06 EN0193 Homo sapiens cDNA
6926	18804	29698	1.37	1.0E-66	AA069883.1	EST_HUMAN	sa0604.41 NCL_OGAP_G0B1 Homo sapiens cDNA clone IMAGE:327262 3'
8312	18189	28438	2.39	1.0E-66	AF111167.2	NT	Homo sapiens Jun dimerization protein gene, partial cds; clone gene, complete cds; and unknown gene
9200	18965		2.09	9.0E-67	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
4929	14711					EST_HUMAN	ES101750 Subcloned Hippocampus, Striatum (cat. #536208) Homo sapiens cDNA clone HHOPN31 similar to L1 repetitive element
376	10390	20184	6.19	7.0E-67	AW162932.1	EST_HUMAN	sa15602.11 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782083 3' similar to gb:U37104
1350	11299	21122	2.63	7.0E-67	AA383416.1	EST_HUMAN	ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
1535	11439	21298	1	7.0E-67	W65947.1	EST_HUMAN	EST168812 Testis Homo sapiens cDNA 5 and similar to similar to C. elegans hypothetical protein, contid
1535	11439	21297	1	7.0E-67	W65947.1	EST_HUMAN	EST168812 Testis Homo sapiens cDNA 5 and similar to similar to C. elegans hypothetical protein, contid
1988	11891	21773	1.06	7.0E-67	7657243	NT	216353
1988	11891	21774	1.06	7.0E-67	7657243	NT	216353
2779	10390	20184	7.07	7.0E-67	AW162932.1	EST_HUMAN	sa15602.11 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782083 3' similar to gb:U37104
5793	18696	28507	2.04	7.0E-67	11428572	NT	ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
5793	18696	28507	2.04	7.0E-67	11428572	NT	Homo sapiens adaptor-related protein complex 2, beta 1 subunit (AP2B1), mRNA
9039	18828	29111	1.96	7.0E-67	11430460	NT	Homo sapiens adaptor-related protein complex 2, beta 1 subunit (AP2B1), mRNA
9039	18828	29112	1.96	7.0E-67	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
9501	19116	25252	3.33	7.0E-67	AB011399.1	NT	Homo sapiens gene for AP-5, complete cds
9686	19571		1.43	7.0E-67	11421527	NT	Homo sapiens calcium channel, voltage-dependent, alpha 2delta subunit 1 (CACNA2D1), mRNA
647	10488	20297	1.32	6.0E-67	X09088.1	NT	H. sapiens mRNA for acyl-CoA carboxylase
778	10798	20547	1.5	6.0E-67	Y17227.1	NT	Homo sapiens mRNA for transmembrane receptor protein
1262	11369	21008	0.93	6.0E-67	Y14320.1	NT	Homo sapiens FM1069 gene, exons 3,4,5,6 & 7
3131	13066	22856	1.24	6.0E-67	Y14320.1	NT	Homo sapiens riboflavin 1 (including riboflavin) (RBI) mRNA
3391	13308	23106	1.2	6.0E-67	4509434	NT	Homo sapiens Synapain III (SYNS) mRNA, and translated products
3391	13308	23107	1.2	6.0E-67	4507332	NT	Homo sapiens Synapain III (SYNS) mRNA, and translated products
4035	13938	23714	1.28	6.0E-67	AL193201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4035	13938	23715	1.28	6.0E-67	AL193201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4607	14495	24283	3.37	6.0E-67	7657020	NT	Homo sapiens DNK-ZP43P211 protein (DNK-ZP43P211), mRNA
4607	14495	24284	3.37	6.0E-67	7657020	NT	Homo sapiens DNK-ZP43P211 protein (DNK-ZP43P211), mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Diffract Source	Top Hit Descriptor
5126	14761		2.1	6.0E-67	490748	NT	Homo sapiens tubulin specific protease 13 (lipoelastase 1-3) (LSP13) mRNA
3164	13109	22913	2.45	5.0E-67	AF009600.1	NT	Homo sapiens T cell receptor beta locus, TCRBV/TS2 to TORBV/TS2 region
8332	18228		2.1	5.0E-67	BE010038.1	EST_HUMAN	PMB-BN0176-100400-001-g04 BN0176 Homo sapiens cDNA
1306	11213	21069	1.83	4.0E-67	R06819.1	EST_HUMAN	yk02411.1 Scores addit brn1 N24-HF8667 Homo sapiens cDNA IMAGE:197253 5'
6883	16762		1.22	4.0E-67	BF37321.1	EST_HUMAN	RC4-H1093-1-150600-026-033 HT0594 Homo sapiens cDNA
8416	18290		2.3	4.0E-67	AA714294.1	EST_HUMAN	nm004071.x1 NCL_OGAP_S51 Homo sapiens cDNA clone IMAGE:123472 3' similar to TR-O10385 OT0385
2792	10553	20395	0.93	3.0E-67	AA333768.1	EST_HUMAN	PRO-POL-DUTPASE POLYPROTEIN;
3407	13324	23125	1.14	3.0E-67	BE064410.1	EST_HUMAN	EST37903 Embryo, 9 week Homo sapiens cDNA 5' end
4566	14484	24270	3.14	3.0E-67	AW659159.1	EST_HUMAN	RC4-BT0311-141195-011-H06 BT0311 Homo sapiens cDNA
6790	16936		1.22	3.0E-67	BF189068.1	EST_HUMAN	MP3-SN0068-040500-008-01 SN0036 Homo sapiens cDNA
5563	18451		18.27	3.0E-67	AA4827874.1	EST_HUMAN	HP105.x1 NCL_OGAP_X411 Homo sapiens cDNA clone IMAGE:3134913 3' similar to SW-RHOP_MOUSE
180	10152	19897	1.94	2.0E-67	BE346354.1	EST_HUMAN	QI1085 OT-RHO BINDING PROTEIN 1;
827	10754	20694	6	2.0E-67	AW816505.1	EST_HUMAN	hm1807.x1 Scores_NFL1_GBC_S1 Homo sapiens cDNA clone IMAGE:1541355 3'
1089	11095		1.74	2.0E-67	AF167480.1	NT	hw16509.x1 NCL_OGAP_Lu24 Homo sapiens cDNA clone IMAGE:3183198 3' similar to WP F23H11.9
1841	11737	21614	1.5	2.0E-67	BE303037.1	EST_HUMAN	OV4-S10234-181109-037-605 S10234 Homo sapiens cDNA
1841	11737	21615	1.5	2.0E-67	BE303037.1	EST_HUMAN	Homo sapiens double stranded RNA activated protein kinase (RPR) gene, exons 2a, 2, 3, and 4
2336	12216	22116	0.98	2.0E-67	AF308611.1	NT	hw2205.x1 NHL_MGC_20 Homo sapiens cDNA clone IMAGE:2205576 5' similar to TR-O4492 O4492
2391	12291	22153	1.2	2.0E-67	AF308611.1	NT	KIA01798 PROTEIN;
3422	13339	23141	3.9	2.0E-67	AF62575.1	EST_HUMAN	hw2205.x1 NHL_MGC_20 Homo sapiens cDNA clone IMAGE:2205576 5' similar to TR-O4492 O4492
3821	13630	23910	2.33	2.0E-67	AL163900.2	EST_HUMAN	Homo sapiens K5A8 zinc finger protein ZF58 mRNA, complete cds
5724	16651	25734	4.22	2.0E-67	BF207088.1	NT	Homo sapiens developmentally regulated GTP-binding protein 1 (DRG5), mRNA
5803	15708	25920	2.17	2.0E-67	AF5091763.1	EST_HUMAN	2321901.x1 Scores_NHL_MGC_20 Homo sapiens cDNA clone IMAGE:145392 3'
5903	15708	25921	2.17	2.0E-67	AF5091763.1	NT	Homo sapiens chromosome 21 segment HS21C100
7202	17078	27264	1.34	2.0E-67	AW502935.1	EST_HUMAN	0018/535191 NHL_MGC_55 Homo sapiens cDNA clone IMAGE:087183 5'
7202	17078	27265	1.34	2.0E-67	AW502935.1	EST_HUMAN	Homo sapiens mRNA for NADPH-cytochrome P-450 reductase, complete cds
8408	18768		3.26	2.0E-67	BC295714.1	NT	RC4-BT0568-170100-011-c07 BT0568 Homo sapiens cDNA
8538	18428	28098	1.77	2.0E-67	BC295714.1	EST_HUMAN	hw16509.x1 NCL_OGAP_Lu24 Homo sapiens cDNA clone IMAGE:1541355 3'
8751	17800	28114	2.26	2.0E-67	BF371708.1	EST_HUMAN	001175702P1 NHL_MGC_17 Homo sapiens cDNA
9398	19577	25069	2.6	2.0E-67	11418180	NT	PM2-TN0103-040900-001-c02 TN0103 Homo sapiens cDNA
							Homo sapiens thyroid autoantigen 70kD (Ku antigen) (G23P1), mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
253	10219	20306	4.37	1.0E-87	4502166	NT	Homo sapiens glyvixid beta (A4) precursor protein (protease activator-1, Alzheimer disease) (APP), mRNA
2120	12017	21915	2.46	8.0E-68	B6370732.1	EST_HUMAN	G0143558F NIH_MGC_65 Homo sapiens cDNA clone IMAGE:365224.5
3794	13706	23492	4.96	8.0E-68	A0209466.1	EST_HUMAN	AB040101 Shiga toxin B chain (STxB) (P02728) Homo sapiens cDNA clone IMAGE:346193.5 similar to SV1 SAV_SULAC COTR98 SAV PROTEIN_1
3794	13706	23493	4.96	8.0E-68	A0209466.1	EST_HUMAN	AB040101 Shiga toxin B chain (STxB) (P02728) Homo sapiens cDNA clone IMAGE:346193.5 similar to SV1 SAV_SULAC COTR98 SAV PROTEIN_1
1846	11743		2.2	6.0E-66	E15503842.1	EST_HUMAN	UHP-BND-4B-C07-SJUT1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3076924.5
7971	17821	28064	2.49	6.0E-68	11420680	NT	Homo sapiens predixin A-inhibited guanine nucleotide-exchange protein 7 (GIG2), mRNA
8469	18627		1.42	6.0E-68	AF153901.1	NT	Homo sapiens interleukin 15 (IL15) precursor protein (interleukin receptor 2-2) (KIR22Z) genes, partial cds
9676	16234		1.82	6.0E-68	BE153901.1	EST_HUMAN	01462007F1 NHL_MGC_66 Homo sapiens cDNA clone IMAGE:3855761.5
9816	18391	25176	1.36	6.0E-68	BF150076.1	EST_HUMAN	010840302F2 NHL_MGC_19 Homo sapiens cDNA clone IMAGE:412414.5
7851	12052	20555	0.87	5.0E-68	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
7851	12042	20556	0.87	5.0E-68	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
7802	12031	20572	3.87	5.0E-68	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
802	10731	20573	3.87	5.0E-68	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
3168	13334	22830	2.62	5.0E-68	AE037882.1	NT	Homo sapiens mRNA for KIAA1431 protein, partial cds
2480	12356	22247	1.01	4.0E-68	11421388	NT	Homo sapiens transcription factor NRF (NRF), mRNA
2480	12356	22248	1.01	4.0E-68	11421388	SWISSPROT	Homo sapiens transcription factor NRF (NRF), mRNA
6001	16044	26168	5.64	4.0E-68	P04040	SWISSPROT	GLYERALDEHYDE 3-PHOSPHATE DEHYDROGENASE LIVER
6001	16044	26169	5.64	4.0E-68	11055997	NT	Homo sapiens serine carboxypeptidase 1 precursor protein (HSC91), mRNA
6001	16044	26180	5.64	4.0E-68	11055997	NT	Homo sapiens serine carboxypeptidase 1 precursor protein (HSC91), mRNA
7225	17102	27391	5.41	4.0E-68	DQ34719.2	NT	Homo sapiens mRNA for KIAA0145 protein, partial cds
7225	17102	27391	5.41	4.0E-68	DQ34719.2	NT	Homo sapiens mRNA for KIAA0145 protein, partial cds
7295	17171	27371	2.36	4.0E-68	A03040916.1	NT	Homo sapiens mRNA for KIAA1485 protein, partial cds
3511	13325	23312	5.61	3.0E-68	AF236082.1	NT	Mus musculus G-protein coupled receptor GPR73 (Gpr73) mRNA, complete cds
7441	14544		4.44	3.0E-68	A343233.1	EST_HUMAN	THR-12 THR repetitive element
7997	17947	26066	1.45	3.0E-68	F28784.1	EST_HUMAN	HSPD18178 HMG Homo sapiens cDNA clone s300023D09
9872	19802		1.53	3.0E-68	A0304488.1	EST_HUMAN	QV1-D10072-510200-056-105 D10072 Homo sapiens cDNA
2832	15076		12.26	2.0E-68	D00522.1	NT	Cereulic acid long-chain fatty acids (CFA) for EF-1 alpha, complete cds
4983	14073	24361	1.06	2.0E-68	A0006861.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
6110	18919		1.6	2.0E-68	B450688.1	EST_HUMAN	p35904.s1 Sures for brain N1B1 Homo sapiens cDNA clone IMAGE:34960.3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
15391	11440		1.35	3.0E-69	T05914.1	EST_HUMAN	y005402.1 Scores Infant brain 1NB Homo sapiens cDNA clone IMAGE:24890 5' similar to SP-A49303
2325	12209		0.86	3.0E-60	5728910	NT	A49303 SPECIFIC III-EGF REPEAT-CONTAINING FIBROPELIN-LIKE PROTEIN - SEA URCHIN ;
3500	13557	23674	0.86	3.0E-60	A1705898.1	EST_HUMAN	Homo sapiens lymphatic vessel endothelial hyaluronan receptor 1 (LYVE-1) mRNA
6293	15057	25105	1.34	3.0E-60	U62351.1	NT	wh05503.X1 NC1, GQAP, Kd11 Homo sapiens cDNA clone IMAGE:2385758 3'
6357	16249	28410	6.97	3.0E-60	U62351.1	NT	Homo sapiens acylase 2, mitochondrial (ACO2), mRNA
6457	16318	28485	6.43	3.0E-60	AF269075.1	NT	Homo sapiens arm-repet protein INRAP/hauglumpin (CTNND2) mRNA, partial cds
7091	16568		1.26	3.0E-60	AF269075.1	EST_HUMAN	Homo sapiens TRAF6-binding protein, TBGP mRNA, complete cds
7417	17264	27491	1.54	3.0E-60	X13223.1	NT	EST83807.7 TRAFC172 cells II Homo sapiens cDNA 5' end similar to ribosomal protein S18
7463	17363	27598	2.24	3.0E-60	X06293.1	NT	H sapiens mRNA for N-acetylglucosaminide-(beta 1-4)-galactosyltransferase
8036	17826	28174	3.07	3.0E-60	X06293.1	NT	Human mRNA for calcium-binding protein in macrophages (MRP-14) macrophage migration inhibitor factor (MIF)-related protein
8245	18068		7.12	3.0E-60	A4370399.1	EST_HUMAN	Homo sapiens ribosomal protein S15a (RPS15A), mRNA
9195	18911		4.19	3.0E-60	11419167	NT	EST83807.7 HSC172 cells II Homo sapiens cDNA 5' end similar to ribosomal protein S16
124	10344	20170	1	2.0E-60	AF160282.1	NT	Homo sapiens HSC56.2 protein (HSC56.2), mRNA
124	10344	20171	1	2.0E-60	AF160282.1	NT	Homo sapiens KIA0353 protein gene, complete cds, and alpha-1b protein gene, partial cds
368	10344	20170	4.94	2.0E-60	AF160282.1	NT	Homo sapiens KIA0353 protein gene, complete cds, and alpha-1b protein gene, partial cds
368	10344	20171	4.94	2.0E-60	AF160282.1	NT	Homo sapiens KIA0353 protein gene, complete cds, and alpha-1b protein gene, partial cds
1842	11738	21610	1.2	2.0E-60	BC227897.1	EST_HUMAN	BC010824-4F1 NH_LMC-10 Homo sapiens cDNA clone IMAGE:330074 9'
2813	12742	21446	2.73	2.0E-60	A4331167.1	EST_HUMAN	zw71922.1 Scores_1beta_NBT Homo sapiens cDNA clone IMAGE:731682 5'
1678	11577	21446	2.35	1.0E-60	AF037083.1	NT	Rat brain neocortex brain specific core-actin-binding protein CBP-90 mRNA, partial cds
5651	16556	26068	3.98	1.0E-60	AW353669.1	EST_HUMAN	CYC-11010-021165-046-007 T10010 Homo sapiens cDNA
5651	16556	26211	1.95	1.0E-60	7682263	NT	Homo sapiens KIA00716 gene product (KIA00716), mRNA
6081	16053	26212	1.95	1.0E-60	7682263	NT	Homo sapiens KIA00716 gene product (KIA00716), mRNA
6081	16053	26213	2.93	1.0E-60	AB032973.1	NT	Homo sapiens mRNA for KIAA1147 protein, partial cds
6081	16053	26214	2.93	1.0E-60	AB032973.1	NT	Homo sapiens mRNA for KIAA1147 protein, partial cds
7847	17657	27642	5.25	1.0E-60	BE246070.1	EST_HUMAN	TGAP-PIEX78 Podiatric pre-B cell acute lymphoblastic leukemia Baylor-HQSC project=TCBA Homo sapiens cDNA clone TGAP2678
7847	17657	27643	5.25	1.0E-60	BE246070.1	EST_HUMAN	TGAP-PIEX78 Podiatric pre-B cell acute lymphoblastic leukemia Baylor-HQSC project=TCBA Homo sapiens cDNA clone TGAP2678
6246	18126		23.27	1.0E-60	4804918	NT	Homo sapiens keratin 8 (KR18) mRNA
9105	18872	28785	1.63	1.0E-60	BF126897.1	EST_HUMAN	80762502F1 NH_LMC-20 Homo sapiens cDNA clone IMAGE:4028765 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9510	19124		2.82	1.0E-66	AB009994.1	EST_HUMAN	Wf40d8.x1 Sorens_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2960390 3' similar to contains Alu repetitive element/containing element MIR repetitive element;
2284	12717	22865	1.52	8.0E-70	AA230303.1	EST_HUMAN	nc13412.1f1 NOL CGAP_P1 Homo sapiens cDNA clone IMAGE:1008023
4271	14176	23954	2.16	8.0E-70	L77866.1	NT	Homo sapiens DGS-1 mRNA, 3' end
1771	11670	21547	1.93	7.0E-70	AA497807.1	EST_HUMAN	tm5901.x1 NOL CGAP_Bnc25 Homo sapiens cDNA clone IMAGE:2768308 3'
1771	11670	21548	1.93	7.0E-70	AA497807.1	EST_HUMAN	tm5901.x1 NOL CGAP_Bnc25 Homo sapiens cDNA clone IMAGE:2768308 3'
1888	11784	21660	1.93	7.0E-70	AA282855.1	EST_HUMAN	21504.1f1 NOL CGAP_GG51 Homo sapiens cDNA clone IMAGE:713239 5'
2018	11809		3.67	7.0E-70	5031689	NT	Homo sapiens tumor suppressor deleted in oral cancer-related 1 (DCC-1R) mRNA
4132	14032	23807	3.96	7.0E-70	475723	NT	Homo sapiens adenylylate cyclase 3 (ADCY3) mRNA
5359	15289	25124	5.28	7.0E-70	AB023269.1	NT	Homo sapiens MST mRNA, partial cds
5359	15289	25124	5.28	7.0E-70	AB023269.1	NT	Homo sapiens MST mRNA, partial cds
5138	15885	26120	1.99	7.0E-70	AJ000092.1	NT	Homo sapiens gene encoding splicing factor SFI1, exons 2-8
6610	16788	26660	2.96	7.0E-70	AB037715.1	NT	Homo sapiens mRNA for KIAA1284 protein, partial cds
6610	16788	26661	2.96	7.0E-70	AB037715.1	NT	Homo sapiens mRNA for KIAA1284 protein, partial cds
7063	16940	27131	3.98	7.0E-70	M74098.1	NT	Homo sapiens displacement protein (GCAP1) mRNA
7063	16940	27132	3.98	7.0E-70	M74098.1	NT	Homo sapiens displacement protein (GCAP1) mRNA
7263	17160	27367	3.72	7.0E-70	X65941.1	NT	Human PBX3 mRNA
7263	17160	27368	3.72	7.0E-70	X65941.1	NT	Human PBX3 mRNA
7263	17160	27369	3.72	7.0E-70	AF163715.1	NT	Homo sapiens phospholamban class 1 gene, exon 1 and 5' flanking region
7445	16457	26649	1.56	7.0E-70	11625964	NT	Homo sapiens leucoprotein beta 2b, transcript (TRN2) mRNA
7445	16457	26649	1.56	7.0E-70	11625964	NT	Homo sapiens leucoprotein beta 2b, transcript (TRN2) mRNA
8875	16887	28978	1.78	7.0E-70	11625319	NT	Homo sapiens HR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA
8875	16887	28979	1.78	7.0E-70	11625319	NT	Homo sapiens HR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA
883	10780	20690	1.93	8.0E-70	4802189	NT	Homo sapiens amyloid beta (A4) precursor protein (protease resistant), Alzheimer disease (APP), mRNA
2300	11679	21974	1.36	6.0E-70	M00038.1	NT	Human Ku (p70) subunit mRNA, complete cds
2491	12398	22232	0.99	6.0E-70	6623994	NT	Homo sapiens CMP-H-acyltransferase acid synthase (LOC55907), mRNA
2505	12723	22298	1.83	5.0E-70	7662307	NT	Homo sapiens KIAA0762 gene product (KIAA0762), mRNA
2505	12723	22299	1.83	5.0E-70	7662307	NT	Homo sapiens KIAA0762 gene product (KIAA0762), mRNA
9116	16879		1.73	5.0E-70	JE160084.1	EST_HUMAN	MF3-4T0487-150000-115-408 HT0487 Homo sapiens cDNA
1571	11475	21332	0.99	3.0E-70	BC017196.1	EST_HUMAN	RC0-8T0482-071295-011-412 BT0522 Homo sapiens cDNA
1571	11475	21333	0.99	3.0E-70	BC017196.1	EST_HUMAN	RC0-8T0482-071295-011-412 BT0522 Homo sapiens cDNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5945	15751	25985	3.88	3.0E-70	BF685233.1	EST_HUMAN	602141591F1 INH1.MGC_48 Homo sapiens cDNA clone IMAGE:4302806 5'
5945	15751	25986	3.88	3.0E-70	BF685233.1	EST_HUMAN	602141591F1 INH1.MGC_48 Homo sapiens cDNA clone IMAGE:4302806 5'
674	10608	20426	13.15	2.0E-70	N42161.1	EST_HUMAN	SW-D3H1_RAT P23266 3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR ;
674	10608	20427	13.15	2.0E-70	N42161.1	EST_HUMAN	SW-D3H1_RAT P23266 3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR ;
689	10622	20449	2.01	2.0E-70	AI24869.1	EST_HUMAN	SW-D3H1_RAT P23266 3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR ;
1004	10522	20765	1.7	2.0E-70	8622968	NT	SW-D3H1_RAT P23266 3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR ;
1167	11079	20024	1.95	2.0E-70	7661993	NT	q951101.X1 NOL_OGAP_Part1 Homo sapiens cDNA clone IMAGE:2004813 3'
1167	11079	20025	1.95	2.0E-70	7661993	NT	Homo sapiens hypothetical protein FLJ20758 (FLJ20758), mRNA
1337	11262	21148	0.97	2.0E-70	BE467311.1	EST_HUMAN	Homo sapiens KIA00193 gene product (KIA00193), mRNA
1708	11609	21479	2.09	2.0E-70	AL163202.2	NT	h254c12.X1 NOL_OGAP_Lu24 Homo sapiens cDNA clone IMAGE:3212758 3'
2272	12166		3.62	2.0E-70	AAC540.10	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C032
3693	13370	23648	3.95	2.0E-70	M69181.1	NT	248q04.r1 Scores retina N2644R Homo sapiens cDNA clone IMAGE:380214 5' similar to SW-GAG_HTL1A
5305	15304	25156	8.05	2.0E-70	X72662.1	NT	P03345 GAG POLYPROTEIN ;
5305	15304	25157	8.05	2.0E-70	X72662.1	NT	Human nonmuscle myosin heavy chain-B (MYH10) mRNA, partial cds
5755	15673	25700	1.42	2.0E-70	AF131019.1	NT	H sapiens gene for schwannomin (CS3)
5755	15673	25700	1.42	2.0E-70	AF131019.1	NT	H sapiens gene for schwannomin (CS3)
5939	15904	26038	1.88	2.0E-70	D12823.1	NT	Homo sapiens MALP1 mRNA, complete cds
8010	15915	26042	9.83	2.0E-70	AF123074.1	NT	Human mRNA for NF1 protein isoform (ras-grafted protein isoform), complete cds
8010	15915	26043	9.83	2.0E-70	AF123074.1	NT	Human sapiens cytoplasmic dyane intermediate chain 1 mRNA, complete cds
8177	15134	24653	1.69	2.0E-70	1142942	NT	Homo sapiens cytoplasmic dyane intermediate chain 1 mRNA, complete cds
8818	15498	25685	7.67	2.0E-70	M21471.1	NT	Homo sapiens sialyltransferase 6 (N-acetylglucosaminidase alpha 2,3-sialyltransferase) (SIA7), mRNA
7835	17685	27950	1.3	2.0E-70	AF123033.1	NT	Human glutamine nucleotide-binding protein alpha subunit gene (G-2-alpha), exons 4 and 5
8422	18266	28550	3.19	2.0E-70	8623420	NT	Homo sapiens calcium-binding transporter mRNA, partial cds
8422	18266	28551	3.19	2.0E-70	8623420	NT	Homo sapiens hypothetical protein FLJ20450 (FLJ20450), mRNA
8908	18716	29010	5.62	2.0E-70	4603520	NT	Homo sapiens hypothetical protein FLJ20450 (FLJ20450), mRNA
9499	19114	25289	2.58	2.0E-70	11430460	NT	Homo sapiens eukaryotic translation initiation factor 3, subunit 8 (48kD) (EIF-355) mRNA
9499	19114	25290	2.58	2.0E-70	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
3347	13287		2.97	1.0E-70	4507478	NT	Homo sapiens transglutaminase 3 (E polypeptide, protein-glutamine-gamma-glutamyltransferase) (TGMA3) mRNA
7642	17492		2.57	1.0E-70	AA42292.1	EST_HUMAN	z64c033.r1 Scores, testis, NHT Homo sapiens cDNA clone IMAGE:757444 5'
8305	18162	28429	13.73	1.0E-70	AV1788538.1	EST_HUMAN	AV1788538.1 Homo sapiens cDNA clone cBLBGB70 5'

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5621	15536	25621	6.04	9.0E-71	AI43870.1	EST_HUMAN	q64f01.x1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:73809 3' similar to TRO1045
5621	15536	25622	6.04	9.0E-71	AI43870.1	EST_HUMAN	O14045 PHOSPHOTRANSFERASE ; q64f01.x1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:73809 3' similar to TRO1045
6192	16077	28226	1.88	9.0E-71	AI654903.1	EST_HUMAN	O14045 PHOSPHOTRANSFERASE ; wk3205.x1 NCL CGAP G03 Homo sapiens cDNA clone IMAGE:209289 3' similar to TR-P97213 P97213
8811	16077	28226	4.65	9.0E-71	AI654903.1	EST_HUMAN	CD42, CDU1, TCCD, TCDB, TCDE, TODA, TDCG, CDD1, CDD2, CDD3, AND CDD4 GENES ; wk3205.x1 NCL CGAP G03 Homo sapiens cDNA clone IMAGE:209289 3' similar to TR-P97213 P97213
7245	17122		1.97	8.0E-71	AA174451.1	EST_HUMAN	CD42, CDU1, TCCD, TCDB, TCDE, TODA, TDCG, CDD1, CDD2, CDD3, AND CDD4 GENES ; 257411.r1 Strikwerwa neuroepithelium (987233) Homo sapiens cDNA clone IMAGE:610101 5' similar to
9303	16226	28396	7.91	7.0E-71	AA174451.1	EST_HUMAN	TR-61143091 G1143091 STRAIN X334.POL ; p69705.x1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:758075 5'
7037	16914	27103	1.32	7.0E-71	AA1705437.1	EST_HUMAN	g91cds.x1 Soares, fetal liver, spleen, INR.L.S. S1 Homo sapiens cDNA clone IMAGE:462228 3'
8943	16807	28766	4.18	7.0E-71	AA163210.2	NT	g91cds.x1 Soares, fetal liver, spleen, INR.L.S. S1 Homo sapiens cDNA clone IMAGE:462228 3'
2183	12080	21691	3.45	5.0E-71	AF056322.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS27C010 Homo sapiens SP7100-HMG nuclear autoantigen (SP7100) mRNA, complete cds
4030	13933	23710	1.38	5.0E-71	AF056322.1	EST_HUMAN	O143570231.61169-207.651570231 Homo sapiens cDNA O143570231.61169-207.651570231 Homo sapiens cDNA
6141	16011	21762	3.2	5.0E-71	AI629196.1	EST_HUMAN	wf1910.x1 NCL CGAP UN Homo sapiens cDNA clone IMAGE:242331 5'
5596	15501	25577	2.14	5.0E-71	492740	NT	Homo sapiens cytochrome oxidase subunit 9 (COX9) mRNA
8434	16265	25167	1.59	5.0E-71	M63106.1	NT	Human neuroendocrine protein type 9 (HNP9) mRNA, complete cds
6548	16406	20565	19.78	5.0E-71	AF072810.1	NT	Human Prk4 gene for Alzheimer's disease A1 amyloid protein precursor (Apo 2)
7792	17552		2.26	5.0E-71	X13467.1	NT	Human Prk4 gene for Alzheimer's disease A1 amyloid protein precursor (Apo 2)
8348	18225	28477	1.19	5.0E-71	11438514	NT	Homo sapiens pro-platelet basic protein (includes platelet basic protein, oste-thromboglobulin, connective tissue-activating peptide II, neutrophil-activating peptide-2) (PBP), mRNA
8128	18400	28668	2	5.0E-71	11438065	NT	Homo sapiens similar to hypothetical protein FLJ20183 (H. sapiens) (LOC838325), mRNA
9037	18548	29116	1.84	5.0E-71	11417862	NT	Homo sapiens calcitonin binding protein 1 (KIA00330), mRNA
9411	19063		1.62	5.0E-71	11418639	NT	Homo sapiens calcitonin binding protein 1 (KIA00330), mRNA
97	10032	19899	1.13	4.0E-71	4507892	NT	Homo sapiens tumor necrosis factor (ligand) superfamily, member 10 (TNFSF10) mRNA
347	10305	20123	115.93	4.0E-71	AF17626.1	NT	Homo sapiens tumor necrosis factor (ligand) superfamily, member 10 (TNFSF10) mRNA
347	10305	20124	115.93	4.0E-71	AF17626.1	NT	Equus caballus glyceraldehyde-3-phosphate dehydrogenase mRNA, partial cds
2850	12778	22566	0.98	4.0E-71	7705414	NT	Equus caballus glyceraldehyde-3-phosphate dehydrogenase mRNA, partial cds
2850	12778	22567	0.98	4.0E-71	7705414	NT	Homo sapiens hook1 protein (HOOK1), mRNA
2851	12785	22567	0.98	4.0E-71	7705414	NT	Homo sapiens hook1 protein (HOOK1), mRNA
2851	12785	22567	0.98	4.0E-71	7705414	NT	Homo sapiens planninogen (PLO) mRNA
4330	14227	24069	3.35	4.0E-71	AF063322.1	NT	Homo sapiens SP100-HMG nuclear autoantigen (SP100) mRNA, complete cds
4913	14792	24587	4.99	4.0E-71	7657602	NT	Homo sapiens putative heme-binding protein (SOL), mRNA

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8077	17968	28218	3.32	3.0E-71	AA505683.1	EST_HUMAN	h45h10.x1 INCL COAP_P41 Homo sapiens cDNA clone IMAGE:1040803 similar to contains P1R5.6 P1R5 respective element;
1210	11119	20068	2.62	2.0E-71	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C036
5259	15161	24657	6.96	2.0E-71	D07462.1	NT	Human mRNA for KIA0272 gene, partial cds
5259	15161	24658	6.96	2.0E-71	D07462.1	NT	Human mRNA for KIA0272 gene, partial cds
8022	17672	28114	2.56	2.0E-71	AF065703.1	NT	Homo sapiens short chain L3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene encoding mitochondrial protein, complete cds
8022	17672	28115	2.56	2.0E-71	AF065703.1	NT	Homo sapiens short chain L3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene encoding mitochondrial protein, complete cds
8079	17970	28219	2.3	2.0E-71	BC018477.1	EST_HUMAN	BB11A05.v1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048754 5' similar to SW_R22B_HUMAN
9181	19920		6.22	2.0E-71	T95469.1	EST_HUMAN	P51727 UV EXCISION REPAIR PROTEIN PROTEIN RAD23 HOMOLOG B.1
922	10559	20371	2.11	1.0E-71	A007927.1	EST_HUMAN	y63c09.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:120520 5' contains LOR1.32 LOR1 repetitive element;
926	10551	20069	1.93	1.0E-71	7706281	NT	Homo sapiens neuronal cell death-related protein (LOC51616) mRNA
1054	11000	20841	4.01	1.0E-71	AF205990.1	NT	Homo sapiens fibroblast-2 gene, exon 2 through 16 and complete cds
1317	11224	21690	10.59	1.0E-71	AF012072.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (pIK230) mRNA, complete cds
2036	11927	21821	1.23	1.0E-71	AB017007.1	NT	Homo sapiens PAK5L16 mRNA, partial cds
2036	11927	21822	1.23	1.0E-71	AB017007.1	NT	Homo sapiens PAK5L16 mRNA, partial cds
2681	12538	22416	4.95	1.0E-71	7687153	NT	Homo sapiens purpurinase-oligolactonase with YRPV motif like (HEVL) mRNA
3457	13375	22179	1.17	1.0E-71	AF119355.1	NT	Homo sapiens synaptic phospholipase mRNA, complete cds
3546	13452	22356	4.73	1.0E-71	AF232161.1	NT	Homo sapiens SVARE protein kinase SNAR mRNA, complete cds
3546	13452	22357	4.73	1.0E-71	AF242619.1	NT	Homo sapiens SVARE protein kinase SNAR mRNA, complete cds
3597	13511	22398	0.94	1.0E-71	BE122690.1	EST_HUMAN	02_16 Human Epidermal Keratinocyte Subtraction Library: Upregulated Transcripta Homo sapiens cDNA
3597	13511	22399	0.94	1.0E-71	BE122690.1	EST_HUMAN	02_16 Human Epidermal Keratinocyte Subtraction Library: Upregulated Transcripta Homo sapiens cDNA
3681	13595	22391	1.87	1.0E-71	AF121800.1	NT	clone 02_15 5' similar to Homo sapiens chromosome 19
4370	14295	24050	1.86	1.0E-71	D39476.1	NT	Homo sapiens atrophic precursor (ATRN) gene, exon 19
6044	15947	26079	1.4	1.0E-71	11428162	NT	Human mRNA for KIA0045 gene, complete cds
6326	16169	26351	10.32	1.0E-71	U08703.1	NT	Homo sapiens OCN5 (general control of amino-acid synthesis, yeast, homolog) like 2 (GON6L2) mRNA
6750	16929	26816	6.96	1.0E-71	11125430	NT	Homo sapiens myosin (M-protein) 2 (1950D) (MYO2D) mRNA
6916	10794	26946	4.18	1.0E-71	8022511	NT	Homo sapiens hypothetical protein FLJ10995 (FLJ10988) mRNA

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6916	16794	26687	4.18	1.0E-71	8922811	NT	Homo sapiens hypochlorite protein FLJ10996 (FLJ10996), mRNA
7748	17698	27620	6.49	1.0E-71	AV707943.1	NT	Homo sapiens cytochrome c oxidase subunit VIIa-related protein gene, complete cds
7792	17642		3.39	1.0E-71	AV781217.1	EST_HUMAN	AV781217 MDS Homo sapiens cDNA clone MDS/EA03 5'
8164	18052		4.87	1.0E-71	AV781217.1	EST_HUMAN	AV781217 MDS Homo sapiens cDNA clone MDS/EA03 5'
8250	18193	28363	3.2	1.0E-71	11418603	NT	Homo sapiens coagulation factor XIII, A1 polypeptide (F13A1), mRNA
8460	18359	28623	2.33	1.0E-71	11417107	NT	Homo sapiens leucyl/tyrosyl aminopeptidase (LNPEP), mRNA
8466	18359	28624	2.33	1.0E-71	11417107	NT	Homo sapiens leucyl/tyrosyl aminopeptidase (LNPEP), mRNA
9547	19147		4.48	1.0E-71	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
401	10347	20173	1.15	9.0E-72	AB87635.1	EST_HUMAN	wk5593.x1 NCI CGAP Lur10 Homo sapiens cDNA IMAGE:2433183 3' similar to TR-O8705 O8705
401	10347	20174	1.15	9.0E-72	AB87635.1	EST_HUMAN	HYPOTHETICAL 38.6 KD PROTEIN, contains Alu repetitive element.
4023	13626	23700	5.23	7.0E-72	4801669	NT	HYPOTHETICAL 38.6 KD PROTEIN, contains Alu repetitive element.
4023	13626	23701	5.23	7.0E-72	4801669	NT	Homo sapiens scotinase 2, mitochondrial (AC02), nuclear gene encoding mitochondrial protein, mRNA
4023	13626	23702	5.23	7.0E-72	4801669	NT	Homo sapiens scotinase 2, mitochondrial (AC02), nuclear gene encoding mitochondrial protein, mRNA
6238	18064	28344	2.84	7.0E-72	S41894.1	NT	[pseudo] PFM22-profilin alpha [human, Genomic, 1102 nt, segment 2 of 3]
6885	18764		3.72	6.0E-72	AL183246.2	NT	Homo sapiens chromosome 21 segment HS21C046
8788	18603	28863	2.22	6.0E-72	BF099578.1	EST_HUMAN	TK53405.x1 NCI CGAP G05 Homo sapiens cDNA clone IMAGE:346080 3' similar to SVT/KML_C_8481T
891	10043	19854	0.86	5.0E-72	BF333707.1	EST_HUMAN	P97313 MYOSIN LIGHT CHAIN KINASE SKELETAL MUSCLE,
891	10043	19855	0.86	5.0E-72	BF333707.1	EST_HUMAN	QY0-C59010-15900-398-411 C59010 Homo sapiens cDNA
891	10043	19856	2.89	5.0E-72	BF333707.1	EST_HUMAN	QY0-C59010-15900-398-411 C59010 Homo sapiens cDNA
891	10043	19857	2.89	5.0E-72	BF333707.1	EST_HUMAN	QY0-C59010-15900-398-411 C59010 Homo sapiens cDNA
1122	11037		2.79	5.0E-72	L11048.1	NT	Homo sapiens alpha-tubulin mRNA, complete cds
6190	10023	26763	1.47	5.0E-72	AW126844.1	EST_HUMAN	AW126844 NT2P22 Homo sapiens cDNA clone NT2P2203751 5'
7097	10674	27167	3.85	5.0E-72	AW161274.1	EST_HUMAN	subQ3.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782864 5' similar to TR-O89768 O89768 HYPOTHETICAL 32.4 KD PROTEIN, contains element MSR1 repetitive element;
8569	18437	28706	3.18	5.0E-72	BF331671.1	EST_HUMAN	MF4-8170598-010500-405-405 BT10598 Homo sapiens cDNA
8569	18437	28707	3.18	5.0E-72	BF331671.1	EST_HUMAN	MF4-8170598-010500-405-405 BT10598 Homo sapiens cDNA
9253	19700		2.43	5.0E-72	BE920046.1	EST_HUMAN	QV1-BT10532-289000-342-410 BT10532 Homo sapiens cDNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4716	14602		1.06	4.0E-72	110344944	NT	Homo sapiens hypothetical protein dJ1067820.2 (U1067820.2), mRNA
6380	16242	28402	1.42	4.0E-72	5726887	NT	Homo sapiens heart domain and RLD 2 (HERC2), mRNA
7633	17484	27706	1.42	4.0E-72	8529989	NT	Homo sapiens hypothetical protein FLJ20758 (FLJ20758), mRNA
8815	18828	28917	7.32	4.0E-72	HY9421.1	EST_HUMAN	h33da03.1 Scores field liver spleen INFLS Homo sapiens cDNA clone IMAGE:225084 5'
8928	18737	29030	2.76	4.0E-72	TH910.1	EST_HUMAN	h33da03.1 Scores field liver spleen INFLS Homo sapiens cDNA clone IMAGE:109549 3'
9603	19185	26249	4.2	4.0E-72	AJ27546.2	NT	Homo sapiens WEE1 gene for protein kinase and partial ZNF143 gene for zinc finger transcription factor
885	10811		4.88	3.0E-72	AA729823.1	EST_HUMAN	h183a03.1 Scores, testis, NHT Homo sapiens cDNA clone 1310290 3'
1139	11053	20884	6.06	3.0E-72	U16306.1	NT	Human chondroin sulfate proteoglycan versican V0 splice-variant precursor peptide mRNA, complete cds
1139	11053	20885	6.06	3.0E-72	U16306.1	NT	Human chondroin sulfate proteoglycan versican V0 splice-variant precursor peptide mRNA, complete cds
3037	12995	22759	10.51	3.0E-72	AJ22904.1	NT	Homo sapiens 559 kb contig between AAL1 and CBR1 on chromosome 21q22, segment 3/3
3241	13194	22993	2.63	3.0E-72	9623548	NT	Homo sapiens hypothetical protein FLJ20685 (FLJ20685), mRNA
3760	13953	23445	2.51	3.0E-72	S77599.1	NT	TOR V delta 2-C alpha 1-coil receptor delta and C alpha fusion gene (alternatively spliced, splice junction)
4445	14339	24129	3.22	3.0E-72	11416190	NT	Human, precursor B-cell line REH, mRNA Partial, 21 nt
4835	14717	24500	0.94	3.0E-72	A054337.1	EST_HUMAN	Homo sapiens hypothetical protein (FLJ1127), mRNA
5639	15552	26543	2.4	3.0E-72	A070387.1	NT	Homo sapiens growth factor receptor-bound protein 10 (GRB10) gene, exon 5
5639	15552	26544	2.4	3.0E-72	A070387.1	NT	Homo sapiens growth factor receptor-bound protein 10 (GRB10) gene, exon 5
5743	15651	26758	4.36	3.0E-72	A022004.1	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds
5743	15651	26758	4.36	3.0E-72	A022004.1	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds
5858	15593	25016	3.02	3.0E-72	4626887	NT	Homo sapiens ribosomal protein L2-like (RPL2) mRNA
6476	16334	28501	2.92	3.0E-72	U60017.1	NT	Homo sapiens basic transcription factor 2p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (nrip) and survival motor neuron protein (smn) genes, complete cds
6765	16544	28822	1.28	3.0E-72	9031982	NT	Homo sapiens nuclear receptor subfamily 1, group H, member 3 (NR1H3), mRNA
7990	17610	29051	1.3	3.0E-72	X93899.1	NT	Homo sapiens S100A12 gene for Calgranulin C, exon 2 and joined cds
9516	19759	25282	1.85	3.0E-72	A001399.1	NT	Homo sapiens gene for AF-6, complete cds
9122	18010	28237	4.45	2.0E-72	AA798277.1	EST_HUMAN	h28a03.1 Scores, testis, NHT Homo sapiens cDNA clone 1381609 3' similar to gb-X02067 H.sapiens mRNA for 75L RNA pseudogene (HUMAN)
9630	19182	25248	3.74	2.0E-72	AF182714.1	NT	Rattus norvegicus putative phosphatidylphosphorylase translocator cDNA, complete cds
2030	11921	21812	2.91	1.0E-72	AA046525.1	EST_HUMAN	h85402.1 Scores, parathyroid, tumor, NHT.Homo sapiens cDNA clone IMAGE:138795 3'
5624	15441	26508	3.16	1.0E-72	7957976	NT	Homo sapiens viceroid protein sorting 41 (yeast homolog) (VPS41), mRNA
5948	16854	25976	19.78	1.0E-72	11321576	NT	Homo sapiens myosin, heavy polypeptide 13, skeletal muscle (MYH13), mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5649	15854	25077	19.78	1.0E-72	11321578	NT	Homo sapiens myosin, heavy polypeptide 13, skeletal muscle (MYH13), mRNA
6501	16360	26533	3.82	1.0E-72	BE175434.1	EST_HUMAN	RC4-HT0578-170300-012-g02 HT0578 Homo sapiens cDNA
6501	16360	26534	3.82	1.0E-72	BE175434.1	EST_HUMAN	RC4-HT0578-170300-012-g02 HT0578 Homo sapiens cDNA
7532	17383	27594	6.06	1.0E-72	AF222742.1	NT	Homo sapiens synaptic glycoprotein SC22 (SC2), complete cds
7532	17383	27595	6.06	1.0E-72	AF222742.1	NT	Homo sapiens synaptic glycoprotein SC22 (SC2), complete cds
1443	11348	21213	1.23	9.0E-73	AW374968.1	EST_HUMAN	MR0-CT0063-071002-002-h11 CT0063 Homo sapiens cDNA
8320	18197		23.9	9.0E-73	11424059	NT	Homo sapiens ribosomal protein L13a (RPL13a), mRNA
1022	10839	20782	1.03	8.0E-73	AW071755.1	EST_HUMAN	ves5506x1 NCL CGAP_Bm25 Homo sapiens cDNA clone IMAGE2501038.3 similar to TR-066300
1369	11304	21163	3.06	8.0E-73	A024877.1	EST_HUMAN	Q03900 HYPOTHETICAL PROTEIN M1156 ;
5659	15894	25986	4.6	8.0E-73	11420469	NT	Homo sapiens lysosome homodig (LOC57151), mRNA
0716	16565	25765	2	8.0E-73	AF113123.1	NT	Homo sapiens vesicular A11Phase isoform VA68 mRNA, complete cds
7345	17354	27459	15.88	8.0E-73	BE019020.1	EST_HUMAN	1482046.V1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE-3030034.5 similar to ab204098.cds1 ACTIN
7014	17465	27682	2.22	8.0E-73	11526037	NT	CYTOLASMIC 2 (HUMAN); gb121495 Mouse cytoskeletal gamma-actin mRNA, complete cds (MOLISE);
7014	17465	27683	2.22	8.0E-73	11526037	NT	Homo sapiens hickulin 12 repeat, beta 1 (IL12RB1), mRNA
8445	19081	25382	2.12	8.0E-73	AB02055.1	NT	Homo sapiens hickulin 12 repeat, beta 1 (IL12RB1), mRNA
9554	19217	25255	2.69	8.0E-73	11418169	NT	Homo sapiens DNA for Human P23X1, complete cds
1178	11033	20376	0.78	7.0E-73	8923260	NT	Homo sapiens hybrid autoantigen 7800 (K0 antigen) (G22F.1), mRNA
3261	13194	22983	1.06	7.0E-73	AL163262.2	NT	Homo sapiens chromosome 21 segment H521C006
4863	14743		1.62	7.0E-73	AL163262.2	NT	Homo sapiens chromosome 21 segment H521C006
152	10726		2.37	6.0E-73	AL163218.2	NT	Homo sapiens chromosome 21 segment H521C018
6255	16721	28274	3.36	6.0E-73	BE166574.1	EST_HUMAN	QY0-HT0494-020300-137-403 HT0494 Homo sapiens cDNA
5215	15138	24532	2.05	4.0E-73	11422159	NT	Homo sapiens HELG protein (FAM441), mRNA
1818	11715	21556	0.99	3.0E-73	11435913	NT	Homo sapiens helix-binding protein (HEBP), mRNA
1818	11715	21586	0.99	3.0E-73	11435913	NT	Homo sapiens helix-binding protein (HEBP), mRNA
833	10760	20010	1.75	2.0E-73	AF109897.1	NT	Homo sapiens BAS3 (BAS3) mRNA, partial cds
1902	11768		1.48	2.0E-73	AW898081.1	EST_HUMAN	RC3-NN0066-270-000-011-c04 NN0066 Homo sapiens cDNA
2251	12135		1.1	2.0E-73	U01317.1	NT	Homo beta globin region on chromosome 11
3144	13069	22889	3.48	2.0E-73	4502982	NT	Homo sapiens catenase 3, apoptosis-related cysteine protease (CASP3) mRNA
3503	13420	23221	0.96	2.0E-73	7699539	NT	Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, perlin (PARK2), transcript variant 3, mRNA

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Probe SEQ ID NC:	Exon SEQ ID NC:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5503	13420	23222	0.96	2.0E-73	7696938	NT	Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, putkin (PARK2), transcript variant 3, mRNA
5902	15908	25933	7.6	2.0E-73	AB04811.1	NT	Homo sapiens mRNA for KIAA1501 protein, partial cds
6023	15927	26068	1.35	2.0E-73	11431471	NT	Homo sapiens Interleukin 4 receptor (IL4R), mRNA
6023	15927	26069	1.35	2.0E-73	11431471	NT	Homo sapiens Interleukin 4 receptor (IL4R), mRNA
7556	17806	28048	1.34	2.0E-73	4804106	NT	Homo sapiens guanine synthetase (GSS) mRNA
7553	17843	28065	2.45	2.0E-73	11469960	NT	Homo sapiens superinfectin (SVIL), transcript variant 1, mRNA
7553	17843	28066	2.45	2.0E-73	11469960	NT	Homo sapiens superinfectin (SVIL), transcript variant 1, mRNA
8138	18026	28272	4.14	2.0E-73	11431568	NT	Homo sapiens KIAA1080 protein, Cggl-associated, gamma-adaptin ear containing ARF-binding protein 2 (KIAA1080), mRNA
8408	18284	28537	3.79	2.0E-73	4557612	NT	Homo sapiens galactose-4-epimerase (Krebs disease) (GALC), mRNA
8408	18284	28538	3.79	2.0E-73	4557612	NT	Homo sapiens galactose-4-epimerase (Krebs disease) (GALC), mRNA
8432	18300	28562	1.78	2.0E-73	AB028982.1	NT	Homo sapiens mRNA for KIAA1059 protein, partial cds
8447	17798	28562	1.72	2.0E-73	AB028982.1	NT	Homo sapiens mRNA for KIAA1059 protein, partial cds
1743	11644	21512	1.97	1.0E-73	AF165809.1	EST_HUMAN	RCSAN0066:270400-011-041 NU0068 Homo sapiens cDNA
1743	11644	21512	1.97	1.0E-73	AF165809.1	EST_HUMAN	RCSAN0066:270400-011-041 NU0068 Homo sapiens cDNA
2434	12311	22207	0.83	1.0E-73	AF198348.1	NT	Galus gallus Dactyl protein (Dact2), mRNA, complete cds
7489	17326	27534	1.36	1.0E-73	AI147427.1	EST_HUMAN	qf6107.1 Source: testis, NBT Homo sapiens cDNA clone IMAGE:636687 5 similar to contains element
8747	17866	28140	2.67	1.0E-73	BE385477.1	EST_HUMAN	MEV22 repeat element, 1
723	10855	20485	1.39	8.0E-74	4557428	NT	601276077.F1 NIH_MGC_28 Homo sapiens cDNA clone IMAGE:3817105 5
6606	15521	25903	1.84	8.0E-74	S83164.1	NT	Homo sapiens CD38-like 4 (CD38L4) mRNA
6606	15521	25903	1.84	8.0E-74	S83164.1	NT	CD38-like 4 (CD38L4) mRNA
1806	11801	21679	3.01	7.0E-74	AJ001686.1	NT	CD38-like 4 (CD38L4) mRNA
3285	13207	28007	0.96	7.0E-74	AI163462.2	NT	Homo sapiens NK622 gene, exon 10
7327	17231	27432	2	7.0E-74	BE97432.1	EST_HUMAN	Homo sapiens chromosome 21 segment H27C048
9533	19216	28234	2.61	7.0E-74	BE20005.1	EST_HUMAN	601646294.F1 NIH_MGC_73 Homo sapiens cDNA clone IMAGE:3902987 5
11068	11022	20865	2.58	6.0E-74	AF108907.1	NT	601161027.F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3939585 5
1809	11514	21713	1.03	6.0E-74	AF108907.1	NT	Homo sapiens S164 gene, partial cds; P51 and hypothetical protein genes, complete cds; and S171 gene, partial cds
2268	12152	22050	9.96	6.0E-74	BE38290.1	EST_HUMAN	601283527.F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3905463 3
2268	12152	22051	9.96	6.0E-74	BE38290.1	EST_HUMAN	601283527.F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3905463 3
2834	12762	22553	1.39	6.0E-74	AF104396.1	EST_HUMAN	UHH-BIO-aab-H-03-0-UI-1st NO1 CGAP Sub1 Homo sapiens cDNA clone IMAGE:2769865 3
2834	12762	22554	1.39	6.0E-74	AF104396.1	EST_HUMAN	UHH-BIO-aab-H-03-0-UI-1st NO1 CGAP Sub1 Homo sapiens cDNA clone IMAGE:2769865 3
3952	13266	23352	2.93	6.0E-74	BE04846.1	EST_HUMAN	UHH-BIO-aab-H-03-0-UI-1st NO1 CGAP Sub1 Homo sapiens cDNA clone IMAGE:313232 3

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3032	13906	23353	2.63	6.0E-74	BE04846.1	EST_HUMAN	h5c611x1 NC1_OGAP_KcH1 Homo sapiens cDNA clone IMAGE:373232 3'
5294	13215	25071	2.49	6.0E-74	11066013	NT	Homo sapiens actin filament associated protein (AFAP), mRNA
887	10813	20061	2.58	5.0E-74	AIJ020986.1	EST_HUMAN	hFT7c09 y1 Marton Fetal Cochlea Homo sapiens cDNA clone IMA:OE-2483704 5'
2086	12534	20061	5.19	5.0E-74	AIJ0362756.1	EST_HUMAN	PMD-OT0289-271036-001-007 CT0289 Homo sapiens cDNA
5320	15240	25045	2.15	5.0E-74	11425417	NT	Homo sapiens phosphatidylinositol glycan, class L (PIGL), mRNA
5539	15450	25526	10.48	5.0E-74	X55670.1	NT	H sapiens mRNA for TPOR18 protein
5563	15470	25532	6.74	5.0E-74	4507866	NT	Homo sapiens VAMP (vesicle-associated membrane protein)-associated protein A (38kD) (VAPA), mRNA, and translated products
5902	13516	23594	1.85	5.0E-74	11431471	NT	Homo sapiens interleukin 4 receptor (IL4R), mRNA
5902	13516	23595	1.85	5.0E-74	11431471	NT	Homo sapiens interleukin 4 receptor (IL4R), mRNA
6120	16014	26132	3.73	5.0E-74	7682263	NT	Homo sapiens KIA00716 gene product (KIA00716), mRNA
6894	16564	26738	2.69	5.0E-74	11345483	NT	Homo sapiens hypothetical protein FLJ13222 (FLJ13222), mRNA
8117	18006	28232	1.88	5.0E-74	Y09420.1	NT	H sapiens mRNA for JIP-1
8117	18006	28232	1.88	5.0E-74	Y09420.1	NT	H sapiens mRNA for JIP-1
278	10243	20063	1.89	4.0E-74	D03675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
834	10781	20611	4.95	4.0E-74	AB028042.1	NT	Homo sapiens mRNA for KIAA1070 protein, partial cds
1010	11814	21682	2.44	4.0E-74	AB028688.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
1010	11814	21683	2.44	4.0E-74	AB028688.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
2027	11018	21808	4.34	4.0E-74	4506162	NT	Homo sapiens proteasome (prosome, macropain) subunit, beta type, 1 (PSMB1), mRNA
2027	11018	21809	4.34	4.0E-74	4506162	NT	Homo sapiens proteasome (prosome, macropain) subunit, beta type, 1 (PSMB1), mRNA
2085	11978	21870	1.21	4.0E-74	AB033564.1	NT	Homo sapiens mRNA for KIAA1168 protein, partial cds
2377	12257	22148	0.99	4.0E-74	AJ006976.1	NT	Homo sapiens PTP gene
3032	12979	22772	4.44	4.0E-74	AJ006976.1	NT	Homo sapiens PTP gene
3483	13369	23204	0.65	4.0E-74	AL16370.2	NT	Homo sapiens chromosome 21 segment HS21O010
3973	13980	23655	1.31	4.0E-74	AL16370.2	NT	Homo sapiens chromosome 21 segment HS21O047
4457	14351	24142	1.57	4.0E-74	AL16370.2	NT	Homo sapiens KIA00689 gene product (KIA00689), mRNA
4512	14405	24192	0.82	4.0E-74	Z17227.1	NT	Homo sapiens mRNA for transmembrane receptor protein
5006	14880	24644	3.76	4.0E-74	4504326	NT	Homo sapiens hydroxyl-Coenzyme A dehydrogenase/3-ketocyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (thiolase protein), beta subunit (HADHB), mRNA
5006	14880	24645	3.76	4.0E-74	4504326	NT	Homo sapiens hydroxyl-Coenzyme A dehydrogenase/3-ketocyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (thiolase protein), beta subunit (HADHB), mRNA
6077	18854		5.03	3.0E-74	AA300378.1	EST_HUMAN	EST13131 Thymus tumor III Homo sapiens cDNA 5' end similar to ribosomal protein L37

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7394	17312	27519	2.42	3.0E-74	M76984.1	EST_HUMAN	EST101132 Subtracted Hippocampus, Striatum (cat. #53205) Homo sapiens cDNA clone HHCPT81
7621	17771	28010	2.22	3.0E-74	AA091493.1	EST_HUMAN	nt017055.t1 NCL CGAP_Pier Homo sapiens cDNA clone IMAGE:1100894.3
942	10867	20714	126.24	2.0E-74	7866467	NT	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GAPD), mRNA
942	10867	20714	126.24	2.0E-74	7866467	NT	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GAPD), mRNA
1158	11071	20016	1.01	2.0E-74	AF020692.1	NT	Human endogenous retrovirus HERV-K147D
1224	11132	20886	1.16	2.0E-74	AI650538.1	EST_HUMAN	w51870.x1 NCL CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2547204.3 similar to SW:GG95_HUMAN
1577	11481	21340	2.84	2.0E-74	4655169	NT	Homo sapiens epidermal growth factor receptor (avian erythroblast leukemia viral (v-erb-b) oncogene homolog) (EGFR) mRNA
1577	11481	21341	2.84	2.0E-74	4655169	NT	Homo sapiens epidermal growth factor receptor (avian erythroblast leukemia viral (v-erb-b) oncogene homolog) (EGFR) mRNA
2558	12430	22323	1.09	2.0E-74	AI557280.1	EST_HUMAN	PT2.L1B.311.f1 tumor2 Homo sapiens cDNA 3'
4637	14815	24982	1.95	2.0E-74	AL356092.1	NT	Novel human gene mapping to chromosome 22
4637	14815	24983	1.95	2.0E-74	AL356092.1	NT	Novel human gene mapping to chromosome 22
4642	14820	24988	1.89	2.0E-74	J02993.1	NT	Human placid, glycoprotein IIb, mRNA, 3' end
5543	19448	25530	1.84	2.0E-74	BE711134.1	EST_HUMAN	RC8.H10578.220505.01.1.C38.H10578 Homo sapiens cDNA
5584	19448	25584	1.98	2.0E-74	11435857	NT	Homo sapiens PDZ-73 protein (PDZ-73/NY-CO-38), mRNA
5584	19448	25584	1.98	2.0E-74	11435857	NT	Homo sapiens PDZ-73 protein (PDZ-73/NY-CO-38), mRNA
5620	19448	25584	2.87	2.0E-74	11435857	NT	Homo sapiens PDZ-73 protein (PDZ-73/NY-CO-38), mRNA
5620	19448	25585	2.87	2.0E-74	11435857	NT	Homo sapiens PDZ-73 protein (PDZ-73/NY-CO-38), mRNA
8219	19448	25585	1.35	2.0E-74	BF000784.1	EST_HUMAN	Homo sapiens PDZ-73 protein (PDZ-73/NY-CO-38), mRNA
8219	19448	25585	1.43	2.0E-74	AB037616.1	NT	60150720471 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3927546.5
8631	16511	26700	1.54	2.0E-74	AA109181.1	EST_HUMAN	Homo sapiens mRNA for KNA1938 protein, partial cds
7358	17316	27523	6.54	2.0E-74	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
5397	19047	25196	1.48	2.0E-74	AF166698.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C004
5653	16590	25196	1.26	2.0E-74	AW816405.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C004
47	10035	19941	0.97	1.0E-74	7857334	NT	Homo sapiens chromosome 21 segment HS21C004
354	10293	20109	3.6	1.0E-74	AF166698.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C004
491	10434	20247	1.16	1.0E-74	AW816405.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C004
467	10439	20252	2.7	1.0E-74	X02344.1	NT	Homo sapiens hypothetical protein FLJ11028 (FLJ11028), mRNA
580	10524	20331	1.36	1.0E-74	4596020	NT	Homo sapiens beta 2 gene
580	10524	20331	1.36	1.0E-74	4596020	NT	Homo sapiens zinc finger protein 289 (ZNF289) mRNA
983	10906	20751	2.17	1.0E-74	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C048
2179	12066	21968	6.16	1.0E-74	AB020050.1	NT	Homo sapiens DNA for Human P2X4, complete cds
3100	13026	22822	5.05	1.0E-74	4759597	NT	Homo sapiens mannosidase, alpha, class 2A, member 1 (MAN2A1), mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3887	13788	23684	4.56	1.0E-74	AF162882.2	NT	Homo sapiens chromosome 21 segment HS21C088
3974	13381	23685	0.9	1.0E-74	BE060300.1	EST_HUMAN	RC2-BT0542-270300-016-06 BT0542 Homo sapiens cDNA
4170	14070	23846	0.9	1.0E-74	BE-687789.1	EST_HUMAN	h37308.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE3213665 3' similar to WP-B05111.12
5112	14080	24754	1.19	1.0E-74	DG3327.1	NT	Homo sapiens DORR1 mRNA, partial cds
6684	16574	26765	1.83	1.0E-74	BE549105.1	EST_HUMAN	801070039P1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE346260 5'
6694	16574	26765	1.83	1.0E-74	BE549105.1	EST_HUMAN	801070039P1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE346260 5'
7112	16595	27182	3.92	1.0E-74	AF214692.1	NT	Homo sapiens tracheal epithelium enriched protein (PLUNC) gene, complete cds
7688	17838	28079	1.31	1.0E-74	11420346	NT	Homo sapiens hypothalamic protein FLJ10783 (FLJ10783), mRNA
8024	18818	29108	1.6	1.0E-74	11417860	NT	Homo sapiens gliothione S-transferase beta 2 (GSTB2), mRNA
8106	18873	29108	2.83	1.0E-74	11417860	NT	Homo sapiens gliothione S-transferase beta 2 (GSTB2), mRNA
8249	12685	21968	4.14	1.0E-74	AB002069.1	NT	Homo sapiens DNA for Human P2XL complete cds
9720	16281		1.36	1.0E-74	AF240796.1	NT	Homo sapiens gliothione S-transferase beta 2 (GSTB2) and gliothione S-transferase beta 1 (GSTB1) genes, complete cds
2007	12475		4.07	8.0E-76	AF176238.1	NT	Homo sapiens DNA cyclinE5 methyltransferase 3B (DNMT3B) mRNA, complete cds
9406	18099		1.67	8.0E-76	AF160302.2	NT	Homo sapiens chromosome 21 segment HS21C092
2273	12157	22065	0.88	6.0E-76	A1817418.1	EST_HUMAN	4285408.1 NCL_CGAP_P221 Homo sapiens cDNA clone IMAGE2417654 3' similar to gb:U14183_cde4
5128	14695		0.86	6.0E-76	A1762285.1	EST_HUMAN	RETROVIRUS-RELATED POLYPROTEIN (HUMAN),
5102	14670	24746	1.04	5.0E-76	BE841305.1	EST_HUMAN	g36063.1 Source: GENBANK Homo sapiens cDNA clone IMAGE2417654 3' similar to TR-Q16377 Q16377.Y.
7395	17513	27520	1.22	5.0E-76	BF662354.1	EST_HUMAN	CHROMOSOME RNA RECOMBINATION MOTIF PROTEIN;
7876	17728	27599	3.1	5.0E-76	A1658623.1	EST_HUMAN	MGC-SN045-080000-004-05 SN0450 Homo sapiens cDNA
107	10088	19003	1.05	4.0E-76	BE081333.1	EST_HUMAN	602169516P1 NIH_MGC_40 Homo sapiens cDNA clone IMAGE4288738 3'
481	10395		1.23	4.0E-76	N36757.1	EST_HUMAN	151612.1 NCL_CGAP_CGS Homo sapiens cDNA clone IMAGE32242390 3' similar to TR-P67361 P67361
1728	11629	21498	1.5	4.0E-76	AW89720.1	EST_HUMAN	HYPOPHYSICAL 20.1 KD PROTEIN;
2818	12747	22540	4.85	4.0E-76	BE-094824.1	EST_HUMAN	QVH-BT0632-270300-078-02 BT0632 Homo sapiens cDNA
67932	16608	28006	4.39	4.0E-76	6579457	NT	g40808.1 Source: GENBANK Homo sapiens cDNA clone IMAGE280656 5'
67932	16603	28084	1.58	4.0E-76	11417946	NT	g40808.1 Source: GENBANK Homo sapiens cDNA clone IMAGE280656 5'
6032	16563	28086	1.55	4.0E-76	11417946	NT	CMD-NN0057-159400-335-411 NN0057 Homo sapiens cDNA
8072	17663	28214	8.72	4.0E-76	7696505	NT	CMD-NN0057-159400-335-411 NN0057 Homo sapiens cDNA
595	10509	20754	2.91	3.0E-76	AF157623.1	NT	80130396P1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE368344 5'
987	10509	20754	2.25	3.0E-76	AF157623.1	NT	Homo sapiens NIPSNAP_C, elegans, homolog 1 (NIPSNAP1), mRNA
							Homo sapiens NIPSNAP_C, elegans, homolog 1 (NIPSNAP1), mRNA
							Homo sapiens myosin, heavy polypeptide 1, skeletal muscle, adult (MYH1), mRNA
							Homo sapiens HTRA serine protease (PRSS11) gene, complete cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1795	11603	21659	1.38	3.0E-76	A3011183.1	NT	Homo sapiens mRNA for KIAA0581 protein, partial cds
2095	11655	21852	1.05	3.0E-76	4807334	NT	Homo sapiens synapsin I (SYNJ1), mRNA
2373	12253	22144	3.86	3.0E-76	4759153	NT	Homo sapiens synapsin-associated protein, 25kD (SNAP-25) mRNA
2948	12016	22711	1.19	3.0E-76	AL193201.2	NT	Homo sapiens chromosome 21 segment HS210001
3162	13071	22877	1.33	3.0E-76	A3011183.1	NT	Homo sapiens mRNA for KIAA0581 protein, partial cds
3306	13227	23031	1.01	3.0E-76	M72383.1	NT	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
3306	13227	23031	1.01	3.0E-76	M72383.1	NT	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
4077	18670	23745	1.43	3.0E-76	D67275.1	NT	Homo sapiens DNA for amplified precursor protein, complete cds
4336	14233	24015	0.36	3.0E-76	7862423	NT	Homo sapiens KIAA0671 protein (KIAA0671), mRNA
6058	16041	26183	1.33	3.0E-76	11526319	NT	Homo sapiens HIR (hirsone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA
6058	16041	26184	1.33	3.0E-76	11526319	NT	Homo sapiens HIR (hirsone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA
8234	15100	26246	3.83	3.0E-73	7852203	NT	Homo sapiens KIAA0623 gene product (KIAA0623), mRNA
8234	15100	26249	3.83	3.0E-73	7852203	NT	Homo sapiens KIAA0623 gene product (KIAA0623), mRNA
8464	16583	26522	2.82	3.0E-73	4685633	NT	Homo sapiens Oncogene TM (TM) mRNA
8464	16583	26523	2.82	3.0E-73	4685633	NT	Homo sapiens Oncogene TM (TM) mRNA
7163	17070	27259	1.23	3.0E-73	11420604	NT	Homo sapiens Chordin TM (TM) mRNA
5460	15400		1.5	2.0E-75	AV74650.1	EST_HUMAN	AV734650 cDNA Homo sapiens cDNA clone cABE02.5
7082	16569	27162	1.73	2.0E-75	AB11783.1	EST_HUMAN	q091462.x1 NC1_OGAP_104 Homo sapiens cDNA clone IMAGE:1915698 3' similar to TR_Q06386 Q06386 POLYOM. GENE.
2285	12739	22037	5.09	1.0E-75	AY108135.1	EST_HUMAN	X90402.x1 NC1_OGAP_104 Homo sapiens cDNA clone IMAGE:2302707 3' similar to contains PFR7.11
2916	12843	22844	3.17	1.0E-75	X52221.1	NT	H.sapiens ERG22 gene, exons 1 & 2 (partial)
6903	16781		4.13	1.0E-76	AA38970.1	EST_HUMAN	257703.s1 Source: testis, NM1 Homo sapiens cDNA clone IMAGE:726465 3' similar to gb:MT3632 403
7423	17250	27466	3.73	1.0E-76	BF313545.1	EST_HUMAN	RIBOSOMAL PROTEIN S17 (HUMAN)
7423	17250	27466	3.73	1.0E-76	BF313545.1	EST_HUMAN	001900294F1 NIH.MGC_19 Homo sapiens cDNA clone IMAGE:4126678 5'
8257	18137		3.56	1.0E-76	AA694377.1	EST_HUMAN	ac777008.s1 Stathemine lmg (MS7210) Homo sapiens cDNA clone IMAGE:805588 3'
8441	18315	28573	2.6	1.0E-75	AF223391.1	NT	Homo sapiens channel chemical alphas1E subunit (CANA1E) gene, exons 7-46, and partial cds, alternatively spliced
8256	15700	24852	1.86	1.0E-75	BF684192.1	EST_HUMAN	001437130F1 NIH.MGC_72 Homo sapiens cDNA clone IMAGE:5922303 5'
38	10028	15825	1.46	9.0E-76	AI652648.1	EST_HUMAN	W83010.x1 NC1_OGAP_G05 Homo sapiens cDNA clone IMAGE:2307163 3' similar to TR_Q75335 Q75335 TMF1.

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38	10026	19826	1.45	9.0E-76	AI652648.1	EST_HUMAN	W630101x1 NC1_CGAP_G08 Homo sapiens cDNA clone IMAGE:2307163 3' similar to TR-075238 075235 TRAMP1 ;
2394	12244		1.16	9.0E-76	AA702415.1	EST_HUMAN	265007.51 Scores_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:447541 3'
7697	17547	27770	23.8	9.0E-76	MT2337.1	NT	Homo keratin Heavy subunit mRNA, complete cds
923	10848	20095	1.60	8.0E-76	4504374	NT	Homo sapiens H factor 1 (complement) (HF1) mRNA
923	10848	20096	1.60	8.0E-76	4504374	NT	Homo sapiens H factor 1 (complement) (HF1) mRNA
2890	12807	22603	1.06	8.0E-76	7708724	NT	Homo sapiens mediator (Sur2) mRNA
5744	15652	25790	5.38	8.0E-76	11421442	NT	Homo sapiens LIM domain kinase 1 (LIMK1) mRNA
8421	16282	29443	1.3	8.0E-76	11438219	NT	Homo sapiens serine/threonine kinase 2 (STK2) mRNA
8057	17848	28198	6.44	8.0E-76	10442821	NT	Homo sapiens baculoviral IAP repeat-containing 6 (BIRC6) mRNA
8636	19207		1.44	8.0E-76	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330) mRNA
759	10659	20527	4.12	7.0E-76	5018692	NT	Homo sapiens dihydropyrimidine dehydrogenase (E3 component of pyruvate dehydrogenase complex, 2-oxo- glutarate complex, branched chain keto acid dehydrogenase complex) (DLD) mRNA
3294	13177	22975	2.64	7.0E-76	AF094940.1	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds
3300	13163	22982	7.08	7.0E-76	4505052	NT	Homo sapiens lymphocyte antigen 75 (LY75) mRNA, and translated products
5293	19216	23017	1.1	7.0E-76	4157919	NT	Homo sapiens core-binding factor, runt domain, alpha subunit 2; translocated to, t, cyclin D-related (CBF421) mRNA
4275	14174	23951	4.3	7.0E-76	4507184	NT	Homo sapiens saposin reductase (7,8-dihydrocholesterol-NADPH: oxidoreductase) (SPR) mRNA
4275	14174	23952	4.3	7.0E-76	4507184	NT	Homo sapiens saposin reductase (7,8-dihydrocholesterol-NADPH: oxidoreductase) (SPR) mRNA
1214	11122		10.95	6.0E-76	BE596233.1	EST_HUMAN	601312016P1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3685757 5'
8781	17970	28164	2.89	6.0E-76	BE272501.1	EST_HUMAN	601142253F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3685757 5'
1899	11795	21673	3.69	5.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
1899	11795	21674	3.69	5.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
1899	11795	21675	3.69	5.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
7759	17609	27834	5.6	4.0E-76	D81925.1	EST_HUMAN	HUM178001B Human fetal brain (Tfujilwara) Homo sapiens cDNA clone GENL-178001 5'
7759	17609	27835	5.6	4.0E-76	D81925.1	EST_HUMAN	HUM178001B Human fetal brain (Tfujilwara) Homo sapiens cDNA clone GENL-178001 5'
613	10549	20390	1.78	3.0E-76	BF516292.1	EST_HUMAN	UHH-BW1-anz-B-04-CUL1 NC1_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3083862 3'
613	10549	20390	1.78	3.0E-76	BF516292.1	EST_HUMAN	UHH-BW1-anz-B-04-CUL1 NC1_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3083862 3'
1591	11485	21345	2.78	3.0E-76	4503479	NT	Homo sapiens eukaryotic translation elongation factor 1 beta 2 (EEF1B2) mRNA
1591	11485	21346	2.78	3.0E-76	4503479	NT	Homo sapiens eukaryotic translation elongation factor 1 beta 2 (EEF1B2) mRNA
3382	13300	23009	4.18	3.0E-76	BF375680.1	EST_HUMAN	RC5-ST0300-180100-053-A03 ST0300 Homo sapiens cDNA
3382	13300	23100	4.18	3.0E-76	BF375680.1	EST_HUMAN	RC5-ST0300-180100-053-A03 ST0300 Homo sapiens cDNA
8204	15084	23104	9.13	3.0E-76	Z41314.1	EST_HUMAN	HSC2D042 normalized infant brain cDNA Homo sapiens cDNA clone c-2404 3'

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5942	15748	25861	7.85	3.0E-76	AF286598.1	NT	Homo sapiens angiotensin binding protein 1 mRNA, complete cds
6737	16616	28606	1.92	3.0E-76	N12071.1	EST_HUMAN	Y50410.1 Soares_melroy28616 Homo sapiens cDNA clone IMAGE:271842 5'
7602	17453	27687	3.2	3.0E-76	AW299533.1	EST_HUMAN	z54901.x1 NCBI_GCGP_Kid1 Homo sapiens cDNA clone IMAGE:277000 3'
7615	17466	27684	1.32	3.0E-76	AA442069.1	EST_HUMAN	z54901.x1 Soares_16616 Homo sapiens cDNA clone IMAGE:277000 3'
7615	17466	27685	1.32	3.0E-76	AA442069.1	EST_HUMAN	z54901.x1 Soares_16616 Homo sapiens cDNA clone IMAGE:277000 3'
8014	19537	25062	2.13	3.0E-76	AW967984.1	EST_HUMAN	EST380059 IMAGE resequences, MAGJ Homo sapiens cDNA
8120	19745	24895	3.75	3.0E-76	AW966454.1	EST_HUMAN	EST380059 IMAGE resequences, MAGJ Homo sapiens cDNA
280	10245	20065	1.22	2.0E-76	D64256.1	NT	Human mRNA for possible protein TFRDII, complete cds
339	10298	20112	3.66	2.0E-76	D64295.1	NT	Human mRNA for possible protein TFRDII, complete cds
339	10298	20113	3.66	2.0E-76	D64295.1	NT	Human mRNA for possible protein TFRDII, complete cds
453	10397		2.17	2.0E-76	4657662	NT	Homo sapiens immunoglobulin (CD79A) binding protein 1 (GBPI1) mRNA
575	10513	20320	1.07	2.0E-76	463944	NT	Homo sapiens glucagon (GCG) mRNA
1014	10932	20778	1.03	2.0E-76	4758053	NT	Homo sapiens cAMP responsive element binding protein 1 (CREB1) mRNA
1518	11423	21281	1.53	2.0E-76	4694028	NT	Homo sapiens GMP guanoside activator protein (GV2A) mRNA
1518	11423	21282	1.53	2.0E-76	4694028	NT	Homo sapiens GMP guanoside activator protein (GV2A) mRNA
1806	11782	21638	1.43	2.0E-76	AA263954.1	EST_HUMAN	z54901.x1 Singapore schizo brain S11 Homo sapiens cDNA clone IMAGE:701925 3'
2811	12740	22536	2.83	2.0E-76	P23268	SWISSPROT	FACTORY RECEPTOR-LIKE PROTEIN FRS
3257	13180	22978	2.01	2.0E-76	AA445692.1	EST_HUMAN	z54902.x1 Soares_16616 Homo sapiens cDNA clone IMAGE:760968 3' similar to SW/ITB5_HUMAN
3257	13180	22980	2.01	2.0E-76	AA445692.1	EST_HUMAN	z54902.x1 Soares_16616 Homo sapiens cDNA clone IMAGE:760968 3' similar to SW/ITB5_HUMAN
4043	12455	20065	0.94	2.0E-76	D64255.1	NT	Human mRNA for possible protein TFRDII, complete cds
4867	17477	24527	6.33	2.0E-76	AW879618.1	EST_HUMAN	Human mRNA for possible protein TFRDII, complete cds
5088	14088	24710	1.25	2.0E-76	5031660	NT	Homo sapiens EGF-like repeats and disordered-like domains 3 (EDL3), mRNA
5403	15374	25432	4.74	2.0E-76	AB029004.1	NT	Homo sapiens mRNA for KIAA1087 protein, partial cds
6518	16377	25554	1.79	2.0E-76	11427410	NT	Homo sapiens TFCR6 protein (HSTPCR6P), mRNA
7898	17748	27988	3.28	2.0E-76	11437211	NT	Homo sapiens similar to ribosomal protein S26 (H. sapiens) (LOC83150), mRNA
8253	18172	28476	2.76	2.0E-76	7646807	NT	Homo sapiens HIRA interacting protein 4 (dna-like) (HIRP4), mRNA
4200	14100	23881	2.18	1.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
4200	14100	23882	2.18	1.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
5345	15266	25093	5.29	1.0E-76	BC796537.1	EST_HUMAN	80159959P1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:394302 5'
6137	15984	26116	3.98	9.0E-77	BC886525.1	EST_HUMAN	80152459P1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:39137 5'
4421	14315	24101	1.65	8.0E-77	BF205181.1	EST_HUMAN	80180620P1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:410903 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5347	15268	25055	2.46	8.0E-77	490220	NT	Homo sapiens prolactinase (prolactin, macropain) 28S subunit, non-ATPase, 7 (Mox44 homolog) (PSMD7) mRNA
6951	18578	28681	2.12	8.0E-77	AA01970.1	EST_HUMAN	z626202.11 Soares retina N24-HR Homo sapiens cDNA clone IMAGE:393578 5'
8651	18578	28852	2.12	8.0E-77	AA01970.1	EST_HUMAN	z626202.11 Soares retina N24-HR Homo sapiens cDNA clone IMAGE:393578 5'
9771	19269	25232	7.25	8.0E-77	R00245.1	EST_HUMAN	y69104.x1 Soares fetal liver spleen 11NLS Homo sapiens cDNA clone IMAGE:123007 3' similar to contains MER10 repetitive element:
1887	17183	21650	3.28	7.0E-77	AA626755.1	EST_HUMAN	z491401.x1 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:74592 3'
2360	12240	22135	2.1	7.0E-77	405944	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide E (280) (POLR2E) mRNA
2360	12240	22137	2.1	7.0E-77	405944	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide E (280) (POLR2E) mRNA
262	10227	20043	4.25	6.0E-77	450400	NT	Homo sapiens interferon (alpha, beta and omega) receptor 2 (IFNA2) mRNA
1125	11040	20882	0.9	6.0E-77	AW597753.1	EST_HUMAN	EST396823 IMAGE: ressequencing, IMAGE Homo sapiens cDNA
1524	11429	21287	17.64	6.0E-77	A2040983.1	EST_HUMAN	q67112.x1 Soares, fetal lung, NHL1971 Homo sapiens cDNA clone IMAGE:1745003 3'
1216	11124	20973	1.78	5.0E-77	AF041015.1	NT	7 Homo sapiens glucokinase (GCK) gene, exon 2
1337	11243	21101	1.16	5.0E-77	4557250	NT	Homo sapiens dilute/leg and metalloproteinase domain 10 (ADAM10) mRNA
2790	12968	22462	0.97	5.0E-77	493160	NT	Homo sapiens cullin 1 (CUL1) mRNA
4695	14453	24260	2.02	5.0E-77	5031650	NT	Homo sapiens EGF-like repeats and discordin 1-like domain 3 (EDIL3) mRNA
4695	14453	24261	2.02	5.0E-77	5031650	NT	Homo sapiens EGF-like repeats and discordin 1-like domain 3 (EDIL3) mRNA
4853	14733	24261	2.05	5.0E-77	AL043953.1	EST_HUMAN	DKFZ454G1728.11 A31 (corynor) beta3 Homo sapiens cDNA clone DKFZ454G1728 5'
8573	16753	28547	1.35	5.0E-77	11428348	NT	Homo sapiens 3-hydroxyacyl-CoA:Coenzyme A hydrolase (H3H3) mRNA
8573	16753	28547	1.35	5.0E-77	11428348	NT	Homo sapiens 3-hydroxyacyl-CoA:Coenzyme A hydrolase (H3H3) mRNA
7519	17338	27943	2.85	5.0E-77	11421028	NT	Homo sapiens sorting nexin 5 (SNX5) mRNA
7519	17338	27944	2.85	5.0E-77	11421028	NT	Homo sapiens sorting nexin 5 (SNX5) mRNA
7560	17840	28080	1.95	5.0E-77	AB022987.1	NT	Human mRNA for KIAA0258 gene, partial cds
1926	11824	21705	1.12	3.0E-77	5730039	NT	Human sapiens CYP17 gene, 5' end
1926	11824	21706	1.12	3.0E-77	5730039	NT	Human sapiens CYP17 gene, 5' end
8246	18129	28377	3.31	2.0E-77	BF336971.1	EST_HUMAN	Homo sapiens SET domain and major transposase fusion gene (SETMAR) mRNA
1330	11237	20953	1.71	2.0E-77	AV754617.1	EST_HUMAN	PV3-MT0078-090900-005-403 MT0078 Homo sapiens cDNA
1414	11320	21185	1.73	2.0E-77	AW597712.1	EST_HUMAN	AV754617 MDS Homo sapiens cDNA clone MOSB110 5'
2044	11935	21830	0.84	2.0E-77	L41826.1	NT	RC3-BN0053 170200 011-101 BN0053 Homo sapiens cDNA
2056	11948	21842	2.54	2.0E-77	7700319	NT	Homo sapiens CYP17 gene, 5' end
2549	12724	22312	2.02	2.0E-77	AB037836.1	NT	Homo sapiens CG-19 protein (LOC51634), mRNA
2549	12724	22312	2.02	2.0E-77	AB037836.1	NT	Homo sapiens mRNA for KIAA1415 protein, partial cds
2546	12724	22313	2.02	2.0E-77	AB037836.1	NT	Homo sapiens mRNA for KIAA1415 protein, partial cds

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Table 4
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Probe SEQ ID NC:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Mean Similar (Top Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3947	13355	23029	1.33	2.0E-77	BE043616.1	EST_HUMAN	h04305.x1 Source_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3040113 3' similar to SW-GAGC2_HUMAN P1024 RETROVIRUS-RELATED GAG POLYPROTEIN ;
4315	14312	23895	0.89	2.0E-77	A1819519.1	EST_HUMAN	w02202.x1 NCL_GGAP_Bns5 Homo sapiens cDNA clone IMAGE:3284468 3' similar to TR.Q65245
4315	14312	23895	0.89	2.0E-77	A1819519.1	EST_HUMAN	O65245 F21E10.7 PROTEIN ;
4492	14366		3.48	2.0E-77	4504068	NT	O65245 F21E10.7 PROTEIN ; Homo sapiens glutamate-oxaloacetate transaminase 2, mitochondrial (aspartate aminotransferase 2) (GOT2), nuclear gene encoding mitochondrial protein, mRNA
4650	14545	24334	3.80	2.0E-77	AA683025.1	EST_HUMAN	n95912.s1 NCL_GGAP_P2 Homo sapiens cDNA clone IMAGE:1168538 similar to SW:RL28_HUMAN
5625	15540	25629	1.8	2.0E-77	BE29540.1	EST_HUMAN	P47914.605 RIBOSOMAL PROTEIN L20, [1] contains element MSR1 repetitive element ;
5745	15553	25761	1.34	2.0E-77	BE1787143.1	EST_HUMAN	001116652F1 NHL_MGC_17 Homo sapiens cDNA clone IMAGE:3029435 5'
6257	16123	28276	12.74	2.0E-77	A1833003.1	EST_HUMAN	001476022F1 NHL_MGC_68 Homo sapiens cDNA clone IMAGE:3879505 5'
7469	17359	27564	4.99	2.0E-77	U63321.1	NT	G13311 TAXI-BINDING PROTEIN TXBP19, [1] ;
7469	17359	27564	4.99	2.0E-77	U63321.1	NT	Human protein kinase G substrate BXX-H (PRKGSH) gene, exon 7
37	10024	19921	0.97	1.0E-77	AB033102.1	NT	Human protein kinase G substrate BXX-H (PRKGSH) gene, exon 7
37	10024	19922	0.97	1.0E-77	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
271	10237	20064	1.87	1.0E-77	4502169	NT	Homo sapiens amyloid beta (A4) precursor protein (protease neurin-L, Alzheimer disease) (APP), mRNA
271	10237	20065	1.87	1.0E-77	4502169	NT	Homo sapiens amyloid beta (A4) precursor protein (protease neurin-L, Alzheimer disease) (APP), mRNA
887	12679	20335	4.95	1.0E-77	4502169	NT	Homo sapiens amyloid beta (A4) precursor protein (protease neurin-L, Alzheimer disease) (APP), mRNA
887	12679	20336	4.95	1.0E-77	4502169	NT	Homo sapiens amyloid beta (A4) precursor protein (protease neurin-L, Alzheimer disease) (APP), mRNA
2394	12272	22168	1.22	1.0E-77	AB02024.1	NT	Homo sapiens mRNA for KIAA1107 protein, complete cds
3071	12935	22727	2.52	1.0E-77	4903300	NT	Homo sapiens 2,4-dienoyl CoA reductase 1, mitochondrial (DECR1), mRNA
4256	14165	23830	2.89	1.0E-77	7706298	NT	Homo sapiens CG-60 protein (LOC51625), mRNA
4423	14317	24203	14.73	1.0E-77	AJ25041.1	NT	Homo sapiens 650 kb contig between AML1 and ORF1 on chromosome 21q22.5 segment 1f3
4452	14445	24229	1.95	1.0E-77	6552322	NT	Homo sapiens breast cancer 1, early onset (BRCA1), transcript variant R1A1+exon, mRNA
5179	15043	24810	2.89	1.0E-77	AW175254.1	EST_HUMAN	CMV4.6 Human cardiac muscle expression library/Homo sapiens cDNA clone 4151935 similar to CMV4.6 Cardemphopathy associated gene 5

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5610	15525	25507	1.93	1.0E-77	AF086944.1	NT	Homo sapiens dynactin 1 (DCTN1) gene, exons 27 and 28
5610	15525	25508	1.93	1.0E-77	AF086944.1	NT	Homo sapiens dynactin 1 (DCTN1) gene, exons 27 and 28
5688	15597	25666	1.56	1.0E-77	M25944.1	NT	Human von Willebrand factor gene, exon 20
8197	15957	26069	11.39	1.0E-77	5881412	NT	Human von Willebrand factor gene, exon 20
8197	17892	26069	1.22	1.0E-77	AB023696.1	NT	Homo sapiens alpha-1-antitrypsin (AAT) gene, complete cds
8002	17892	26064	1.22	1.0E-77	AB023696.1	NT	Homo sapiens alpha-1-antitrypsin (AAT) gene, complete cds
8013	17893	28108	2.53	9.0E-78	AF073302.1	EST_HUMAN	Homo sapiens alpha-1-antitrypsin (AAT) gene, complete cds
5860	15768	25507	2.97	8.0E-78	AF047051.1	EST_HUMAN	Homo sapiens alpha-1-antitrypsin (AAT) gene, complete cds
5860	15768	25508	2.97	8.0E-78	AF047051.1	EST_HUMAN	Homo sapiens alpha-1-antitrypsin (AAT) gene, complete cds
80	10064	19881	1.93	8.0E-78	AF018789.1	EST_HUMAN	Human alpha-1-antitrypsin (AAT) gene, complete cds
80	10064	19882	1.93	8.0E-78	AF018789.1	EST_HUMAN	Human alpha-1-antitrypsin (AAT) gene, complete cds
6950	15855		2.51	8.0E-78			Homo sapiens alpha-1-antitrypsin (AAT) gene, complete cds
2111	10182	19968	1.1	1.1E-24	11422460	NT	Homo sapiens alpha-1-antitrypsin (AAT) gene, complete cds
2515	12389	22261	4.1	5.0E-78	AF073241.1	EST_HUMAN	Homo sapiens alpha-1-antitrypsin (AAT) gene, complete cds
3338	13289	23068	3.81	5.0E-78	M65956.1	NT	Homo sapiens alpha-1-antitrypsin (AAT) gene, complete cds
3023	15243	25048	2.39	5.0E-78	AF068536.1	NT	Homo sapiens alpha-1-antitrypsin (AAT) gene, complete cds
5422	15243	25048	9.35	5.0E-78	11416663	NT	Homo sapiens alpha-1-antitrypsin (AAT) gene, complete cds
6244	16710	26582	2.17	5.0E-78	AF093120.1	EST_HUMAN	Homo sapiens alpha-1-antitrypsin (AAT) gene, complete cds
7248	17125	27318	6.5	5.0E-78	M06089.1	NT	Human alpha-1-antitrypsin (AAT) gene, complete cds
7249	17126	27319	3.75	5.0E-78	BC060893.1	EST_HUMAN	Homo sapiens alpha-1-antitrypsin (AAT) gene, complete cds
1502	11409	21265	1.6	4.0E-78	AL356941.1	NT	Novel human gene mapping to chromosome 22
1629	11633	21393	1.93	4.0E-78	AB065094.1	EST_HUMAN	w97412.x1 NC_004711 Homo sapiens alpha-1-antitrypsin (AAT) gene, complete cds
2270	12154	22053	2.21	4.0E-78	AF107405.1	NT	Human alpha-1-antitrypsin (AAT) gene, complete cds
4227	14126	23699	1.39	4.0E-78	7666879	NT	Homo sapiens alpha-1-antitrypsin (AAT) gene, complete cds
4664	14590	24340	1.27	4.0E-78	4505900	NT	Homo sapiens alpha-1-antitrypsin (AAT) gene, complete cds
4664	14590	24341	1.27	4.0E-78	4505900	NT	Homo sapiens alpha-1-antitrypsin (AAT) gene, complete cds
7967	17817	28058	1.94	4.0E-78	11590151	NT	Homo sapiens alpha-1-antitrypsin (AAT) gene, complete cds
7967	17817	28059	1.94	4.0E-78	11590151	NT	Homo sapiens alpha-1-antitrypsin (AAT) gene, complete cds
8721	18938	28622	1.97	4.0E-78	AF169148.1	NT	Homo sapiens alpha-1-antitrypsin (AAT) gene, complete cds
8814	18966	28944	3	4.0E-78	X05844.1	NT	Human transforming growth factor-beta precursor gene, exons 4-5 (end joined mature peptide)
9684	19224	25239	2.85	4.0E-78	AF011399.1	NT	Homo sapiens alpha-1-antitrypsin (AAT) gene, complete cds
155	10729	19944	1.6	3.0E-78	AF096501.1	NT	Homo sapiens alpha-1-antitrypsin (AAT) gene, complete cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
165	10139	19945	1.6	3.0E-78	AF056901.1	NT	Homo sapiens cRF1 gene, complete cds
3178	13103	22905	0.91	3.0E-78	4607164.1	NT	Homo sapiens nuclear antigen Sp100 (SP100) mRNA
4018	13657	23436	0.93	3.0E-78	4607334.1	NT	Homo sapiens synapjanin 1 (SYNJ1), mRNA
7802	17732	28478	5.65	3.0E-78	BE144765.1	EST_HUMAN	CM6-HT10160-04-099-065-c07 HT10180 Homo sapiens cDNA
8349	18238	28478	5.65	3.0E-78	BE16618.1	EST_HUMAN	CM6-HT10367-150206-114-069 HT10367 Homo sapiens cDNA
3953	13010		2.28	2.0E-78	BC1493.1	NT	Homo sapiens Dna V collagen alpha 5 chain (COL4A5) gene, exon 20
3952	13841		1.08	2.0E-78	A311972.1	EST_HUMAN	EST163583, Jurkat T-cells VI Homo sapiens cDNA 5' end
6412	16274	26435	1.46	2.0E-78	AY142306.1	EST_HUMAN	UHLF-BK0-0465-10-0-U1.1 NH MSG_36 Homo sapiens cDNA clone IMAGE:3054139 5'
6412	16274	26436	1.46	2.0E-78	AY142306.1	EST_HUMAN	UHLF-BK0-0465-10-0-U1.1 NH MSG_36 Homo sapiens cDNA clone IMAGE:3054139 5'
6517	16405	26654	3.88	2.0E-78	BC59600.1	EST_HUMAN	UHLF-BK0-0465-10-0-U1.1 NH MSG_36 Homo sapiens cDNA clone IMAGE:3054139 5'
6657	16557	26761	2.73	2.0E-78	AY141477.1	EST_HUMAN	AY171417.1 D59 Homo sapiens cDNA clone D59A170 5'
6621	16769	26961	1.94	2.0E-78	A057506.1	EST_HUMAN	P21.L6 B077 tunic2 Homo sapiens cDNA 3'
6621	16799	26962	1.84	2.0E-78	A057506.1	EST_HUMAN	P21.L6 B077 tunic2 Homo sapiens cDNA 3'
8429	18303	28559	4.5	2.0E-78	AI197857.1	EST_HUMAN	q50M5.ut NO, COG6, Brn25 Homo sapiens cDNA clone IMAGE:165961 3' similar to WIP50.1
8487	18340	28605	3.28	2.0E-78	A05951.1	EST_HUMAN	CG6325 PROTEIN KINASE 1
5247	15170	24943	2.9	1.0E-78	11417304	NT	28481251 Soares testis liver spleen NHL5 Homo sapiens cDNA clone IMAGE:295623 3'
6743	16922		1.86	1.0E-78	U52373.1	NT	Homo sapiens GAP-like protein (LOC51300), mRNA
9189	18924	28350	5.14	1.0E-78	11430460	NT	Human serine/threonine kinase M5B (m5b) mRNA, complete cds
9294	18986	28327	1.26	1.0E-78	11435903	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
4900	14488	24274	4.46	9.0E-79	11628991	NT	Homo sapiens similar to lymphocyte activation-associated protein (H sapiens) [LOC38140], mRNA
4765	14643	24431	2.48	9.0E-79	BC000837.1	EST_HUMAN	Homo sapiens perlecan (PPV), mRNA
5335	15255	28078	12.03	9.0E-79	A0228070.1	NT	RC3-BN0074-090300-014-c12 BN0074 Homo sapiens cDNA
						NT	Homo sapiens mRNA for activator of S phase Kinase, complete cds
5827	15733	28644	2.18	9.0E-79	5454145	NT	Homo sapiens ubiquitin-conjugating enzyme E2C 3 (homologous to yeast UBC4/5) [UBC2E3] mRNA
7243	17120	27315	4.56	9.0E-79	A02855.1	NT	Homo sapiens casein kinase II alpha subunit mRNA, complete cds
7243	17120	27315	4.56	9.0E-79	A02855.1	NT	Homo sapiens casein kinase II alpha subunit mRNA, complete cds
7953	17803	28042	1.31	9.0E-79	AF093246.1	NT	Homo sapiens zinc finger protein 216 splice variant 1 (ZNF210) mRNA, complete cds
7953	17803	28043	1.31	9.0E-79	AF093246.1	NT	Homo sapiens zinc finger protein 216 splice variant 1 (ZNF210) mRNA, complete cds
8419	15203	28547	1.82	9.0E-79	AY008273.1	NT	Homo sapiens TRAF6-regulated IKK activator 1 beta UtrA mRNA, complete cds
8419	15203	28547	1.82	9.0E-79	AY008273.1	NT	Homo sapiens TRAF6-regulated IKK activator 1 beta UtrA mRNA, complete cds
8802	18616	28906	2.82	9.0E-79	11423827	NT	Homo sapiens suppressor of white apicron homolog 2 (SWAP2), mRNA
8802	18616	28907	2.82	9.0E-79	11423827	NT	Homo sapiens suppressor of white apicron homolog 2 (SWAP2), mRNA
9584	18947	28213	1.49	9.0E-79	11417677	NT	Homo sapiens gamma-glutamyltransferase 1 (GGT1), mRNA

Table 4

Probe SEQ ID NC:	Exon SEQ ID NC:	ORF SEQ ID NC:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
3692	13566	23362	1.2	8.0E-70	AI1592.0.2	NT	Homo sapiens chromosome 21 segment H521C010
4301	14237	24260	0.94	8.0E-70	U128476.1	NT	Human mRNA for KIAA0455 gene, complete cds
4301	14237	24070	0.94	8.0E-70	U28476.1	NT	Human mRNA for KIAA0455 gene, complete cds
9107	15097	24690	1.4	8.0E-76	8667387.1	NT	Homo sapiens perlecan (Perlecanin) homolog 3 (PER3), mRNA
3274	13138	22441	6.85	7.0E-79	BE510648.1	EST_HUMAN	00147270217.NH.MGC: 581 Homo sapiens cDNA clone IMAGE:3875657.3 39464.41 Soares, F.H., spleen, IVF-LS. S1 Homo sapiens cDNA clone IMAGE:489568.3 similar to TRQ316408.Q16408 NEUTRAL PROTEASE-LARGE SUBUNIT1;
6760	18027		1.29	8.0E-76	AA666626.1	EST_HUMAN	Homo sapiens chromosome 21 segment H521C006
9040	19501	28691	4.15	8.0E-70	AI103822.2	NT	Homo sapiens chromosome 21 segment H521C082
3130	13564		1.12	4.0E-79	8622325.1	EST_HUMAN	001874522P.NH.MGC: 54 Homo sapiens cDNA clone IMAGE:4701246.5 801874522P.NH.MGC: 54 Homo sapiens cDNA clone IMAGE:4701246.5
9112	10272		1.33	4.0E-79	BF1210869.1	EST_HUMAN	Homo sapiens intercell short isoform (ITSN) mRNA, complete cds
962	10865	20733	2.88	3.0E-79	AF124488.1	NT	Homo sapiens catenin short isoform (ITSN) mRNA, complete cds
3060	12587	22776	1.36	3.0E-79	U05401.1	NT	Human zinc finger protein ZNF131 mRNA, partial cds
5291	15212	25011	4.52	3.0E-79	AI10322.1	NT	Homo sapiens MSTP016 (MST016) mRNA, complete cds
5509	15424	25468	1.71	3.0E-79	AB502089.1	NT	Homo sapiens mRNA for KIAA0892 protein, partial cds
5525	15442	25508	3.47	3.0E-79	AI126770.1	NT	Homo sapiens retin-1 (NTRN1), mRNA
5525	15442	25508	3.47	3.0E-79	AI126770.1	NT	Homo sapiens retin-1 (NTRN1), mRNA
8200	16800	28091	3.28	3.0E-79	AB014520.1	NT	Homo sapiens mRNA for KIAA0620 protein, partial cds
8200	16800	28091	3.28	3.0E-79	AB014520.1	NT	Homo sapiens mRNA for KIAA0620 protein, partial cds
618	10555	20367	1.05	2.0E-79	BE370626.1	EST_HUMAN	001180419P2.NH.MGC: 53 Homo sapiens cDNA clone IMAGE:3951107.57
912	10836	20985	1.14	2.0E-76	4757841.1	EST_HUMAN	Homo sapiens BCL-2-like 2 (BCL2.L2) mRNA
1019	10837		1.43	2.0E-76	AI23744.1	EST_HUMAN	00180471.NC.GAP: P28 Homo sapiens cDNA clone IMAGE:118665.3 18180471.NC.GAP: P28 Homo sapiens cDNA clone IMAGE:118665.3
2101	11880	21689	14.14	2.0E-79	4395865.1	NT	Homo sapiens phosphodiesterase 8A, cGMP-specific, rat, alpha (PDE8A), mRNA
2101	11880	21689	14.14	2.0E-79	4395865.1	NT	Homo sapiens phosphodiesterase 8A, cGMP-specific, rat, alpha (PDE8A), mRNA
2146	12034	21931	0.99	2.0E-79	AJ271408.1	NT	Homo sapiens mRNA for Fae-associated factor, FAF1 (Faf1), mRNA
2255	12451	22049	1.84	2.0E-79	AF124193.1	NT	Homo sapiens mRNA for Fae-associated factor, FAF1 (Faf1), mRNA
3838	13749	23542	0.86	2.0E-70	AF170492.1	NT	Homo sapiens hepatocellular carcinoma-associated antigen 88 (HCA88) mRNA, complete cds
4074	13976	23854	1.17	2.0E-70	AJ271403.1	NT	Homo sapiens chloride channel CLC4 (CLC4) mRNA, complete cds
4590	14478	24265	0.95	2.0E-70	AI103203.2	NT	Homo sapiens mRNA for Fae-associated factor, FAF1 (Faf1), mRNA
6251	15117	25270	1.83	2.0E-79	7382478.1	NT	Homo sapiens chromosome 21 segment H521C006
6251	15117	25271	1.83	2.0E-79	7382478.1	NT	Homo sapiens Rho GTPase activating protein 6 (ARHGAP6), transcript variant 4, mRNA
6556	15834	27023	2.6	2.0E-79	7382479.1	NT	Homo sapiens Rho GTPase activating protein 6 (ARHGAP6), transcript variant 4, mRNA
7608	17558	27696	1.44	2.0E-70	11427428.1	NT	Homo sapiens Rho GTPase activating protein FL11005 (FLJ11005), mRNA
7608	17558	27696	1.44	2.0E-70	S72869.1	NT	H4D105170 putative cytoskeletal protein (human, thyroid, mRNA, 3011 nt)
7608	17558	27696	1.44	2.0E-70	S72869.1	NT	H4D105170 putative cytoskeletal protein (human, thyroid, mRNA, 3011 nt)

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8391	18287	28516	4.22	2.0E-76	BE064386.1	EST_HUMAN	RC4-BT0310-110000-016-F10 BT0310 Homo sapiens cDNA
8391	18287	28517	4.22	2.0E-76	BE064386.1	EST_HUMAN	RC4-BT0310-110000-016-F10 BT0310 Homo sapiens cDNA
8078	15066	24888	2.6	2.0E-76	7692357	NT	Homo sapiens KIA0076 protein (KIA0076), mRNA
9161	18007	23341	4.23	2.0E-76	AB020640.1	NT	Homo sapiens mRNA for KIA00833 protein, partial cds
8391	19050	25307	1.96	2.0E-76	11418322	NT	Homo sapiens cadherin EGF-LAM even-skip C-type receptor 1 (CELSR1), mRNA
5571	19456		2.78	1.0E-76	BF363071.1	EST_HUMAN	MFO-NN0087-200900-07-F10 NN0087 Homo sapiens cDNA
8884	18704	28666	2.74	1.0E-76	BF087405.1	EST_HUMAN	QY241H540-120900-358-J05 HT0540 Homo sapiens cDNA
3107	13033	22826	3.79	9.0E-80	AA72848.1	EST_HUMAN	423406.41 Scores, testis, NHT Homo sapiens cDNA clone 1343848.3
3107	13033	22829	3.79	9.0E-80	AA72848.1	EST_HUMAN	423406.41 Scores, testis, NHT Homo sapiens cDNA clone 1343848.3
7751	17601	27824	1.28	9.0E-80	BE786003.1	EST_HUMAN	801681052F1 NH1_MGC.7 Homo sapiens cDNA clone IMAGE3935051.5
8557	18464	28735	11.05	9.0E-80	11433524	NT	Homo sapiens solute carrier family 7 (cationic amino acid transporter, y ⁺ system), member 8 (SLC7A8), mRNA
8597	18464	28736	11.05	9.0E-80	11433524	NT	Homo sapiens solute carrier family 7 (cationic amino acid transporter, y ⁺ system), member 8 (SLC7A8), mRNA
3551	13466		0.95	8.0E-80	U94387.1	NT	Homo sapiens Y chromosome spermatogenesis candidate protein (RBM) pseudogene mRNA, partial cds
8465	18343	28512	2.83	8.0E-80	11422847	NT	Homo sapiens KIA00724 gene product (KIA00724), mRNA
8465	18343	28513	2.83	8.0E-80	11422847	NT	Homo sapiens KIA00724 gene product (KIA00724), mRNA
7409	17276	27482	1.19	8.0E-80	6005923	NT	Homo sapiens tripe functional domain (PTFRF interacting) (TRIO), mRNA
7409	17276	27483	1.19	8.0E-80	6005923	NT	Homo sapiens tripe functional domain (PTFRF interacting) (TRIO), mRNA
882	10808	20457	2.24	6.0E-80	AA22167.1	EST_HUMAN	H69403.4 NCL CC4JP_Eln28 Homo sapiens cDNA clone IMAGE2103465.3 similar to SW_NUEM_HUMAN
1624	11324	21381	2.05	6.0E-80	U6466.1	NT	Q16795 NADH-L-lysine NADPH-dependent oxidoreductase 38 kD subunit precursor 1
4188	14088	28865	1.09	6.0E-80	A030281.1	NT	Homo sapiens NRC conversion RNA, complete cds
4188	14088	28866	1.09	6.0E-80	A030281.1	NT	Homo sapiens mRNA for KIA01169 protein, partial cds
5545	15461	25532	2.58	6.0E-80	11421463	NT	Homo sapiens mRNA for KIA01169 protein, partial cds
5702	15670	25512	2.58	6.0E-80	AJ404468.1	NT	Homo sapiens malate dehydrogenase 2, NAD (mitochondrial) (MDH2), mRNA
5776	15683	25191	3.84	6.0E-80	11436796	NT	Homo sapiens mRNA for dyx19 heavy chain (mitochondrial) (DHC19), mRNA
7123	17000	27191	3.07	6.0E-80	11529454	NT	Homo sapiens tubby like protein 3 (TULP3), mRNA
7214	17091	27281	3.07	6.0E-80	11529454	NT	Homo sapiens G protein-coupled receptor 51 (GPR51), mRNA
7672	17522	27748	1.08	6.0E-80	U0211.1	NT	Homo sapiens cytochrome 21 segment HS21C101
8311	18188	28437	2.81	6.0E-80	11427300	NT	Human c-myc photoreceptor cGMP-phosphodiesterase alpha' subunit gene, exon 21
							Homo sapiens A-inhibited guanine nucleotide-exchange protein 1 (G01), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
8656	18426	28604	60.71	6.0E-80	AF226730.1	NT	Homo sapiens CY10 mRNA, complete cds
2047	10808	20557	1.86	6.0E-80	AA422197.1	EST_HUMAN	HS5403.21 NCI, COAP. Bm23 Homo sapiens cDNA clone IMAGE:210459.9 similar to SW_NUEM_HUMAN CH5765 NADPH-KINETONE OXIDOREDUCTASE 99 KD SUBUNIT PRECURSOR ;
8172	19822		1.62	6.0E-80	AF40786.1	NT	Homo sapiens glutathione S-transferase Theta 2 (GSTT2) and glutathione S-transferase Theta 1 (GSTT1) genes, complete cds
8371	19337		4.56	6.0E-80	AB023300.1	NT	Homo sapiens GSTT1 gene for carboxylester sulfotransferase, exon 1, 2, 3, 4, 5
8647	19363		2.25	6.0E-80	AF153127.1	NT	Homo sapiens mRNA for sodium glucose cotransporter (SGLT2) gene
573	10331	20319	1.11	5.0E-80	4266228	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-alpha (Pase, 3 (PSMD3) mRNA
817	10745	20522	1.26	5.0E-80	AF108350.1	NT	Homo sapiens serine-threonine protein kinase (NRP1) mRNA, complete cds
817	10745	20569	1.26	5.0E-80	AF108350.1	NT	Homo sapiens serine-threonine protein kinase (NRP1) mRNA, complete cds
817	10745	20569	4.77	5.0E-80	X91647.1	NT	H. sapiens nact gene (exon 12)
1172	11094		2.28	5.0E-80	AF163263.2	NT	Homo sapiens chromosome 21 segment HS21C0B3
1440	11345		1.34	5.0E-80	AF163263.2	NT	Human K1001 protein homolog mRNA, complete cds
2311	12152		0.92	5.0E-80	U89336.1	NT	Homo sapiens mRNA for KMA14.54 protein, partial cDNA
2560	12256	22152	3.98	5.0E-80	AB037855.1	NT	Homo sapiens HLA class II histone family class II member 3 (H2-3) mRNA
2784	12526	22618	1.13	5.0E-80	AB942923	NT	Homo sapiens HLA class II histone family class II member 3 (H2-3) mRNA
3953	13361	23936	1.07	5.0E-80	AB0110036.1	NT	Homo sapiens HLA class II histone family class II member 3 (H2-3) mRNA
3953	13361	23937	1.07	5.0E-80	AB0110036.1	NT	Homo sapiens HLA class II histone family class II member 3 (H2-3) mRNA
4872	14742	24631	1.74	5.0E-80	AF163268.2	NT	Homo sapiens chromosome 21 segment HS21C0B8
6866	16745	26038	1.48	5.0E-80	9910293	NT	Human musclic keratin complex 2, gene 1g (K2G1g), mRNA
7333	17237	27441	7.48	4.0E-80	F526915.1	EST	HS2P13156 Hm3 Homo sapiens cDNA clone s4000046703
210	10181		4.71	3.0E-80	AF163270.2	EST	Homo sapiens chromosome 21 segment HS21C010
4410	14456		1.43	3.0E-80	BF085090.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C010
4818	14767	24487	4.97	3.0E-80	BC517465.1	EST_HUMAN	PMO-GBN0316-040000-002-E13 GN0316 Homo sapiens cDNA
4914	14701		4.97	3.0E-80	BC517465.1	EST_HUMAN	PMO-GBN0316-040000-002-E13 GN0316 Homo sapiens cDNA
6654	16470	25541	2.05	3.0E-80	AB091675.1	EST_HUMAN	ad23121.1 Soares, NIG-1. PAF_9W_OT_PAF_951 Homo sapiens cDNA clone IMAGE:1667054.3 similar to TR G191370
1757	11656	21627	0.39	2.0E-80	RH5321.1	EST_HUMAN	TR G191370
1816	11713	21963	1.91	2.0E-80	AA44824.1	EST_HUMAN	ye55508.1 Soares infant brain IN16 Homo sapiens cDNA clone IMAGE:38000.5
2009	11901	21791	6.8	2.0E-80	AL049112.2	EST_HUMAN	BE1 487 embryonic retinal cDNA library Homo sapiens cDNA clone RET487
1597	11567	20715	1.86	2.0E-80	AL049112.2	EST_HUMAN	DKE-Zp43HD1322.1 R34 (epytam: hias) Homo sapiens cDNA clone DKFZp434D1322.6
6132	15971	20715	1.86	2.0E-80	AL049112.2	EST_HUMAN	Homo sapiens Gp2 transport complex protein (Gp2) (GTG50), mRNA
8243	18123	28373	3.05	2.0E-80	AA393392.1	EST_HUMAN	G191012.1 Soares, Isells. NHT Homo sapiens cDNA clone IMAGE:72727.5 similar to TR G191315
337	10296		1.82	1.0E-80	AF169303.2	NT	G191012.1 Soares, Isells. NHT Homo sapiens cDNA clone IMAGE:72727.5 similar to TR G191315
782	10712	20551	1.12	1.0E-80	AF231920.1	NT	Homo sapiens chromosome 21 segment HS21C103
837	10712		1.12	1.0E-80	AF231920.1	NT	Homo sapiens chromosome 21 segment HS21C103

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Mean Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1911	11806		3.13	1.0E-90	M72956.1	EST_HUMAN	mt0f12.s6 NC1_GGAP_Co3 Homo sapiens cDNA clone IMAGE:1076466 3' similar to contains OFR.11 OFR repetitive element 4A
4359	14254	24039	0.96	1.0E-90	AF77883.1	NT	Homo sapiens cullin 4A (CUL4A) mRNA, complete cds
5192	15055	24819	0.97	1.0E-90	AI16378.2	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C078
5205	15187		5.93	1.0E-90	BE369916.1	NT	601274065F1 NR1_MGC_70 Homo sapiens cDNA clone IMAGE:3616433 5'
5633	15847	25635	6.41	1.0E-90	110347.1	NT	Human pro-alpha1 type II collagen (COL2A1) gene exons 1-54, complete cds
5916	15822	25847		1.0E-90	5174540	NT	Homo sapiens malate dehydrogenase 2, NAD (mitochondrial) (MDH2), nuclear gene encoding mitochondrial protein, mRNA
6470	16329	26498	2.68	1.0E-90	AB48731.1	EST_HUMAN	w025035.x1 NC1_GGAP_KdR1 Homo sapiens cDNA clone IMAGE:2472268 3'
6470	16329	26497	2.60	1.0E-90	AB48731.1	EST_HUMAN	w025035.x1 NC1_GGAP_KdR1 Homo sapiens cDNA clone IMAGE:2472268 3'
7360	17218	27417	1.23	1.0E-90	AF74519.1	NT	Homo sapiens probable mannose binding C-type lectin DC-SIGNR mRNA, complete cds
7360	17218	27418	1.23	1.0E-90	AF74519.1	NT	Homo sapiens probable mannose binding C-type lectin DC-SIGNR mRNA, complete cds
7657	17807	28049	1.19	1.0E-90	D63470.2	NT	Homo sapiens mRNA for KIA0145 protein, partial cds
8044	17835	28163	7.43	1.0E-90	11641278	NT	Homo sapiens similar to rat myomesin (LOC54182), mRNA
8044	17835	28164	7.43	1.0E-90	11641278	NT	Homo sapiens similar to rat myomesin (LOC54182), mRNA
8443	18079	28261	1.46	1.0E-90	11417601	NT	Homo sapiens mitochondria (disrupted in balanced translocation) 1 (NN1), mRNA
8443	18211	28268	1.98	1.0E-90	AB30340.1	NT	Homo sapiens mRNA for KIA0853 protein, partial cds
85070	18229	28268	1.98	1.0E-90	AB30340.1	NT	Homo sapiens gene for A-E, complete cds
86711	17862	28212	2.33	8.0E-91	AB231762.1	EST_HUMAN	q184905.x1 Soares_NF1_T_OB6_S1 Homo sapiens cDNA clone IMAGE:1854298 3'
86711	17862	28213	2.33	8.0E-91	AB231762.1	EST_HUMAN	q184905.x1 Soares_NF1_T_OB6_S1 Homo sapiens cDNA clone IMAGE:1854298 3'
8484	18377	28531	4.96	5.0E-91	BE344525.1	EST_HUMAN	61731035F1 NR1_MGC_74 Homo sapiens cDNA clone IMAGE:362070 5'
5300	18164	28521	3.00	7.0E-91	AB22115.1	EST_HUMAN	259100.35 Soares_Fetal_lung_NB-L191 Homo sapiens cDNA clone IMAGE:26976 3'
4290	14188	23871	4.84	5.0E-91	BE256829.1	EST_HUMAN	601111970F1 NR1_MGC_76 Homo sapiens cDNA clone IMAGE:3362840 5'
4290	14188	23872	4.84	5.0E-91	BE256829.1	EST_HUMAN	601111970F1 NR1_MGC_76 Homo sapiens cDNA clone IMAGE:3362840 5'
5229	15153	24920	1.93	6.0E-91	4901848	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
5229	15153	24921	1.93	6.0E-91	4901848	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
7325	17201	27401	1.34	6.0E-91	AB300017.1	EST_HUMAN	EST109129 Fetal_lung_H1 Homo sapiens cDNA 3' end
9075	19190	26269	1.87	6.0E-91	AB176022.1	EST_HUMAN	602153065F1 NR1_MGC_83 Homo sapiens cDNA clone IMAGE:4284601 5'
9879	19166	26270	1.62	6.0E-91	BE208042.1	EST_HUMAN	602153065F1 NR1_MGC_83 Homo sapiens cDNA clone IMAGE:4284601 5'
2170	12657	21860	3.14	5.0E-91	BE208042.1	EST_HUMAN	601127005F1 NR1_MGC_8 Homo sapiens cDNA clone IMAGE:3344480 5'
6901	18780	20974	3.47	5.0E-91	AB300782.1	NT	Homo sapiens mRNA for KIA00454 protein, partial cds
6901	18780	20975	3.47	5.0E-91	AB300782.1	NT	Homo sapiens mRNA for KIA00454 protein, partial cds
8865	18187	28968	0.81	5.0E-91	9608324	NT	Homo sapiens hypothetical protein (FLJ11045), mRNA
214	10155	19998	2.57	4.0E-91	A1765257.1	NT	Homo sapiens CYP2 binding protein mRNA, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF-SEQ ID NO:	Expression Signal	Most Similar (Top) Htt BLAST E Value	Top Htt Accession No.	Top Htt Database Source	Top Htt Descriptor
1778	11678	21566	0.99	4.0E-81	AW779612.1	EST_HUMAN	Int69402.x1 NC1_GGAP_Cor14 Homo sapiens cDNA clone IMAGE:3035907 3' similar to SW-GOPG_BOVIN
3134	13059	22888	3.79	4.0E-81	AE037769.1	NT	P59620 COATOMER GAMMA SUBUNIT ; Homo sapiens mRNA for KIAA1345 protein, partial cds
3576	13490	23280	1.18	4.0E-81	AW004608.1	EST_HUMAN	W59103.x1 NC1_GGAP_C03 Homo sapiens cDNA clone IMAGE:2605289 3' similar to TR-O43815 O43815
4098	13070	23746	2.14	4.0E-81	AF263306.1	NT	Homo sapiens rab3 interacting protein variant 2 mRNA, partial cds
4098	13070	23746	2.14	4.0E-81	AF263306.1	NT	Homo sapiens rab3 interacting protein variant 2 mRNA, partial cds
8621	16700	28823	3.16	4.0E-81	X06989.1	NT	Human mRNA for amyloid A4(76) protein
8673	16850	27041	3.4	4.0E-81	U01697.1	NT	Human cone photoreceptor cGMP-phosphodiesterase alpha subunit gene, exons 2 and 3
8673	16850	27042	3.4	4.0E-81	U01697.1	NT	Human cone photoreceptor cGMP-phosphodiesterase alpha subunit gene, exons 2 and 3
7320	17190	27395	8.65	4.0E-81	AB018001.1	NT	Homo sapiens mRNA for Dual-specific protein kinase 2, complete cds
7816	17690	27608	1.49	4.0E-81	11426261	NT	Homo sapiens base 1 DNA-ATP-dependent (LIG1) mRNA
8522	18394	28558	2.24	4.0E-81	4736055	NT	Homo sapiens vesicle trafficking protein sec22b (SEC22B) mRNA
8522	18394	28558	2.24	4.0E-81	4736055	NT	Homo sapiens vesicle trafficking protein sec22b (SEC22B) mRNA
9069	19627	29007	3.81	4.0E-81	11417652	NT	Homo sapiens calcineurin binding protein 1 (KJAA0330) mRNA
9069	19627	29008	3.81	4.0E-81	11417652	NT	Homo sapiens calcineurin binding protein 1 (KJAA0330) mRNA
8612	19191	25253	2.62	4.0E-81	11417671	NT	Homo sapiens beta-irradiation-inducible protein (LOC51733) mRNA
8612	19191	25254	2.62	4.0E-81	11417671	NT	Homo sapiens beta-irradiation-inducible protein (LOC51733) mRNA
8750	18276	28228	2.67	4.0E-81	11417674	NT	Homo sapiens transcobalamin II, microcytic anemia (TCA2) mRNA
1246	11153	21000	9.38	3.0E-81	Y18000.1	NT	Homo sapiens NF2 gene
1246	11153	21001	9.38	3.0E-81	Y18000.1	NT	Homo sapiens NF2 gene
2320	12201	22100	1.7	3.0E-81	AF07188.1	NT	Homo sapiens cullin 4A (CUL4A) mRNA, complete cds
2981	12888	22885	5.12	3.0E-81	4900260	NT	Homo sapiens plectrophin (heparin binding growth factor 8, neurite growth-promoting factor 1) (PTN) mRNA
2981	12888	22886	5.12	3.0E-81	4900260	NT	Homo sapiens plectrophin (heparin binding growth factor 8, neurite growth-promoting factor 1) (PTN) mRNA
4633	14811	22931	0.77	3.0E-81	AL165283.2	NT	Homo sapiens chromosome 21 segment H321C083
2802	12732	22530	1.77	2.0E-81	BE794636.1	EST_HUMAN	801747075F1 NIH_VGC_98 Homo sapiens cDNA clone IMAGE:3877121 5'
2802	12732	22531	1.77	2.0E-81	BE794636.1	EST_HUMAN	801747075F1 NIH_VGC_98 Homo sapiens cDNA clone IMAGE:3877121 5'
3707	13620	23434	0.96	2.0E-81	AW11542.1	EST_HUMAN	hg55001.x1 NC1_GGAP_Kd11 Homo sapiens cDNA clone IMAGE:2952384 3'
4579	14469	24246	0.95	2.0E-81	5453871	NT	Homo sapiens placental-derived growth factor receptor-like (PDGFRL) mRNA
9888	13620	23404	1.74	2.0E-81	AW11542.1	EST_HUMAN	hg55001.x1 NC1_GGAP_Kd11 Homo sapiens cDNA clone IMAGE:2952384 3'
6888	10375	25194	1.35	2.0E-81	8667387	NT	Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA
1403	11308	21159	3.32	1.0E-81	W26536.1	EST_HUMAN	3338 Human retina cDNA randomly primed sublibrary/Homo sapiens cDNA

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Prote SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3902	13516	23304	2	1.0E-81	AA1900568.1	EST_HUMAN	EST177250 IMAGE resequences, MAGF Homo sapiens cDNA
4414	14308	24051	3.07	1.0E-81	AA040370.1	EST_HUMAN	2454809.1 Soares_fragments, NHPHU Homo sapiens cDNA clone IMAGE:48825 5' similar to
4546	14439	24222	7.85	1.0E-81	BE047966.1	EST_HUMAN	PK-352437 SS2437 CDP-diacylglycerol synthase - fruit fly
5203	15089	25103	9.03	1.0E-81	187928.1	NT	tz4503a.yf NC1 CGAP Bin52 Homo sapiens cDNA clone IMAGE:2291520 5'
5284	15206	24692	4.01	1.0E-81	11432808	NT	Human acetylcholinesterase (AOC2) gene, exon 3
5284	15206	24692	4.01	1.0E-81	11432808	NT	Homo sapiens polymerase (DNA directed), gamma (POLG), mRNA
5468	15388	25446	3.54	1.0E-81	152351.1	NT	Homo sapiens polymerase (DNA directed), gamma (POLG), mRNA
5468	15388	25446	3.54	1.0E-81	152351.1	NT	Homo sapiens arm-repeat protein NRPAP1/neurogranin (CTNND2) mRNA, partial cds
5737	15649	25750	3.15	1.0E-81	BF74641.1	EST_HUMAN	60217894F1 NHL_MGC_83 Homo sapiens cDNA clone IMAGE:4274535 5'
5967	16429	26060	6.4	1.0E-81	11432808	NT	Homo sapiens polymerase (DNA directed), gamma (POLG), mRNA
7831	17482	27702	2.62	1.0E-81	BE98278.1	EST_HUMAN	60164051F1 NHL_MGC_56 Homo sapiens cDNA clone IMAGE:3602228 5'
7831	17482	27703	2.62	1.0E-81	BE98278.1	EST_HUMAN	60164051F1 NHL_MGC_56 Homo sapiens cDNA clone IMAGE:3602228 5'
7726	17576	27769	4.81	1.0E-81	BE654567.1	EST_HUMAN	601343180F1 NHL_MGC_53 Homo sapiens cDNA clone IMAGE:3635483 5'
7919	17659	27969	2.83	1.0E-81	BE74454.1	EST_HUMAN	601577336F1 NHL_MGC_9 Homo sapiens cDNA clone IMAGE:383280 5'
7919	17659	27970	2.83	1.0E-81	BE74454.1	EST_HUMAN	601577336F1 NHL_MGC_9 Homo sapiens cDNA clone IMAGE:383280 5'
8000	17860	28051	1.46	1.0E-81	AA1907450.1	EST_HUMAN	CU333339F1 NHL_MGC_147400:147412:NN0059 Homo sapiens cDNA
8438	18212	28658	1.98	1.0E-81	AA194098.1	EST_HUMAN	MR0-CT10096-261598-019 CT10096 Homo sapiens cDNA
8438	18212	28659	1.98	1.0E-81	AA194098.1	EST_HUMAN	MR0-CT10096-261598-019 CT10096 Homo sapiens cDNA
8564	18316	23304	2.42	1.0E-81	BF204353.1	EST_HUMAN	EST177250 IMAGE resequences, MAGF Homo sapiens cDNA
8510	18524	28919	1.80	1.0E-81	AF161065.1	NT	601867714F1 NHL_MGC_17 Homo sapiens cDNA clone IMAGE:4110459 5'
8276	18581	25325	3.62	1.0E-81	AF161065.1	NT	Homo sapiens protein (similar to apolipoprotein B mRNA editing protein) [D745C10.2], mRNA
121	9588	19765	1.87	8.0E-82	AF161065.1	NT	Homo sapiens HSP-68B mRNA, partial cds
101	9588	19765	1.26	8.0E-82	AF161065.1	NT	Homo sapiens HSP-68B mRNA, partial cds
263	10228	20044	1.60	8.0E-82	U08986.1	NT	Human CRP4 gene, partial cds
797	10728	20566	2.17	8.0E-82	U08986.1	NT	Human CRP4 gene, partial cds
860	10795	20545	1.11	8.0E-82	U08986.1	NT	Human CRP4 gene, partial cds
1476	11390	21244	1.12	8.0E-82	AB037748.1	NT	Homo sapiens mRNA for KIAA1327 protein, partial cds
1636	11540	21400	1.24	8.0E-82	671560.1	NT	Homo sapiens glutathione peroxidase 5 (epididymal androgen-related protein), (GPX5), transcript variant 2, mRNA
4180	14050	23825	0.81	8.0E-82	8922432	NT	Homo sapiens hypothetical protein FLJ20461 (FLJ20461), mRNA
1434	11339	22465	1.27	7.0E-82	BF03527.1	EST_HUMAN	60146883F1 NHL_MGC_66 Homo sapiens cDNA clone IMAGE:3862085 5'
2739	12801	22465	1.82	7.0E-82	AU144060.1	EST_HUMAN	AU144060 HEMBA1 Homo sapiens cDNA clone HEIMBA1000752 3'
4634	13837	23719	0.81	5.0E-82	AA115512.1	EST_HUMAN	tt08411.at NC1 CGAP C3b Homo sapiens cDNA clone IMAGE:522198 3'

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Prote SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1947	11851	21412	6.51	4.0E-82	AF081484.1	NT	Homo sapiens alpha-tubulin isoform 1 mRNA, complete cds
8954	18761	29054	6.47	4.0E-82	AI937300.1	EST_HUMAN	wf75600.x1 NCI CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2467624 3' similar to TR.O76276
9519	19130		6.19	4.0E-82	AF026701.2	NT	OT576 PCD1: Homo sapiens presenilin-1 gene, exons 1 and 2
276	10242	20051	13.76	3.0E-82	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease sensitive), Alzheimer disease (APP), mRNA
687	10620	20446	2.19	3.0E-82	BE05705.1	EST_HUMAN	RC3-BN01720-01400-013-022 BCN0120 Homo sapiens cDNA
770	10700	20639	4.44	3.0E-82	5174702	NT	Homo sapiens transforming growth factor beta-activated kinase-binding protein 1 (TAB1), mRNA
852	10779	20629	3.22	3.0E-82	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease sensitive), Alzheimer disease (APP), mRNA
1048	10963		13.76	3.0E-82	A172648.1	EST_HUMAN	423-005.x1 Scores, testis, testis, NHT Homo sapiens cDNA clone 133248 3'
1333	11240	21098	5.47	3.0E-82	AW87678.1	EST_HUMAN	RC3-P10001-190100-021-1902 P10001 Homo sapiens cDNA
1450	11355	21219	2.03	3.0E-82	AL193285.2	NT	Homo sapiens chromosome 21 segment HS21C085
1859	11755	21630	1.82	3.0E-82	BE613232.1	EST_HUMAN	RC1-BN0005-259700-018-g04 BN0005 Homo sapiens cDNA
1981	11655	21744	0.9	3.0E-82	4501922	NT	Homo sapiens adenylate cyclase activating polypeptide 1 (phallos) receptor type 1 (ADCYAP-IR1) mRNA
3234	13158		2.06	3.0E-82	545381.1	NT	Homo sapiens neurotrophic tyrosine kinase, receptor, type 2 (NTRK2) mRNA
4836	14718	24501	0.91	3.0E-82	A1135070.1	EST_HUMAN	2083904.1 Statedene Long carcinoma 93718 Homo sapiens cDNA clone IMAGE:565711 5' similar to SW-620 BOVIN CQ783 POLYPEPTIDE NA-CETYLMALACTOSAMINYLTRANSFERASE
8768	18917	29807	2.84	3.0E-82	11425208	NT	Homo sapiens myosin-like with transmembrane domain 1 (ANKTM), mRNA
7944	17804	27728	3.79	3.0E-82	A802900.1	NT	Homo sapiens mRNA for KIAA1077 protein, partial cds
7854	17804	27728	3.79	3.0E-82	A802900.1	NT	Homo sapiens mRNA for KIAA1077 protein, partial cds
852	10520	20235	1.92	2.0E-82	A8023276.1	NT	Homo sapiens mRNA for KIAA0996 protein, partial cds
852	10520	20237	1.92	2.0E-82	A8023276.1	NT	Homo sapiens mRNA for KIAA0996 protein, partial cds
1650	11952	21428	1.75	2.0E-82	A046390.1	EST_HUMAN	DKFZ-34M177.71 434 (Synonym: hies) Homo sapiens cDNA clone DKFZ-34M177 5'
3772	13954	23463	1.14	2.0E-82	4504116	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4140	14040	23813	1.14	2.0E-82	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
4458	14352	24143	0.98	2.0E-82	A8029019.1	NT	Homo sapiens mRNA for KIAA1006 protein, partial cds
4458	14352	24144	0.98	2.0E-82	A8029019.1	NT	Homo sapiens mRNA for KIAA1006 protein, partial cds
4768	14653	24441	3.18	2.0E-82	AF045955.1	NT	Homo sapiens wister (WBSR1) and wister5 (WBSR5) genes, complete cds, alternatively spliced and replication factor C subunit 2 (RFC2) gene, complete cds
5013	14887	24553	1.96	2.0E-82	4507590	NT	Homo sapiens tumor necrosis factor receptor superfamily, member 5 (TNFRSF5) mRNA
5013	14887	24554	1.96	2.0E-82	4507590	NT	Homo sapiens tumor necrosis factor receptor superfamily, member 5 (TNFRSF5) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5365	15278	25108	2.37	2.0E-82	AB018270.1	NT	Homo sapiens mRNA for KIAA0727 protein, partial cds
5746	15654	25762	4.96	2.0E-82	AF294882.1	NT	Homo sapiens FAM4A1 splice variant a (FAM4A1) mRNA, complete cds
6834	16713	26906	2.23	2.0E-82	11321670	NT	Homo sapiens aII (Drocephila) homolog 3 (SLIT3), mRNA
7821	17671	27912	1.2	2.0E-82	708032.1	NT	Human endogenous retrovirus-K, LTR U5 and gag gene
7821	17671	27912	1.2	2.0E-82	708032.1	NT	Human endogenous retrovirus-K, LTR U5 and gag gene
8628	18493	28765	6.98	2.0E-82	U80736.1	NT	Homo sapiens CAGF9 mRNA, partial cds
8628	18493	28765	6.98	2.0E-82	U80736.1	NT	Homo sapiens CAGF9 mRNA, partial cds
5097	18668	28767	2.23	2.0E-82	NA9560.1	EST_HUMAN	Homo sapiens SRY (sex determining region Y) box 10 (SOX10), mRNA
9632	19205	29717	2.37	2.0E-82	AA011276.1	EST_HUMAN	Homo sapiens SRY (sex determining region Y) box 10 (SOX10), mRNA
9632	19385	29723	1.44	2.0E-82	11419097	NT	Homo sapiens melanoma differentiation associated protein3 (MDA5), mRNA
577	10516	20321	1.48	1.0E-82	11549921	NT	Homo sapiens mRNA for KIAA0538 protein, partial cds
1190	11100	21020	0.9	1.0E-82	BE686106.1	EST_HUMAN	RC4-B170310-11030016-410 B170310 Homo sapiens cDNA
1264	11171	21020	0.9	1.0E-82	BE686106.1	EST_HUMAN	RC4-B170310-11030016-410 B170310 Homo sapiens cDNA
1265	11172	21021	0.83	1.0E-82	AB011110.2	EST_HUMAN	UHHBW1-coat492-2U131 NC2 CGAP Sub7 Homo sapiens cDNA clone IMAGE:3084063 3'
7882	17732	28264	2.97	1.0E-82	AF519388.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C096
8728	18016	28264	2.97	1.0E-82	AL183293.2	NT	Homo sapiens chromosome 21 segment HS21C096
8733	18260	28300	1.79	1.0E-82	AL183248.2	NT	Homo sapiens chromosome 21 segment HS21C096
7937	15634	27124	4.71	8.0E-83	BF17220.1	EST_HUMAN	802180035F1 NH1_MGC_81 Homo sapiens cDNA clone IMAGE:4291581 5'
1382	12877	21165	1.86	8.0E-83	BE683973.1	EST_HUMAN	802180035F1 NH1_MGC_81 Homo sapiens cDNA clone IMAGE:3671382 5'
1656	12647	21422	1.96	8.0E-83	NA9561.1	EST_HUMAN	802180035F1 NH1_MGC_81 Homo sapiens cDNA clone IMAGE:258823 3'
2836	12764		1.64	7.0E-83	AA84065.1	EST_HUMAN	nc12801.1 NC1 CGAP_Phe1 Homo sapiens cDNA clone IMAGE:110497 3' similar to contains AU repetitive element
4710	14966		5.49	7.0E-83	BF21613.1	EST_HUMAN	7037407.x1 NC1 CGAP_P128 Homo sapiens cDNA clone IMAGE:3847993 3' similar to TR-Q97916 Q97916 D1207H1.1
397	10343	20169	1.34	6.0E-83	U63320.1	NT	Homo sapiens plectin cytoplasmic III (p13b) gene, exons 229
1747	11847	21615	1.5	6.0E-83	AW573088.1	EST_HUMAN	h111803.x1 Scores_NFL_T_GGCG_S1 Homo sapiens cDNA clone IMAGE:2993528 3' similar to SW-TPB3_HUEN P44471 HYPOPHYSECTIC PROTEIN H0084. ;
2984	12912	22709	1.09	6.0E-83	AW819435.1	EST_HUMAN	QV4-ST0294-181169-037-405 S10294 Homo sapiens cDNA
3031	12959	22751	0.94	6.0E-83	AA010467.1	EST_HUMAN	258605.1 Scores_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:456080 3'
3515	13431	23231	0.96	6.0E-83	11430241	NT	Homo sapiens hypothetical protein FLU10379 (FLU10379), mRNA
5236	15160	24628	1.72	6.0E-83	4907866	NT	Homo sapiens VAMP (vesicle-associated membrane protein)-associated protein A (380) (VAPA) mRNA, and translated products
5989	15979	25979	2.13	6.0E-83	AA010770.1	NT	Homo sapiens hypoxanthine phosphoribosyl transferase 1-50
6430	16291	25452	1.79	6.0E-83	11422024	NT	Homo sapiens mit proto-oncogene (hepatocyte growth factor receptor) (MET), mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7579	17430	27844	6.77	6.0E-83	4905314	NT	Homo sapiens myomesin (M-protein) 2 (BMD) (MYOM2), mRNA
8817	18630		6.32	6.0E-83	AA486105.1	EST_HUMAN	ad440.0.1 Stooligene Lung (#637210) Homo sapiens cDNA clone IMAGE:640810 3' similar to contains THR12 THR repetitive element
9050	18634		3.11	6.0E-83	AF240788.1	NT	Homo sapiens glutathione S-transferase beta 2 (GSTT2) and glutathione S-transferase beta 1 (GSTT1) genes, complete cds
931	18659		4.14	6.0E-83	U17983.1	NT	Human succinate dehydrogenase iron-protein subunit (sdhB) gene, exon 5
2004	12849		2.1	5.0E-83	AF006305.1	NT	Homo sapiens 3S3 proteasome regulatory subunit (SUG2) mRNA, complete cds
3586	13500	23289	0.92	5.0E-83	AL13207.2	NT	Novel human gene mapping to chromosome X
5071	14895	24651	10.99	5.0E-83	4657013	NT	Homo sapiens caldesin (CAT) mRNA
5071	14895	24652	10.99	5.0E-83	4657013	NT	Homo sapiens caldesin (CAT) mRNA
5094	14994	24739	0.66	5.0E-83	AF068327.1	NT	Homo sapiens dihydropyridine receptor alpha 2 subunit (CACNA2D1) gene, exon 11
624	10591	26373	1.47	4.0E-83	AF224699.1	NT	Homo sapiens neurofilament, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D) genes, complete cds
3489	13395	23190	0.96	4.0E-83	BE68078.1	EST_HUMAN	80157160F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3973195 5'
981	10604		4.5	3.0E-83	AA386311.1	EST_HUMAN	EST179842 Phoenix Homo sapiens cDNA similar to similar to endogenous retrovirus ERV9
2750	12612		1.82	3.0E-83	AA632654.1	EST_HUMAN	p87c007.01 NCL CGAP_Thy1 Homo sapiens cDNA clone IMAGE:1133262 similar to contains THR12 THR repetitive element
1759	11658	21526	1.9	2.0E-83	AA693492.1	EST_HUMAN	af64g05.01 Soares, Iselin, NIH Homo sapiens cDNA clone IMAGE:1621602 3' similar to TR-02614
1759	11658	21530	1.9	2.0E-83	AA693492.1	EST_HUMAN	af64g05.01 Soares, Iselin, NIH Homo sapiens cDNA clone IMAGE:1621602 3' similar to TR-02614
1883	11779	21654	2.23	2.0E-83	AG6961.1	EST_HUMAN	Q92614 MYELOBLAST (M40216)
2821	12760	22542	1.11	2.0E-83	BE826894.1	EST_HUMAN	Q92614 MYELOBLAST (M40216)
3231	13165		1.82	2.0E-83	U1160654	NT	Q92614 MYELOBLAST (M40216)
3708	13921		1	2.0E-83	AF163022.2	NT	Q92614 MYELOBLAST (M40216)
4211	14140	23915	4.47	2.0E-83	AF208791.1	NT	Homo sapiens chromosome 21 segment H521C002
4583	14446	24230	8.13	2.0E-83	7700598	NT	Homo sapiens hematopoietic progenitor cell antigen CD34 precursor (CD34) mRNA, partial cds
4653	14448	24231	8.13	2.0E-83	7700598	NT	Homo sapiens hematopoietic progenitor cell antigen CD34 precursor (CD34) mRNA, partial cds
5359	15279	25109	28.35	2.0E-83	11024711	NT	Homo sapiens ankyrin repeat containing protein A39-2 (LOC51676), mRNA
5359	15279	25110	28.35	2.0E-83	11024711	NT	Homo sapiens ankyrin repeat containing protein A39-2 (LOC51676), mRNA
6396	16258	28419	5.9	2.0E-83	AF129533.1	NT	Homo sapiens myosin, heavy polypeptide 4, skeletal muscle (MYH4), mRNA
6959	16539	28736	1.52	2.0E-83	U67057.1	NT	Homo sapiens F-box protein Fbx6 (FBL35) mRNA, partial cds
8839	16718	28911	2.86	2.0E-83	AF041920.1	NT	Rattus norvegicus desmin-180 mRNA, complete cds
8839	16718	28912	2.86	2.0E-83	AF041920.1	NT	Rattus norvegicus desmin-180 mRNA, complete cds
8839	16718	28912	2.86	2.0E-83	AF041920.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Mod Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7767	17617	27845	3.32	2.0E-33	U22044.1	NT	Human neural cell adhesion molecule (N-CAM) secreted isoform mRNA, 3' end
7767	17617	27846	3.32	2.0E-33	U22044.1	NT	Human neural cell adhesion molecule (N-CAM) secreted isoform mRNA, 3' end
7926	17676	27620	1.21	2.0E-33	U11759.1	EST_HUMAN	AU11759 HEMBAT Homo sapiens cDNA clone HEMBAT100180 5'
8233	18105	26359	3.7	2.0E-33	U143948	NT	Homo sapiens KIAA0985 protein (KIAA0985), mRNA
8238	18171	26422	1.82	2.0E-33	U134452.1	EST_HUMAN	DKF25477135.11.547 (synonym: HbT7) Homo sapiens cDNA clone DKF25477135 5'
8268	18177	26423	1.82	2.0E-33	U134452.1	EST_HUMAN	DKF25477135.11.547 (synonym: HbT7) Homo sapiens cDNA clone DKF25477135 5'
8667	19226		3.48	2.0E-33	AB011396.1	NT	Homo sapiens gene for AF-6, complete cds
1300	11295	21152	18.57	1.0E-33	4504326	NT	Homo sapiens hydroxyacyl-Coenzyme A dehydrogenase/3-ketacyl-Coenzyme A thiolase/acyl-Coenzyme A hydratase (trifunctional protein), beta subunit (HADHB), mRNA
1300	11295	21153	16.57	1.0E-33	4504326	NT	Homo sapiens hydroxyacyl-Coenzyme A dehydrogenase/3-ketacyl-Coenzyme A thiolase/acyl-Coenzyme A hydratase (trifunctional protein), beta subunit (HADHB), mRNA
2323	12468	22378	1.8	1.0E-33	BE36390.1	EST_HUMAN	001973771 NIH, JGCC, 71 Homo sapiens cDNA clone IMAGE3608754 5'
3143	13071	22872	0.84	1.0E-33	7682246	NT	Homo sapiens cell recognition molecule Casp2 (KIAA388), mRNA
3783	13705	23491	3.55	1.0E-33	AF535768.1	NT	Rattus norvegicus brain specific cortactin-binding protein CBP50 mRNA, partial cds
4151	14051	23522	2.22	1.0E-33	Z2632.1	NT	H. sapiens gene for mitochondrial dolichomoy-CoA delta-isomerase, span 3
4789	14574	24161	1.36	1.0E-33	4502168	NT	Homo sapiens amyloid beta (A4) precursor protein (prolase neta-4, Alzheimer disease) (APP), mRNA
6022	15928	26057	1.75	1.0E-33	U027514.1	EST_HUMAN	329303.17 Scarsa, beta1, NNT Homo sapiens cDNA clone IMAGE164561 5' similar to g1546241 OM
3727	13639	23425	2.82	1.0E-33	BE907205.1	EST_HUMAN	001970231 NIH, JGCC, 21 Homo sapiens cDNA clone IMAGE366553 5'
1273	11180	21028	4.21	6.0E-34	BE36864.1	EST_HUMAN	R23750119-203693-0111-435 FN0119 Homo sapiens cDNA
1273	11180	21029	4.21	6.0E-34	BE36864.1	EST_HUMAN	R23750119-203693-0111-435 FN0119 Homo sapiens cDNA
2348	12226	22125	4.78	6.0E-34	AY70574.1	EST_HUMAN	585863.51 Stages gene spans brain ST1 Homo sapiens cDNA clone IMAGE-97028 3'
5206	15095		0.24	6.0E-34	AL049663.2	EST_HUMAN	DKF254944022.11.424 (synonym: HbT5) Homo sapiens cDNA clone DKF254944022 5'
5338	15307	25180	1.7	6.0E-34	AA97339.1	EST_HUMAN	447393.17 Scarsa, NF1, C8C, S1 Homo sapiens cDNA clone IMAGE146060 3' similar to g154614338
6415	16277	26440	3.17	6.0E-34	BE110371.1	EST_HUMAN	VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);
6706	16566	26774	1.9	6.0E-34	BE770186.1	EST_HUMAN	PMOL10019-10030-004-402 LT0019 Homo sapiens cDNA
8821	18634		1.94	6.0E-34	AY39912.1	EST_HUMAN	PMOL10034-10060-004-402 LT0034 Homo sapiens cDNA
6697	16030	20496	1.06	5.0E-34	AA82811.1	EST_HUMAN	ILD17165-001195-195-005 B10168 Homo sapiens cDNA
2951	12506		1.01	5.0E-34	AF100718.1	NT	Homo sapiens chromosome 3 subtelomeric region
8330	18643	28826	2.76	5.0E-34	U1425740	NT	Homo sapiens regulatory factor X, 3 (influences H1 A class II expression) (RF3), mRNA
1354	11200	21116	1.06	4.9E-34	AB037736.1	NT	Homo sapiens mRNA for KIAA1314 protein, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top 1 hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3390	11294	21151	4.03	4.0E-84	A695321.1	EST_HUMAN	wt7604.x1 Soares_NEL_2_GRC_H1 Homo sapiens cDNA clone IMAGE:230298 3' similar to
4899	14749	24529	1.76	4.0E-84	AF025991.2	NT	SIN-NRDO Homo sapiens myosin light chain kinase isoform 2 (MLCK) mRNA, complete cds
5060	16330	26701	1.27	4.0E-84	U94982.1	NT	Huma 2.4-kilobase cDNA encoding genes, clones 3 and 4
5418	18238	29348	1.31	4.0E-84	I1389168	NT	Homo sapiens protein tyrosine phosphatase, receptor type C (PTPREG) mRNA
6418	18238	29348	1.31	4.0E-84	I1389168	NT	Homo sapiens protein tyrosine phosphatase, receptor type C (PTPREG) mRNA
5791	19297	28955	2.35	4.0E-84	AF049593.1	NT	Homo sapiens histone H2A.X (H2AX) gene, complete cds
6507	19297	28955	2.35	4.0E-84	I1421028	NT	Homo sapiens KLU0783 gene product (KLU0783) gene, complete cds
8280	19109	28413	0.88	4.0E-84	AB032993.1	NT	Homo sapiens mRNA for KIAA1330 protein, partial cds
313	10275	20413	1.38	3.0E-84	AF032600.1	NT	Homo sapiens basophil protein homolog mRNA, partial cds
1137	11011	20951	0.89	3.0E-84	AF798261	NT	Homo sapiens choroideroma sulfate proteoglycan 2 (versican) (SPG2) mRNA
1917	11812	21690	1.16	3.0E-84	5453955	NT	Homo sapiens pericentriolar material 1 (PCM1) mRNA
1962	11836	21745	3.03	3.0E-84	ALJ9580.1	NT	Novel human mRNA containing zinc finger C2H2 type domains (complete cds)
3542	13682	23251	1.18	3.0E-84	AD038988.1	NT	Homo sapiens DNA, DLEC1 to ORC1L4 gene region, section 1/2 (DLEC1, ORC1L4 genes, complete cds)
3690	13682	23259	1.41	3.0E-84	AF071445.1	NT	Homo sapiens X-linked juvenile retinoschisis precursor protein (XLRS1) mRNA, complete cds
8293	18133	21845	7.8	3.0E-84	E445801.1	EST_HUMAN	wht0005.x1 Soares_Dickkopf_3rd_nco HO Homo sapiens cDNA clone IMAGE:2620563 3' similar to
2058	11949	21845	5.89	2.0E-84	B56663397.1	EST_HUMAN	GIM-B10795-190000-372-808 B10795 Homo sapiens cDNA
2058	11949	21846	5.89	2.0E-84	BC5663397.1	EST_HUMAN	GIM-B10795-190000-372-808 B10795 Homo sapiens cDNA
2131	12840	22840	0.95	2.0E-84	AF030943.1	NT	Homo sapiens myelin transcription factor 1-like (MYT1L) mRNA, complete cds
2932	12860	22850	0.95	2.0E-84	X89211.1	NT	H.sapiens DNA for endogenous retroviral like element
2932	12860	22850	0.95	2.0E-84	X89211.1	NT	H.sapiens DNA for endogenous retroviral like element
4982	14598	24364	1.11	2.0E-84	BF308518.1	EST_HUMAN	001887604F.NIH_LMC6_17 Homo sapiens cDNA clone IMAGE:4121727 6'
4982	14598	24364	1.11	2.0E-84	BF308518.1	EST_HUMAN	001887604F.NIH_LMC6_17 Homo sapiens cDNA clone IMAGE:4121727 6'
4982	14598	24366	1.11	2.0E-84	BF308518.1	EST_HUMAN	001887604F.NIH_LMC6_17 Homo sapiens cDNA clone IMAGE:4121727 6'
6996	16575		1.87	2.0E-84	AJ29574.1	EST_HUMAN	msl00202.x1 Lucap_symphlella_Junk-Homo sapiens cDNA clone IMAGE:4990251 3' similar to
6996	16575		1.87	2.0E-84	AJ29574.1	EST_HUMAN	msl00202.x1 Lucap_symphlella_Junk-Homo sapiens cDNA clone IMAGE:4990251 3' similar to
9908	19003	25334	1.89	2.0E-84	BF449000.1	EST_HUMAN	msl000602.x1 Lucap_symphlella_Junk-Homo sapiens cDNA clone IMAGE:4990251 3' similar to
9908	19003	25335	1.89	2.0E-84	BF449000.1	EST_HUMAN	msl000602.x1 Lucap_symphlella_Junk-Homo sapiens cDNA clone IMAGE:4990251 3' similar to
309	10271	20090	1.93	1.0E-84	AF114488.1	NT	Homo sapiens interconvert short isoform (ITSN) mRNA, complete cds
537	10478	20260	5.2	1.0E-84	4807962	NT	Homo sapiens cyclase 3-monoacylglycerol lipophan 5-monooxygenase activation protein, zeta polypeptide (VWHAZ) mRNA
703	10535		0.99	1.0E-84	11427031	EST_HUMAN	Homo sapiens complement component 5 (C5), mRNA
1271	11178	21026	1.92	1.0E-84	AA984379.1	EST_HUMAN	amb9511.x1 Sitagene schizo brain S111 Homo sapiens cDNA clone IMAGE:1028865 3'

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Table 4

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2068	11800	21790	3.13	1.0E-84	BE39237.1	EST_HUMAN	B013000061 NH1_MGC_44 Homo sapiens cDNA clone IMAGE:362927 5'
2176	12063	21984	1.08	1.0E-84	11427187	EST_HUMAN	Homo sapiens pericentriolar material 1 (PCM1), mRNA
3691	13063	23391	2.14	1.0E-84	AA720891.1	EST_HUMAN	Novel human gene mapping to chromosome 13
4319	14216	23866	6.59	1.0E-84	AJ229041.1	NT	Novel human gene mapping to chromosome 13
4601	14480	24275	3.32	1.0E-84	AL040314.2	EST_HUMAN	DKF-ZP44N0323.11.434 (synonym: hta33) Homo sapiens cDNA clone DKFZ44N0323.5'
4601	14480	24276	3.32	1.0E-84	AL040314.2	EST_HUMAN	DKF-ZP44N0323.11.434 (synonym: hta33) Homo sapiens cDNA clone DKFZ44N0323.5'
4623	14216	23866	4.29	1.0E-84	AJ229041.1	NT	Homo sapiens 556 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
4623	14216	23866	4.29	1.0E-84	AJ229041.1	NT	Homo sapiens 556 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
5767	15665	25773	1.32	1.0E-84	S73462.1	NT	Usher's water channel-28 kDa erythrocyte integral membrane protein homolog [human, uterus, mRNA, 1346 nt]
6113	16007	26143	1.49	1.0E-84	AL046784.1	NT	Novel human gene mapping to chromosome 13
6113	16007	26144	1.49	1.0E-84	AL046784.1	NT	Novel human gene mapping to chromosome 13
6220	16066	26236	1.96	1.0E-84	AL046784.1	NT	Novel human gene mapping to chromosome 13
6414	16276	26439	3.12	1.0E-84	639399.0	NT	Homo sapiens polymerase (DNA directed), alpha (POLA), mRNA
6493	16324	26490	1.6	1.0E-84	11430846	NT	Homo sapiens NGF-L1 binding protein 1 (ERG1 binding protein 1) (NAB1), mRNA
7493	17360	24854	2.45	1.0E-84	5031062.1	NT	Homo sapiens nuclear transport factor 2 (nuclear protein 135) (PRT13), mRNA
7639	15001	24854	1.95	1.0E-84	4507948	NT	Homo sapiens ubiquitin specific protease 13 (ubiquitinase 13) (USP13), mRNA
7639	15001	24855	1.95	1.0E-84	4507948	NT	Homo sapiens ubiquitin specific protease 13 (ubiquitinase 13) (USP13), mRNA
8100	18623	26855	2.86	1.0E-84	11417812	NT	Homo sapiens parathyroid receptor P2-like 1, orphan receptor (PARAL1), mRNA
8298	18965	26330	9.8	1.0E-84	11416168	NT	Homo sapiens acylates 2, mitochondrial (ACQ2), mRNA
9611	10875	20816	1.17	9.0E-86	AL163309.2	NT	Homo sapiens chromosome 21 segment HS21C009
10271	10974	20816	2.3	9.0E-86	US1432.1	NT	Homo sapiens nuclear protein Sup mRNA, complete cds
10271	10974	20817	2.3	9.0E-86	US1432.1	NT	Homo sapiens nuclear protein Sup mRNA, complete cds
1560	11465	21322	1.07	9.0E-86	M33262.1	NT	Human plasminogen gene, exon 7
1560	11465	21323	1.07	9.0E-86	M33262.1	NT	Human plasminogen gene, exon 7
1651	11554	21417	4.93	9.0E-86	7057020	NT	Homo sapiens DKFZP434P211 protein (DKFZP434P211), mRNA
4156	14058	23832	0.94	9.0E-86	AL163380.2	NT	Homo sapiens chromosome 21 segment HS21C009
4778	14662	24449	1.14	9.0E-86	5901975	NT	Homo sapiens heat shock transcription factor 2 binding protein (HSF2BP), mRNA
4825	14707	24461	1.01	9.0E-86	AL163388.2	NT	Homo sapiens chromosome 21 segment HS21C009
9819	11554	21417	1.27	9.0E-86	7057020	NT	Homo sapiens DKFZP434P211 protein (DKFZP434P211), mRNA
1120	11036	20877	3.24	7.0E-86	L05094.1	NT	Homo sapiens ribosomal protein L27 mRNA, complete cds
8910	18716		5.81	7.0E-86	AF113210.1	NT	Homo sapiens MSTP030 mRNA, complete cds
8716	16535	26619	2.90	6.0E-86	11439573	NT	Homo sapiens DEAD/H (Aap-Glu-Ala-Asp) box polypeptide 10 (RNA helicase) (DDX10), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8718	18835	28620	2.96	6.0E-65	U138573	NT	Homo sapiens DEADH (Asp-Glu-Ala-Asp) box polypeptide 10 (RNA helicase) (DDX10), mRNA
2285	12168	22066	1.21	5.0E-65	AF18394.2	NT	Homo sapiens chromosome 21 segment H827C084
8462	18335	28598	1.0	5.0E-65	AF224980.1	NT	Homo sapiens mammoside, beta A, yesonin (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
9889	15084		2.45	5.0E-65	AF211180.1	NT	Homo sapiens T-type calcium channel alpha1 subunit Alpha1A isoform (CACNA11) mRNA, complete cds
5738	15646	25751	1.96	4.0E-65	SF677910.1	EST_HUMAN	602094730F1 NH1.MGC_83 Homo sapiens cDNA clone IMAGE4246087 5'
5738	15646	25752	1.96	4.0E-65	SF677910.1	EST_HUMAN	602094730F1 NH1.MGC_83 Homo sapiens cDNA clone IMAGE4246087 5'
8017	17697		1.98	4.0E-65	BE076283.1	EST_HUMAN	RC1-B17623-102020-011-c07 B17623 Homo sapiens cDNA
9237	19549		1.97	4.0E-65	Z18887.1	EST_HUMAN	HSDHEG03 Stratiagene cDNA, library Human heart, cat#923208 Homo sapiens cDNA clone HEG03
1277	11185	21035	1.15	3.0E-65	AF068157.1	NT	Homo sapiens protein phosphatase 2A, BR gamma subunit gene, exon 6
1741	11642	21509	3.37	3.0E-65	T97495.1	EST_HUMAN	yeS3999.1 Scores fetal liver spleen 1NHL3 Homo sapiens cDNA clone IMAGE121564 5'
4219	14117	23864	0.94	3.0E-65	BE267189.1	EST_HUMAN	801189704F2 NH1.MGC_7 Homo sapiens cDNA clone IMAGE3533819 5'
4805	14680	24475	1.73	3.0E-65	11024665	NT	Homo sapiens F-box only protein 24 (FBXO24), mRNA
4805	14680	24476	1.73	3.0E-65	11024665	NT	Homo sapiens F-box only protein 24 (FBXO24), mRNA
4864	14744	24523	0.96	3.0E-65	AF5049783.1	NT	Homo sapiens mRNA for KIAA1553 protein, partial cds
4863	14764	24540	0.94	3.0E-65	Z683443	NT	Homo sapiens disintegrin receptor, family 12, subfamily D, member 2 (ORTD2), mRNA
5729	15558	25739	6.94	3.0E-65	7882203	NT	Homo sapiens KIAA0793 gene product (KIAA0793), mRNA
5729	15558	25740	6.94	3.0E-65	7882203	NT	Homo sapiens KIAA0793 gene product (KIAA0793), mRNA
8162	18025		7.04	3.0E-65	AJ004488.1	NT	Homo sapiens mRNA for drosophila wing disc (Drosophila) gene
6524	18474	28653	1.81	3.0E-65	U44953.1	NT	Homo sapiens DEN1 mRNA, complete cds
7180	17071	27256	4.93	3.0E-65	11430863	NT	Homo sapiens DEN1 mRNA, complete cds
8798	18670	28501	2.28	3.0E-65	5331653	NT	Homo sapiens EG-like repeats and discoidin 1-like domains 3 (EDL3), mRNA
9788	19258		2.96	3.0E-65	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
947	16871	20719	0.97	2.0E-65	7857266	NT	Homo sapiens KIAA0029 protein Mos2 interacting nuclear target (MINT) homolog (KIAA0029), mRNA
1024	10542	20786	1.95	2.0E-65	AF248540.1	NT	Homo sapiens intercalin 2 (ICLN2) mRNA, complete cds
1400	11365	21164	7.1	2.0E-65	5174775	NT	Homo sapiens apolipoprotein C-II (APOC2) mRNA
1400	11365	21165	7.1	2.0E-65	5174775	NT	Homo sapiens apolipoprotein C-II (APOC2) mRNA
2183	12070	21972	2.12	2.0E-65	U10026.1	NT	Human DNA polymerase beta gene, exons 12 and 13
2793	11222		4.24	2.0E-65	7957468	NT	Homo sapiens similar to rat integral membrane glycoprotein POMT21 (POMT21), mRNA
4239	14138	23913	5.42	2.0E-65	4905890	NT	Homo sapiens desminin (PUG) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4822	14705	24489	1.3	2.0E-85 AL16394.2	NT	EST_HUMAN	Homo sapiens chromosome 21 segment H821C084 w/87008.x1 NCI CGAP_K102 Homo sapiens cDNA clone IMAGE:298431 3' similar to contains element MSR1 repetitive element.
7341	17209	27408	1.28	2.0E-85 AF769820.1	EST_HUMAN	EST_HUMAN	601601416F1 NH1.MGC.7 Homo sapiens cDNA clone IMAGE:394819 5'
2241	12125		2.44	1.0E-85 BF794306.1	EST_HUMAN	EST_HUMAN	601482817F1 NH1.MGC.67 Homo sapiens cDNA clone IMAGE:3948021 5'
2341	12224	22121	8.09	1.0E-85 BE518392.1	EST_HUMAN	EST_HUMAN	601482817F1 NH1.MGC.67 Homo sapiens cDNA clone IMAGE:3948021 5'
2341	12224	22122	8.09	1.0E-85 BE518392.1	EST_HUMAN	EST_HUMAN	601482817F1 NH1.MGC.67 Homo sapiens cDNA clone IMAGE:3948021 5'
7632	17483	27704	2.06	1.0E-85 BE257917.1	EST_HUMAN	EST_HUMAN	601109738F1 NH1.MGC.19 Homo sapiens cDNA clone IMAGE:3305653 5'
8290	18175	28410	2.56	1.0E-85 AA78785.1	EST_HUMAN	EST_HUMAN	246703.x1 Scores: field liver spleen, INFLS 51 Homo sapiens cDNA clone IMAGE:493245 3'
8290	18175	28420	2.56	1.0E-85 AA78785.1	EST_HUMAN	EST_HUMAN	246703.x1 Scores: field liver spleen, INFLS 51 Homo sapiens cDNA clone IMAGE:493245 3'
8345	18242	28402	2.28	1.0E-85 BF311552.1	EST_HUMAN	EST_HUMAN	6011897003F1 NH1.MGC.19 Homo sapiens cDNA clone IMAGE:4129440 5'
8345	18242	28403	2.28	1.0E-85 BF311552.1	EST_HUMAN	EST_HUMAN	6011897003F1 NH1.MGC.19 Homo sapiens cDNA clone IMAGE:4129440 5'
9164	19082	25283	2.7	1.0E-85	EST_HUMAN	EST_HUMAN	Homo sapiens calcineurin binding protein 1 (K1AA0330), mRNA
9448	19082	25283	3.43	1.0E-85	EST_HUMAN	EST_HUMAN	Homo sapiens calcineurin binding protein 1 (K1AA0330), mRNA
1410	11315		7.66	11417862.NT	NT	EST_HUMAN	Homo sapiens cDNA clone IMAGE:2687660 5'
220	10190	20001	1.3	7.0E-86 BE27427.1	EST_HUMAN	EST_HUMAN	601120778F1 NH1.MGC.20 Homo sapiens cDNA clone IMAGE:2687660 5'
921	10845	20081	1.33	7.0E-86 AA939091.1	EST_HUMAN	EST_HUMAN	985108.x1 Scores: parathyroid tumor, NHPHA Homo sapiens cDNA clone IMAGE:1403550 3'
921	10845	20082	1.33	7.0E-86 AA939091.1	EST_HUMAN	EST_HUMAN	985108.x1 Scores: parathyroid tumor, NHPHA Homo sapiens cDNA clone IMAGE:1403550 3'
6164	15121	24485	6.91	7.0E-86 11421737	NT	EST_HUMAN	Homo sapiens T-cell leukemia virus type 1 binding protein 1 (TAX1BP1), mRNA
7078	16945	27148	2.91	7.0E-86 33657.1	NT	EST_HUMAN	Homo sapiens RAN binding protein 7 (RANBP7), mRNA
7693	17444		1.63	7.0E-86 6453692	NT	EST_HUMAN	Homo sapiens RAN binding protein 7 (RANBP7), mRNA
7024	17475	27398	2.35	7.0E-86	11823307	NT	Homo sapiens D130000 lymphoma critical region gene 6 (D130000), mRNA
8329	18253	28450	2.15	7.0E-86	11417012	NT	Homo sapiens similar to transcription factor CA150 (H1 spleen) (CC63170), mRNA
8329	18253	28450	2.15	7.0E-86	11417012	NT	Homo sapiens similar to transcription factor CA150 (H1 spleen) (CC63170), mRNA
1272	11179	21027	9.33	6.0E-86 4856492	NT	EST_HUMAN	Homo sapiens octabinic acid dihydrogenase (pseudogene) (CG24), mRNA
204	10755	19960	1.48	4.0E-86 BE547173.1	EST_HUMAN	EST_HUMAN	60117258F1 NH1.MGC.12 Homo sapiens cDNA clone IMAGE:545800 5'
8677	15580	25686	10.18	4.0E-86 BE25943.1	EST_HUMAN	EST_HUMAN	60117258F1 NH1.MGC.12 Homo sapiens cDNA clone IMAGE:545800 5'
8677	15580	25686	10.18	4.0E-86 BE25943.1	EST_HUMAN	EST_HUMAN	60117258F1 NH1.MGC.12 Homo sapiens cDNA clone IMAGE:545800 5'
5435	15355	25411	6.02	3.0E-86 AA340948.1	EST_HUMAN	EST_HUMAN	60117258F1 NH1.MGC.12 Homo sapiens cDNA clone IMAGE:545800 5'
7668	17718	27963	3.31	3.0E-86 BE586497.1	EST_HUMAN	EST_HUMAN	601505066F1 NH1.MGC.71 Homo sapiens cDNA clone IMAGE:3971303 5'
7668	17718	27964	3.31	3.0E-86 BE586497.1	EST_HUMAN	EST_HUMAN	601505066F1 NH1.MGC.71 Homo sapiens cDNA clone IMAGE:3971303 5'
8734	17883	28125	9.01	3.0E-86 AA09240.1	EST_HUMAN	EST_HUMAN	601302333F1 NCI CGAP_P128 Homo sapiens cDNA clone IMAGE:2261371 3'
9163	19500		2.02	3.0E-86 BE410354.1	EST_HUMAN	EST_HUMAN	EST1177322 Jurkat T cells VI Homo sapiens cDNA 5' end
288	10231	20046	1.67	2.0E-86 AA309254.1	EST_HUMAN	EST_HUMAN	EST1177322 Jurkat T cells VI Homo sapiens cDNA 5' end
408	10554		1.37	2.0E-86 AL163203.2	NT	EST_HUMAN	Homo sapiens chromosome 21 segment H821C083

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Table 4

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Probe SEQ ID NO:	Exon ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1173	11095	20929	2.18	2.0E-86	N93077.1	EST_HUMAN	Y21A03.01 Scores, multiple, cdcn2a, 2NHNMSF Homo sapiens cDNA clone IMAGE:283478.5'
2144	12032	21903	2.37	2.0E-86	9835487	NT	Human endogenous retrovirus, complete genome
2222	12107	22011	1.12	2.0E-86	AF033103.1	NT	Homo sapiens mRNA for KIAA1277 protein, partial cds
3369	13298	23087	1.45	2.0E-86	AF066142.1	EST_HUMAN	EST1378216 IMAGE, resequencing, MAGE Homo sapiens cDNA
3668	13569	23365	2.16	2.0E-86	AF159776.1	NT	Homo sapiens hypoxanthine phosphotransferase-deficient (PAA ⁻ -delta) mRNA, complete cds
3693	13593	23386	2.16	2.0E-86	AF159776.1	NT	Homo sapiens hypoxanthine phosphotransferase-deficient (PAA ⁻ -delta) mRNA, complete cds
3854	13592		2.42	2.0E-86	AF151743.1	EST_HUMAN	cd87208.x1 NC1 CGAP G08 Homo sapiens cDNA clone IMAGE:2818242.3
4679	14285	24360	2.8	2.0E-86	AF058460.1	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds
5580	15495	25571	1.53	2.0E-86	Z16411.1	NT	H. sapiens mRNA, encoding phosphodiesterase 8
5580	15495	25572	1.83	2.0E-86	Z16411.1	NT	H. sapiens mRNA, encoding phosphodiesterase 8
6087	16064	27037	2.22	2.0E-86	11437139	NT	Homo sapiens butyrolactone (gamma), 2-oxoglutarate dioxygenase (gamma-butyrolactone hydroxylase) (BBOX), mRNA
6087	16064	27038	2.22	2.0E-86	11437139	NT	Homo sapiens butyrolactone (gamma), 2-oxoglutarate dioxygenase (gamma-butyrolactone hydroxylase) (BBOX), mRNA
7372	17241	27148	1.95	2.0E-86	11422941	NT	Homo sapiens chromosome segregation 1 (yeast homolog) like (CSE1L), mRNA
7669	17819	28081	2.68	2.0E-86	11549448	NT	Homo sapiens basic-Hall-kop-Helix-PAS protein (NPASS), mRNA
7699	17819	28082	2.68	2.0E-86	11549448	NT	Homo sapiens basic-Hall-kop-Helix-PAS protein (NPASS), mRNA
8276	18156	28337	1.83	2.0E-86	4750057	NT	Homo sapiens ribosomal protein S6 kinase, 60kD, polypeptide 5 (RPS6K4) mRNA
8600	19187	29250	2.4	2.0E-86	11418189	NT	Homo sapiens thyroid autoantigen 700D (K0 antigen) (G22P*), mRNA
8772	19280		1.81	2.0E-86	AB011399.1	NT	Homo sapiens gene for AF-9, complete cds
8955	19520	25139	1.47	2.0E-86	11417883	NT	Homo sapiens adenergic, beta, receptor kinase 2 (ADRBK2), mRNA
1579	11483	21343	3.1	1.0E-86	4828856	NT	Homo sapiens NADH dehydrogenase (ubiquinone) Fe-S protein 1 (780D) (NADH-coenzyme Q reductase) (NDUFS1), mRNA
3125	13050	22347	2.06	1.0E-86	5453849	NT	Homo sapiens titulin 5 (TBLN5) mRNA
3197	13122	22327	2.42	1.0E-86	L20492.1	NT	Human gamma glutamyl transpeptidase mRNA, complete cds
3256	13179	22377	1.32	1.0E-86	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C09
3256	13179	22378	1.32	1.0E-86	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C09
3864	13176	23498	1.148	1.0E-86	7709161	NT	Homo sapiens hypochloral protein (LOC131319), mRNA
3864	13176	23499	1.148	1.0E-86	7709161	NT	Homo sapiens hypochloral protein (LOC131319), mRNA
4167	14067	23542	5.76	1.0E-86	AL163200.2	NT	Homo sapiens chromosome 21 segment HS21C100
4832	14714	24497	1.11	1.0E-86	AF100791.1	NT	Homo sapiens FKBP-binding protein FKBP3 isoform mRNA, complete cds
8892	15328	23578	2.15	1.0E-86	AF103284.2	NT	Homo sapiens chromosome 21 segment HS21C084
5297	15309		1.47	9.0E-87	AI150703.1	EST_HUMAN	db77030.x1 Scores, fetal, insert, NHH119W Homo sapiens cDNA clone IMAGE:1706128.3' similar to SW-61C1, MOUSE P02635 KERA1N, TYPE I CYTOSKELETAL 10 ;

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Probe SEQ ID NO.	Even SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4860	14760	24637	0.8	2.0E-87	BE175478.1	EST_HUMAN	ROSH-110160-200300-031-C04 T10550 Homo sapiens cDNA
5472	15363	26467	7.97	2.0E-87	BE1724100.1	EST_HUMAN	601690041F1 NH, MGC, 21 Homo sapiens cDNA, clone IMAGE:3943730.5
5473	15363	26468	7.97	2.0E-87	BE1724100.1	EST_HUMAN	601690041F1 NH, MGC, 21 Homo sapiens cDNA, clone IMAGE:3943730.5
5819	16725	26275	6.27	2.0E-87	BE5607183.1	EST_HUMAN	6017341308F1 NH, MGC, 53 Homo sapiens cDNA, clone IMAGE:3985343.9
6260	17122	26275	1.91	2.0E-87	BE5607183.1	EST_HUMAN	6017341308F1 NH, MGC, 53 Homo sapiens cDNA, clone IMAGE:3985343.9
6567	16288	26430	32.21	2.0E-87	N448728.1	EST_HUMAN	Y24767.1 Soares fetal liver spleen cDNA, clone IMAGE:243308.8
6528	16354	26364	26.31	2.0E-87	N448728.1	EST_HUMAN	Y24767.1 Soares fetal liver spleen cDNA, clone IMAGE:243308.8
9862	10771	23950	3.91	2.0E-87	XG2651.1	EST_HUMAN	Human cytoplasmic gene for cytoplasm (EC 6.2.1.2)
7634	17468	26371	5.11	2.0E-87	BE5511936.1	EST_HUMAN	60127831F1 NH, MGC, 38 Homo sapiens cDNA, clone IMAGE:3819339.8
11058	18248	26371	2.33	1.0E-87	7706083.1	EST_HUMAN	Homo sapiens putative glycosylated transfer protein (L0281049), mRNA
1413	13118	21161	0.84	1.0E-87	AW3501677.1	EST_HUMAN	PH2-210255-11095-001-g04 C10283 Homo sapiens cDNA
1413	13118	21162	0.84	1.0E-87	AW3501677.1	EST_HUMAN	PH2-210255-11095-001-g04 C10283 Homo sapiens cDNA
3646	13353	23349	3.18	1.0E-87	Y00062.1	EST_HUMAN	Human mRNA for T-cell cytolysin
3673	13357	23374	2.47	1.0E-87	4758827.1	NT	Homo sapiens neuron 11 (NRXN3) mRNA
6067	14627	24666	1.04	1.0E-87	U60949.1	NT	Rattus norvegicus taste bud receptor protein TB 641 (TB 641) gene, complete cds
5774	16581	26788	3.39	1.0E-87	AF073371.1	EST_HUMAN	Homo sapiens growth factor receptor-bound protein 10 (GRB10) gene, exon 8
5774	16581	26789	3.39	1.0E-87	AF073371.1	EST_HUMAN	Homo sapiens growth factor receptor-bound protein 10 (GRB10) gene, exon 8
6376	16238	26958	1.6	1.0E-87	11431590.1	NT	Homo sapiens protein kinase C, beta 1 (PRKCB1), mRNA
6724	16704	26763	13.13	1.0E-87	AF214662.1	NT	Homo sapiens tracheal epithelium enriched protein (PLUNC) gene, complete cds
7166	17062	27233	1.19	1.0E-87	AB0302918.1	NT	Homo sapiens mRNA for alpha,3-sialyltransferase ST3Gal VI, complete cds
7166	17062	27234	1.19	1.0E-87	AB0302918.1	NT	Homo sapiens mRNA for alpha,3-sialyltransferase ST3Gal VI, complete cds
7684	17476	27620	2.17	1.0E-87	BE516163.1	EST_HUMAN	ROE-BN0275-050700-012-E02 BN0276 Homo sapiens cDNA
7684	17476	27621	2.17	1.0E-87	BE516163.1	EST_HUMAN	ROE-BN0275-050700-012-E02 BN0276 Homo sapiens cDNA
8114	18003	28248	2.06	1.0E-87	U259897.1	EST_HUMAN	Homo sapiens lect domain and RLD 2 (HERC2), mRNA
8397	18244	28247	1.78	1.0E-87	U10063.1	NT	Homo sapiens RGH-1 gene, retrovirus-like element
9539	19751	20547	2.02	1.0E-87	7657832.1	NT	Homo sapiens sulfotransferase-related protein (SULT3), mRNA
1000	11006	11006	7.39	9.0E-86	AF167485.1	NT	Homo sapiens double stranded RNA activated protein kinase (PKR) gene, exon 12
1327	11264	21090	2	9.0E-86	AB0307820.1	NT	Homo sapiens mRNA for KIAA1399 protein, partial cds
1327	11264	21091	2	9.0E-86	AB0307820.1	NT	Homo sapiens mRNA for KIAA1399 protein, partial cds
3574	13468	23279	1.13	9.0E-86	AF163209.1	NT	Homo sapiens chromosome 21 segment HS210009
4172	14072	23847	2.64	9.0E-86	X91626.1	NT	H. sapiens ECE-1 gene (exon 9)
4172	14072	23848	2.64	9.0E-86	X91626.1	NT	H. sapiens ECE-1 gene (exon 9)
4934	14612	24650	1.23	9.0E-86	AB006898.1	NT	Homo sapiens DNA, DLEC1 to ORC1L4 gene region, section 1/2 (DLEC1, ORC1L3, ORC1L4 genes, complete cds)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (10p) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7216	17093	27284	3.69	6.0E-88	AF008528.1	NT	Homo sapiens X-linked ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
1767	11656		1.19	5.0E-88	7661987	NT	Homo sapiens KIAA0003 gene product (KIAA0003), mRNA
2602	12470	22366	3	5.0E-88	N83699.1	EST HUMAN	K9719P Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K9719 5' similar to ZING
2070	12897	22096	0.92	5.0E-88	AF114488.1	NT	FINGER PROTEIN HZF1
2078	12905	22704	0.94	5.0E-88	AF114488.1	NT	Homo sapiens interactin short isoform (ITSN) mRNA, complete cds
2078	12905	22705	0.94	5.0E-88	AF114488.1	NT	Homo sapiens interactin short isoform (ITSN) mRNA, complete cds
3343	13263						w68h08.41 NCI Q604P L24 Homo sapiens cDNA clone IMAGE:2330788 3' similar to contains A.U. repetitive element/contains element MER22 MER22 repetitive element ;
3491	13407	23212	0.91	5.0E-88	AF114488.1	EST HUMAN	Homo sapiens interactin short isoform (ITSN) mRNA, complete cds
4631	14519	24310	0.87	5.0E-88	AF114488.1	NT	Homo sapiens interactin short isoform (ITSN) mRNA, complete cds
6059	16042	26185	2.64	5.0E-88	H10932.1	EST HUMAN	Hom05070.71 Source infant brain T1B8 Homo sapiens cDNA clone IMAGE:47128 5'
6527	16507	26584	1.84	5.0E-88	AL165264.2	NT	Homo sapiens chromosome 21 segment H521084
1307	11214	21070	1.64	4.0E-88	BF09128.1	EST HUMAN	PM1-TN0028-050900-004-10 TN0028 Homo sapiens cDNA
1307	11214	21071	1.64	4.0E-88	BF09128.1	EST HUMAN	PM1-TN0028-050900-004-10 TN0028 Homo sapiens cDNA
6295	16150	20316	1.93	4.0E-88	4502694	NT	Homo sapiens transforming growth factor, beta-induced, 88kD (TGFB1), mRNA
8291	18100	28402	2.84	4.0E-88	4502694	NT	Homo sapiens cell division cycle 10 homologous to CDG10 of S. cerevisiae (CDG10) mRNA
8790	18595	28883	2.1	4.0E-88	7851947	NT	Homo sapiens KIAA0152 gene product (KIAA0152), mRNA
8790	18595	28884	2.1	4.0E-88	7851947	NT	Homo sapiens KIAA0152 gene product (KIAA0152), mRNA
7715	10547	20475	0.99	3.0E-88	11545000	NT	Homo sapiens hypodermal protein FLJ21634 (FLJ21634), mRNA
1770	11959	20475	4.77	3.0E-88	4596020	NT	Homo sapiens zinc finger protein 267 (ZNF267) mRNA
2018	12845	22647	4.31	3.0E-88	N83699.1	EST HUMAN	2548F12.31 Source fetal liver spleen (NF.S Homo sapiens cDNA clone IMAGE:295623 3'
4147	14047	23810	1.21	3.0E-88	4501912	NT	Homo sapiens a disintegrin and metalloprotease domain 23 (ADAM23) mRNA
4147	14047	23820	1.21	3.0E-88	4501912	NT	Homo sapiens a disintegrin and metalloprotease domain 23 (ADAM23) mRNA
4390	14270	24637	3.17	3.0E-88	1426300	NT	Homo sapiens hypodermal protein FLJ20220 (FLJ20220), mRNA
3242	15103	24637	4.09	3.0E-88	1426300	NT	Homo sapiens vesicular-containing protein (VCP), mRNA
3429	15349	25403	3.84	3.0E-88	6960605	NT	Homo sapiens polyoma virus vira 1, cell surface receptor (PV1), mRNA
5498	15471	25400	3.39	3.0E-88	1426307	NT	Homo sapiens vira human spleen vira oncoprotein homolog A (vira related) (RAVA), mRNA
5204	15954	25098	12.03	3.0E-88	AF276235.1	NT	Homo sapiens putative anion transporter 1 mRNA, complete cds
6452	16313	25479	0.66	3.0E-88	11436400	NT	Homo sapiens reticulon-binding protein 2 (RBP2), mRNA
6520	16500	26888	8.52	3.0E-88	11421726	NT	Homo sapiens growth differentiation factor 5 (cartilage derived morphogenetic protein-1) (CDF5), mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2393	12293	22154	1.97	6.0E-89	4507786	NT	Homo sapiens ubiquitin-conjugating enzyme E2L3 (UBE2L3) mRNA
2393	12293	22155	1.97	6.0E-89	4507786	NT	Homo sapiens ubiquitin-conjugating enzyme E2L3 (UBE2L3) mRNA
2480	13395	22301	0.84	6.0E-89	7691817	NT	Homo sapiens HSPC150 protein (HSPC150) mRNA
4537	14430	24211	3.5	6.0E-89	AB007699.2	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
4537	14430	24212	3.5	6.0E-89	AB007699.2	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
5007	14891	24646	2.77	5.0E-89	BE244323.1	EST_HUMAN	TGAP2P263883 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project-TGAP2
5007	14891	24647	2.77	5.0E-89	BE244323.1	EST_HUMAN	TGAP2P263883 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project-TGAP2
6477	15338	25503	1.33	4.0E-89	BE769749.1	EST_HUMAN	OV34.U1022.469000.219-c33 NT0022 Homo sapiens cDNA
2947	12775	22583	1.61	3.0E-89	AF076781.1	EST_HUMAN	EST338350 MAGI2 (resucopos, MAGN) Homo sapiens cDNA
9698	12541	25215	1.92	3.0E-89	AF076781.1	EST_HUMAN	AF076781.1 DB Homo sapiens cDNA, clone AD85GA01.5
121	10348	20175	1.46	2.0E-89	7706570	NT	Homo sapiens PXR2b protein (PXR2b) mRNA
121	10348	20176	1.46	2.0E-89	7706570	NT	Homo sapiens PXR2b protein (PXR2b) mRNA
402	10348	20175	0.91	2.0E-89	7706570	NT	Homo sapiens PXR2b protein (PXR2b) mRNA
402	10348	20176	0.91	2.0E-89	7706570	NT	Homo sapiens PXR2b protein (PXR2b) mRNA
519	10461	20272	0.83	2.0E-89	AB037763.1	NT	Homo sapiens mRNA for KIAA1542 protein, partial cds
2852	12790	22589	2.01	2.0E-89	AI22206.1	EST_HUMAN	g96006.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:181022.5 similar to gp104131
4053	13955	23731	1.45	2.0E-89	AF069897.1	NT	GAMMA-GLUTAMYL TRANSPEPTIDASE 1 PRECURSOR (HUMAN); contains Ala repetitive element
4051	13953	23740	6.18	2.0E-89	X95742.1	NT	Homo sapiens topoisomerase-related function protein (TRF42) mRNA, partial cds
4051	13953	23741	6.18	2.0E-89	X95742.1	NT	H sapiens HCK gene for tyrosine kinase (PTK), exons 10-11
4395	14292	24076	1.14	2.0E-89	AJ007378.1	NT	H sapiens HCK gene for tyrosine kinase (PTK), exons 10-11
5395	15293	25123	2.5	2.0E-89	AB007546.1	NT	Homo sapiens gene for LEO12, complete cds
5538	15455	25525	1.6	2.0E-89	UC3895.1	NT	Human N-ethylmaleimide-sensitive factor mRNA, partial cds
5520	16379	29537	4.93	2.0E-89	U81004.1	NT	Human GT24 (GT24) mRNA, partial cds
6630	16510	29699	3.73	2.0E-89	11428901	NT	Homo sapiens solute carrier family 24 (sodium/potassium/calcium exchanger), member 2 (SLC24A2), mRNA
6690	18568	29891	2.63	2.0E-89	11434411	NT	Homo sapiens integrin, alpha 3 (enligin CD49c, alpha 3 subunit of VLA-3 receptor) (ITGA3), mRNA
9954	19966	29953	4.87	2.0E-89	11433673	NT	Homo sapiens cell adhesion molecule with homology to L1CAM (close homologue of L1) (OIL1), mRNA
9955	19762	29955	2.24	2.0E-89	U10982.1	NT	Homo sapiens 7 antigen (IMAGE7) pseudogene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5433	15353	25400	2.52	5.0E-50	Z16411.1	NT	H.sapiens mRNA encoding phospholipase c
5523	15353	25400	2.13	5.0E-50	Z16411.1	NT	H.sapiens mRNA encoding phospholipase c
5283	16147	26302	2.26	5.0E-50	AF113708.1	NT	Homo sapiens angiotensin II (ANGII) mRNA, partial cds
5283	16147	26303	2.26	5.0E-50	AF113708.1	NT	Homo sapiens angiotensin II (ANGII) mRNA, partial cds
6454	16323	26450	7.93	5.0E-50	4557259	NT	Homo sapiens adenylylate cyclase 9 (ADCY9) mRNA
6525	16704	26850	4.86	5.0E-50	11345493	NT	Homo sapiens hypothetical protein FLJ13322 (FLJ13322), mRNA
7581	17432	27646	1.24	5.0E-50	11419429	NT	Homo sapiens similar to ectonucleotide pyrophosphatase/phosphodiesterase 3 (H. sapiens) (LOC833214), mRNA
7968	17818	28050	15.41	5.0E-50	11433721	NT	Homo sapiens ATPase, aminophospholipid transporter-like, Class I, type 8A, member 2 (ATP8A2), mRNA
9744	18306		2.16	5.0E-50	AB013359.1	NT	Homo sapiens gene for AIF 3, complete cds
9756	19250		2.37	5.0E-50	AB523369.1	EST_HUMAN	ar/3h03.x1 Barstead acris HPLR68 Homo sapiens cDNA clone IMAGE:2128761 3'
269	10263	20083	1.95	4.0E-50	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
269	10263	20084	1.95	4.0E-50	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
1070	10968	20826	2.94	4.0E-50	4595319	NT	Homo sapiens myosin phosphatase, target subunit 1 (MYPT1), mRNA
1633	11565	21432	9.22	4.0E-50	X92033.1	NT	H.sapiens gene encoding discoidin receptor tyrosine kinase, exon 18
4557	14449	24235	4.07	4.0E-50	D97675.1	NT	Homo sapiens cDNA for amyloid precursor protein, complete cds
4691	14571	24372	1.07	4.0E-50	AB334070.1	NT	Homo sapiens mRNA for KIAA1244 protein, partial cds
4713	14590	24365	1.5	4.0E-50	X95987	NT	Human proboscis oostaining enzyme (NEC2) gene, exon 9
8001	18709	23041	103.82	3.0E-50	BE553533.1	EST_HUMAN	601335JUL19H1.MGC_39 Homo sapiens cDNA clone IMAGE:3869147 5'
207	10178	19951	4.28	2.0E-50	BE553753.1	EST_HUMAN	60104737B1.H1.MGC_10 Homo sapiens cDNA clone IMAGE:348354 5'
1158	11059	20913	3.95	2.0E-50	5631749	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 17 (HMGI7), mRNA
1156	11059	20914	3.95	2.0E-50	5631749	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 17 (HMGI7), mRNA
							q5-4c02.x1 Govers, placenta, 36days, 2H4bP4bCwv Homo sapiens cDNA clone IMAGE:1713410 3'
							similar to SW/OLP3_MOUSE F23275 OLFACTORY RECEPTOR OR3.;
3771	16683	23465	2.91	2.0E-50	AI139213.1	EST_HUMAN	Homo sapiens mRNA for KNU289 gene, partial cds
4588	14476	24264	1.13	2.0E-50	AG006627.1	NT	Homo sapiens GRB2-related adaptor protein (GrAP) mRNA
4820	14703	24488	8.33	2.0E-50	572955	NT	HYPOTHETICAL 35.5 KD PROTEIN.;
5534	15451	25510	4.34	2.0E-50	AW672866.1	EST_HUMAN	
7538	17450	27708	2.9	2.0E-50	11427320	NT	Homo sapiens similar to laminin receptor 1 (67kD, ribosomal protein 3A) (H. sapiens) (LOC334893), mRNA
7638	17480	27709	2.9	2.0E-50	11427320	NT	Homo sapiens similar to laminin receptor 1 (67kD, ribosomal protein 3A) (H. sapiens) (LOC334893), mRNA
7722	17572	27796	1.96	2.0E-50	AU118985	EST_HUMAN	AU118985 HEMBA1 Homo sapiens cDNA clone HEMBA1004795 5'

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Probe SEQ ID NO:	Exon NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7722	17672	27797	1.95	2.0E-60	AU118565.1	EST_HUMAN	AU118565 HEMBA1 Homo sapiens cDNA clone HEMBA1004795 5'
8705	17614	28156	46.27	2.0E-60	11024711	NT	Homo sapiens myosin, heavy polypeptide 4, skeletal muscle (MYH4), mRNA
275	10241	20060	3.39	1.0E-60	4902166	NT	Homo sapiens amyloid beta (A β) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
371	12639	20148	1.21	1.0E-60	AF21820.1	NT	Homo sapiens chromosome 21 unknown mRNA
370	12639	20148	1.04	1.0E-60	AF21820.1	NT	Homo sapiens chromosome 21 unknown mRNA
680	10613	20435	2.03	1.0E-60	AJ237569.1	NT	Homo sapiens mRNA for T-box transcription factor (TBX20 gene), partial
680	10613	20435	2.03	1.0E-60	AJ237569.1	NT	Homo sapiens mRNA for T-box transcription factor (TBX20 gene), partial
713	10945	20472	7.71	1.0E-60	AF244760.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
713	10945	20472	7.71	1.0E-60	AF244760.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1034	11010	20473	2.45	1.0E-60	4607826	NT	Homo sapiens Kruppel-like factor 7 (KLF7), mRNA
1284	11162	21044	9.37	1.0E-60	AF090154.1	NT	Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 3
1284	11162	21044	9.37	1.0E-60	AF090154.1	NT	Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 3
1644	11549	21045	4.92	1.0E-60	BE37584.1	EST_HUMAN	6011595632 UH_MGC_59 Homo sapiens cDNA clone IMAGE3511118 5'
1644	11549	21045	4.92	1.0E-60	BE37584.1	EST_HUMAN	Homo sapiens similar to SULT1 (2) (Drosophila) like (LOC37167), mRNA
1680	11750	21631	4.98	1.0E-60	11420314	NT	Homo sapiens chromosome 8 centromeric frame 2 (CBORF2), mRNA
2523	12782	22345	5.4	1.0E-60	AB020710.1	NT	Homo sapiens mRNA for KIAA0600 protein, partial cds
3771	13589	23473	1.15	1.0E-60	AB020710.1	NT	Homo sapiens mRNA for KIAA0600 protein, partial cds
3771	13589	23474	1.15	1.0E-60	AB020710.1	NT	Homo sapiens soluble interalpha 1 receptor accessory protein (LIRAP) gene, exon 5, alternative splicing and complete cds, alternatively spliced
4326	14223	24005	1	1.0E-60	AF167340.1	NT	Homo sapiens mRNA for KIAA0600 protein, partial cds
5461	15401	25464	2.2	1.0E-60	AB014533.1	NT	Homo sapiens solute carrier family 1 (high affinity aspartate/glutamate transporter), member 9 (SLC14), mRNA
6521	16360	26558	2.85	1.0E-60	11426758	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 2 (BIG2), mRNA
7121	10589	27189	3.78	1.0E-60	11422090	NT	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
7356	17224	27190	1.22	1.0E-60	AF163964.1	NT	Homo sapiens CG1-15 protein (LOC51005), mRNA
7371	17240	27444	1.72	1.0E-60	11422105	NT	Homo sapiens CG1-15 protein (LOC51005), mRNA
7371	17240	27445	1.72	1.0E-60	11422105	NT	Homo sapiens CG1-15 protein (LOC51005), mRNA
9732	19208	28226	1.89	1.0E-60	AB002059.1	NT	Homo sapiens DNA for Human P20A, complete cds
9732	19208	28226	1.89	1.0E-60	AB002059.1	NT	Homo sapiens DNA for Human P20A, complete cds
4101	14001	23780	5.48	8.0E-61	DT1234.1	EST_HUMAN	HUM0005381 Liver HepG2 cell line. Homo sapiens cDNA clone s813 3'
1428	11333	21196	0.88	7.0E-91	AF093708.1	NT	Rattus norvegicus brain specific contactin-binding protein CBP90 mRNA, partial cds
8535	16714	26507	2.05	7.0E-91	AF093708.1	NT	Rattus norvegicus brain specific contactin-binding protein CBP90 mRNA, partial cds
3429	13346	23151	1.47	5.0E-61	AA702794.1	EST_HUMAN	250604.41 Scores, final liver, splice, INFLS, S1 Homo sapiens cDNA clone IMAGE-449015 3'
4415	14309	24092	1.05	5.0E-61	AU143530.1	EST_HUMAN	AU143538 Y9AA1 Homo sapiens cDNA clone Y9AA1002097 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4415	14309	24093	1.05	5.0E-91	AU143538.1	EST_HUMAN	AU13639 Y70AA1 Homo sapiens cDNA clone Y70AA1/002867 5'
4703	14569	24379	0.82	5.0E-91	7110634	NT	Homo sapiens chromosome 22 open reading frame 5 (C22ORF5), mRNA
4703	14569	24380	0.92	5.0E-91	7110634	NT	Homo sapiens chromosome 22 open reading frame 5 (C22ORF5), mRNA
7087	16964	27157	1.34	5.0E-91	AV646278.1	EST_HUMAN	AV646878 GLC Homo sapiens cDNA clone GLC8YR08 3'
7087	16964	27157	1.34	5.0E-91	AV646278.1	EST_HUMAN	Homo sapiens Neophosphatidic acid acyltransferase-delta (LPAAT-delta) mRNA, complete cds
3166	13591	22865	1.3	4.0E-91	AF150776.1	NT	Homo sapiens Neophosphatidic acid acyltransferase-delta (LPAAT-delta) mRNA, complete cds
3166	13591	22865	1.3	4.0E-91	AF150776.1	NT	Homo sapiens Neophosphatidic acid acyltransferase-delta (LPAAT-delta) mRNA, complete cds
5301	18180	28427	3.13	4.0E-91	AL163284.2	NT	Homo sapiens chromosome 21 segment H521C084
9239	18554	28514	1.67	4.0E-91	M77594.1	EST_HUMAN	EST101578 Hippocampus, Striatum (cat. #636205) Homo sapiens cDNA clone HHCNC090 similar to
9239	18554	28514	1.67	4.0E-91	M77594.1	EST_HUMAN	Retrovirus-related gag polyprotein
1901	11596	21566	5.12	3.0E-91	11430163	NT	EST101578 Hippocampus, Striatum (cat. #636205) Homo sapiens cDNA clone HHCNC090 similar to
1901	11596	21566	5.12	3.0E-91	11430163	NT	Retrovirus-related gag polyprotein
1901	11596	21567	5.12	3.0E-91	11430163	NT	Homo sapiens solute carrier family 4, anion exchanger, member 3 (SLC4A3), mRNA
2024	13493	22382	0.96	3.0E-91	AF169455.1	NT	Homo sapiens solute carrier family 4, anion exchanger, member 3 (SLC4A3), mRNA
2024	13493	22383	0.96	3.0E-91	AF169455.1	NT	Homo sapiens beta-unsaturated crotonase (BUP1) gene, exon 6
3297	13216	20020	1.71	3.0E-91	AF163363.2	NT	Homo sapiens beta-unsaturated crotonase (BUP1) gene, exon 6
3418	13333	23169	2.68	3.0E-91	AF593310.1	NT	Homo sapiens chromosome 21 segment H521C083
3418	13333	23169	2.68	3.0E-91	AF593310.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
3720	13532	23418	0.83	3.0E-91	AF046303.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
4457	14351	24168	4.02	3.0E-91	AF036033.1	NT	Homo sapiens cyclin D binding 135-like protein mRNA, complete cds
4505	14788	24560	1.2	3.0E-91	AF163285.2	NT	Human Xu (p708p) subunit mRNA, complete cds
4605	14788	24561	1.2	3.0E-91	AF163285.2	NT	Homo sapiens chromosome 21 segment H521C085
5458	15407	25470	1.48	3.0E-91	11434064	NT	Homo sapiens chromosome 21 segment H521C085
5507	15712		2.39	3.0E-91	400740	NT	Homo sapiens apolipoprotein secretory protein (16-300) (HSP), mRNA
5507	15712		2.39	3.0E-91	400740	NT	Homo sapiens cyclin-dependent kinase 9 (CDK9) mRNA
5967	15872	25966	4.11	3.0E-91	11497911	NT	Homo sapiens gamma-aminobutyric acid (GABA) B receptor, 1 (GABBR1), transcript variant 2, mRNA
5967	15872	25967	4.11	3.0E-91	11497911	NT	Homo sapiens gamma-aminobutyric acid (GABA) B receptor, 1 (GABBR1), transcript variant 2, mRNA
6502	16391	26535	4.4	3.0E-91	U96965.1	NT	Human L-type calcium channel beta-1 subunit (CACGLB1) gene, exons 10 and 11
6502	16391	26536	4.4	3.0E-91	U96965.1	NT	Human L-type calcium channel beta-1 subunit (CACGLB1) gene, exons 10 and 11
7083	16870	27163	3.31	3.0E-91	D16494.1	NT	Human mRNA for very low density lipoprotein receptor, complete cds
9480	19104	28286	1.45	3.0E-91	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds

Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ. ID NO.	Expression Signal	Most Similar (BLAST) E-Value	Top Hit Annotation No.	Top Hit Database Source	Top Hit Description
9812	1262	22382	3.03	3.0E-91 AF169555.1	NIT	Homo sapiens beta-uridocytosinase (BUP1) gene, exon 8	
9813	1262	22383	3.03	3.0E-91 AF169555.1	NIT	Homo sapiens beta-uridocytosinase (BUP1) gene, exon 8	
9814	1030	19833	3.02	3.0E-91 AF163744.2	NIT	Homo sapiens chromosome 21 segment RSJ2 CDBL	
1225	11131	20967	3.98	1.0E-91 AW443964.2	EST_HUMAN	DHFR-like class III cytosolic NCI COAP SIBS Homo sapiens cDNA clone IMAGE:733280.3	
9050	10030	19835	1.7	1.0E-91 BF346182.1	EST_HUMAN	SOD22088T NCI COAP Bim27 Homo sapiens cDNA clone IMAGE:4157804.5	
9050	10030	20176	1.7	1.0E-91 BF346182.1	EST_HUMAN	SOD22088T NCI COAP Bim27 Homo sapiens cDNA clone IMAGE:4157804.5	
9050	10030	20176	1.7	1.0E-91 BF346182.1	EST_HUMAN	SOD22088T NCI COAP Bim27 Homo sapiens cDNA clone IMAGE:4157804.5	
9398	19865		2.42	1.0E-91 H115212.1	EST_HUMAN	JMYD3C3 r1 Soxies infant brain TMS Homo sapiens cDNA clone IMAGE:43687.8	
1221	11130	20981	8.41	9.0E-92 AJ001069.1	NIT	Homo sapiens NKX2D1 gene, exon 10	
1221	11130	20982	8.41	9.0E-92 AJ001069.1	NIT	Homo sapiens NKX2D1 gene, exon 10	
8393	15273	20103	3.98	9.0E-92 JG3007.1	NIT	Human Na ⁺ /K ⁺ -ATPase alpha-subunit mRNA, partial cds	
8442	15352	20148	1.78	9.0E-92	NIT	Homo sapiens hydrophobic protein PLI220387 (PLI20265), mRNA	
8682	15786	20811	3.22	9.0E-92 AF310105.1	NIT	Homo sapiens INALU-T1 mRNA, complete cds	
8878	16757	20954	19.33	9.0E-92 AGO40943.1	NIT	Homo sapiens mRNA for KIAA1512 protein, partial cds	
8878	16757	20955	19.33	9.0E-92 AGO40943.1	NIT	Homo sapiens mRNA for KIAA1512 protein, partial cds	
7342	10071	1112068	1.68	9.0E-92 Y136226.1	NIT	Homo sapiens heparan A-inhibited guanine nucleotide-exchange protein 2 (HG2), mRNA	
87	10071	19897	2.02	9.0E-92 W23697.1	EST_HUMAN	2688 Human retina cDNA randomly primed auxiliary Homo sapiens cDNA	
283	10224	20026	6.9	8.0E-92 BE398393.1	EST_HUMAN	001273513T NIH JMGC_20 Homo sapiens cDNA clone IMAGE:391987.9	
1778	11677	21054	1.29	8.0E-92	NIT	Homo sapiens diacylglycerol kinase, gamma (DGKG), mRNA	
1778	11677	21555	1.29	8.0E-92 AJ006076.1	NIT	Homo sapiens diacylglycerol kinase, gamma (DGKG)(DGKG). mRNA	
5544	16646	20673	1.26	8.0E-92 AJ006076.1	NIT	Homo sapiens MCF-4 gene	
6508	16760	20679	3.01	8.0E-92 LQ4163.1	NIT	Human lens membrane protein (mp18) genes, exon 11	
6508	16760	20679	3.01	8.0E-92 LQ4163.1	NIT	Human lens membrane protein (mp18) genes, exon 11	
7242	17116	27314	2.01	8.0E-92 AB014511.1	NIT	Homo sapiens mRNA for KIAA0511 protein, partial cds	
7760	17610	27836	1.31	8.0E-92 Y13626.1	NIT	Homo sapiens mRNA for MBNL protein	
8160	18067	29316	4.83	8.0E-92 AF074393.1	NIT	Homo sapiens nuclear ribogen- and stress-activated protein kinase-1 (NSK1) mRNA, complete cds	
8687	18556	28841	3.21	8.0E-92	NIT	Homo sapiens dyhydropyrimidine S-succinyltransferase (E2 component of 2-on-glylate complex) (DLST)	
9572	19192	25289	1.43	8.0E-92	NIT	mRNA	
9572	19192	25289	1.43	8.0E-92	NIT	Homo sapiens fragile X mental retardation, autosomal homolog 1 (FXR1), mRNA	
10046	16856		2.64	7.0E-92 AKM0076.1	NIT	Human von Willbrand factor pseudogene corresponding to exons 23 through 34	
236	12692	20021	2.51	7.0E-92 AB018301.1	NIT	Homo sapiens mRNA for KIAA0756 protein, partial cds	
236	12692	20021	2.51	7.0E-92 AB018301.1	NIT	Homo sapiens mRNA for KIAA0756 protein, partial cds	
236	12692	20021	2.51	7.0E-92 AB018301.1	NIT	Homo sapiens mRNA for KIAA0756 protein, partial cds	
676	10514		1.25	7.0E-92 AF007822.1	NIT	Homo sapiens cyclopentanecyclic Surfactant truncated isoform mRNA, complete cds	
1259	11166	21017	1.91	7.0E-92	NIT	Homo sapiens S-cell CLCytoplasmic 7d (BCLT7d) mRNA	

Table 4

Single Exon Probes Exp

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
4191	14091	23856	1.02	2.0E-62	M10376.1	NT	Human endogenous retroviral DNA (4-1), complete retroiral segment
4648	14534	24523	0.79	2.0E-62	AF136523.1	NT	Human sapens ribe salt export pump (BSEP) mRNA, complete cds
4622	14801		2.53	2.0E-62	AL040437.1	EST_HUMAN	DKFZ4640414.7 for KIAA (synonym: hies) Homo sapiens cDNA clone D17CZp43C0414.5
6969	15864	26017	2.49	2.0E-62	AB026891.1	EST	Human sapens mRNA for KIAA1008 protein, partial cds
6420	16273		2.25	2.0E-62	U67780.1	NT	Human NPY Y1-like receptor pseudogene mRNA, complete cds
7141	17018	27271	1.37	2.0E-62	AW34074.1	EST_HUMAN	hM02102.y1 Scores: NFI_2T_GGC_31 Homo sapiens cDNA clone IMAGE:290837.31 similar to TR-002711
8142	18080	28276	5.81	2.0E-62	U1434000	NT	002711 PRO-POU-DUTASE POLYPROTEIN :
9536	19172	25274	2.55	2.0E-62	AB023016.1	NT	Homo sapiens thyroid stimulating hormone receptor (TSHR), mRNA
9859	19421	22381	20.85	2.0E-62	6912457	EST_HUMAN	Homo sapiens calcineurin binding protein 1 (KIAA0930), mRNA
1807	11704	21562	1.11	1.0E-62	R78078.1	EST_HUMAN	y80c08.1 Scores placenta N23Pp Homo sapiens cDNA clone IMAGE:145574.5
1807	11704	21583	1.11	1.0E-62	R78078.1	EST_HUMAN	y80c08.1 Scores placenta N23Pp Homo sapiens cDNA clone IMAGE:145574.5
2028	1819	21610	34.72	1.0E-62	4506566	NT	Homo sapiens ribosomal, large, P1 (RLP1) mRNA
7286	17162	27390	4.04	1.0E-62	AL930353.1	EST_HUMAN	y01802.1 NQ2 CGAP, GL1.1 Homo sapiens cDNA clone IMAGE:2107467.3 similar to SW.PTNE_HUMAN O18055 PROTEIN-TYROSINE PHOSPHATASE D1, contains Alu repetitive element;contains element MER17 repeat element;
7286	17162	27361	4.04	1.0E-62	AL930353.1	EST_HUMAN	y01802.1 NQ2 CGAP, GL1.1 Homo sapiens cDNA clone IMAGE:2107467.3 similar to SW.PTNE_HUMAN O18055 PROTEIN-TYROSINE PHOSPHATASE D1, contains Alu repetitive element;contains element MER17 repeat element;
1963	11678	21760	3.14	9.0E-63	AL171681.1	EST_HUMAN	A1721681 MAMMAL Homo sapiens cDNA clone VAMMA1000736.5
1966	11890		9.21	9.0E-63	AA316723.1	EST_HUMAN	U1216841 HOC cell line (nucleotides) to liver in mouse) H1 Homo sapiens cDNA 5' and similar to ribosomal protein L29
2610	12478		1.46	9.0E-63	AF123391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
3053	13277	23267	0.86	9.0E-63	EE338571.1	EST_HUMAN	00128180771 NIH_LMG_C_41 Homo sapiens cDNA clone IMAGE:3903832.5
8011	18719		9.8	9.0E-63	U11418263	EST	001490521.F11 NIH_LMG_C_46 Homo sapiens cDNA clone IMAGE:3863906.5
9675	18719	26003	2.48	9.0E-63	BF093694.1	EST_HUMAN	Homo sapiens chromosome 21 unknown mRNA
2402	10212	20028	0.24	7.0E-63	AF231919.1	NT	Homo sapiens mRNA for KIAA0611 protein, partial cds
11359	11265	21121	1.25	5.0E-63	AB014511.1	NT	w05c08.x1 NQ2 CGAP P728 Homo sapiens cDNA clone IMAGE:2314670.3
1385	11265	21146	5.38	5.0E-63	AB674184.1	EST_HUMAN	w05c08.x1 NQ2 CGAP P728 Homo sapiens cDNA clone IMAGE:2314670.3
1385	11265	21146	5.38	5.0E-63	AB674184.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C0001
1459	11364		0.95	5.0E-63	AL163201.2	NT	Human skeletal muscle 1.3 kb mRNA for recombinant
3165	13240	28265	2.42	5.0E-63	X043001.1	NT	

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Expr SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
6640	16398	28577	3.97	5.0E-60	AF067108.1	NT	Human sapientin protein phosphatase-1 regulatory subunit 7 (PPP1R7) gene, exon 11, complete cds and alternatively spliced product
7649	17400	27913	2.07	5.0E-93	AF214983.1	NT	Human sapientin secondary pathway component Sacs1B-1 mRNA, alternatively spliced, complete cds
7644	17494	27936	1.31	5.0E-93	56321561	NT	Human sapientin TAR (N1) RNA-binding protein 1 (TARBP1) mRNA
8200	18056	28536	3.01	5.0E-93	111359559	NT	Human sapientin nucleobindin 2 (NUC952) mRNA
9487	19423	28713	1.84	5.0E-93	11417877	NT	Human sapientin gamma-glutamyltransferase 1 (GGT1) mRNA
82	10081		4.72	4.0E-93	AA496933.1	EST_HUMAN	526b069.s1 Soares, Isidoro, Naito, Naito Homo sapiens dRNA clone IMAGE:796688 3' similar to SW.GLPA_RAT
487	10381	20294	1.76	4.0E-93	48587978	NT	P373497 CAL-PONIN, ACIDIC (SOPORM) : Homo sapiens interferon gamma receptor 1 (IFNGR1) mRNA
479	10381	20292	1.76	4.0E-93	48587978	NT	Homo sapiens interferon gamma receptor 1 (IFNGR1) mRNA
7651	10886	20262	1.33	4.0E-93	79857454	NT	Homo sapiens pascadic (zifabrafish) homolog 1, containing BROG domain (PES1), mRNA
7650	10886	20262	1.33	4.0E-93	79857454	NT	Homo sapiens pascadic (zifabrafish) homolog 1, containing BROG domain (PES1), mRNA
11681	11078	20923	2.06	4.0E-93	86239958	NT	Homo sapiens pascadic (zifabrafish) homolog 1, containing BROG domain (PES1), mRNA
1934	11929	21712	5.06	4.0E-93	AF047877.1	NT	Homo sapiens diaphoph (DMD) gene, cluster transcripts 1-3 in raton 6
2349	12226	22120	0.84	4.0E-63	AL183031.2	NT	Homo sapiens chromosome 21 segment HS21G101
2964	12436	22326	2.18	4.0E-63	75686972	NT	Homo sapiens TNF-inducible protein CG12-1 (CG12-1), mRNA
3962	13989	22947	1.44	4.0E-63	4804954	NT	Homo sapiens interferon 18 receptor 1 (IL18R1) mRNA
6486	16386	26446	4.81	4.0E-63	T46864.1	EST_HUMAN	y64c1c12.1 Stragelans liver (8907224) Homo sapiens cDNA clone IMAGE:76838 5' similar to similar to SP-A44381 A44381 SERPIN RESPONSE ELEMENT-BINDING PROTEIN SRE-ZBP - HUMAN ,
8476	16386	28613	19.24	3.0E-63	AF692061.1	EST_HUMAN	19A026057 GK030 Homo sapiens cDNA clone GK030R07 5'
3001	13615	23302	5.99	3.0E-63	BF690630.1	EST_HUMAN	802246654F1 NH1_MGC_62 Homo sapiens cDNA clone IMAGE:4332038 5'
3001	13615	23303	5.99	3.0E-63	BF690630.1	EST_HUMAN	802246654F1 NH1_MGC_62 Homo sapiens cDNA clone IMAGE:4332038 5'
4142	14642	24742	2.7	3.0E-63	AF225896.1	NT	Homo sapiens keratin mRNA, complete cds
5505	15462	25620	1.88	3.0E-63	AF165383.1	EST_HUMAN	h23g03.x1 NCI_CGAP Em25 Homo sapiens cDNA clone IMAGE:2169076 3'
5505	15462	25621	1.58	3.0E-63	AF165383.1	EST_HUMAN	h23g03.x1 NCI_CGAP Em25 Homo sapiens cDNA clone IMAGE:2169076 3'
5962	16857	29979	1.32	3.0E-63	11243182	NT	Homo sapiens GNB6 (general control of amino-acid synthesis, yeast, homolog) like 2 (GNBL2), mRNA
8176	18056	29314	4.15	3.0E-63	AB248291.1	EST_HUMAN	m622005.x1 NCI_CGAP G05 Homo sapiens cDNA clone IMAGE:2304489 3'
163	10165	19970	8.31	2.0E-58	AB015610.1	NT	Chlorocibac ethiops mRNA for ribosomal protein S4X, complete cds
163	10165	19971	8.31	2.0E-58	AB015610.1	NT	Chlorocibac ethiops mRNA for ribosomal protein S4X, complete cds
320	10282	20100	6.69	2.0E-58	AL163286.2	NT	Homo sapiens chromosome 21 segment HS21G085
321	10282	20100	7.68	2.0E-58	AL163286.2	NT	Homo sapiens chromosome 21 segment HS21G085

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1688	11603	21383	1.48	2.0E-63	AF223896.1	NT	Homo sapiens tenascin mRNA, complete cds
2083	11979	21898	1.02	2.0E-63	U40703.1	NT	Human Cdk-associated RS cyclophilin CAR5-Cyp mRNA, complete cds
2436	12131	22210	0.89	2.0E-63	HE22982.1	EST_HUMAN	Homo sapiens cDNA clone IMAGE:338320 5'
5088	14659	24732	1.02	2.0E-63	BE26301.1	EST_HUMAN	601110810F1 NH ₂ MGCC 18 Homo sapiens cDNA clone IMAGE:3367243 5'
6326	15245	25049	4.59	2.0E-63	AW68438.1	EST_HUMAN	EST376458 IMAGE:rescuecons, MAGH Homo sapiens cDNA
6482	15382	25442	1.32	2.0E-63	11430039	NT	Homo sapiens hypothetical protein (LOC61918), mRNA
8014	15618		1.32	2.0E-63	AW62002.1	EST_HUMAN	UHFH-BNO-alk-9-05-Q-UT NH ₂ MGCC 50 Homo sapiens cDNA clone IMAGE:3078329 5'
8069	19476	29063	2.97	2.0E-63	AI32026.1	EST_HUMAN	qp7810.x1 Source, fetal, lung, NH ₂ MGCC 16W Homo sapiens cDNA clone IMAGE:1620715 3'
9395	19476		1.32	2.0E-63	AA126736.1	EST_HUMAN	2536-10.01 Source, pregnant, uterus, NH ₂ MGCC 16W Homo sapiens cDNA clone IMAGE:503346 3'
9465	19695		1.31	2.0E-63	LA1825.1	NT	Homo sapiens CYP17 gene, 5' end
9724	19263		2.75	2.0E-63	BF033327.1	EST_HUMAN	601486531F1 NH ₂ MGCC 66 Homo sapiens cDNA clone IMAGE:3862086 5'
98	10081	18897	1.64	1.0E-63	AF238897.1	NT	Homo sapiens GTR1 pseudogene
98	10081	18898	1.64	1.0E-63	AF238897.1	NT	Homo sapiens GTR1 pseudogene
507	10449	20262	2.56	1.0E-63	7657016	NT	Homo sapiens hypothetical protein (D332E18.C1), mRNA
595	10523	20330	3.75	1.0E-63	AI46755.1	EST_HUMAN	094408.x1 NCL CGAP GL11 Homo sapiens cDNA clone IMAGE:1072503 3' similar to TR-Q82384-Q82384
884	10781	20931	3.32	1.0E-63	D87761.1	NT	ZINC FINGER PROTEIN
1217	11261	20974	8.41	1.0E-63	8622370	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
1217	11261	20975	8.41	1.0E-63	8622370	NT	Homo sapiens hypothetical protein FLJ20291 (FLJ20291), mRNA
1321	11228	20975	8.41	1.0E-63	8622370	NT	Homo sapiens hypothetical protein FLJ20291 (FLJ20291), mRNA
1321	11228	21063	1.95	1.0E-63	AB046738.1	NT	Homo sapiens mRNA for KIAA1553 protein, partial cds
1323	11230	21065	1.98	1.0E-63	AF167106.1	NT	Homo sapiens cytosine-rich repeat-containing protein 332 precursor, mRNA, complete cds
2289	12172	22870	1.01	1.0E-63	AF251981.1	NT	Homo sapiens long chain polynucleotide fatty acid elongation enzyme (HELO), mRNA, complete cds
2415	12292	22190	4.16	1.0E-63	AF950066.1	NT	Homo sapiens MFC class 1 region
2498	12334		1.09	1.0E-63	AL137200.1	NT	Novel human gene mapping to chromosome 1
2762	11181	21030	2.89	1.0E-63	BE287396.1	EST_HUMAN	601177698F1 NH ₂ MGCC 17 Homo sapiens cDNA clone IMAGE:3852955 5'
2762	11181	21031	2.89	1.0E-63	BE287396.1	EST_HUMAN	601177698F1 NH ₂ MGCC 17 Homo sapiens cDNA clone IMAGE:3852955 5'
2903	12830	22627	4.33	1.0E-63	D87076.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4331	14228	24010	1.44	1.0E-63	AL183842.1	NT	Homo sapiens chromosome 21 segment HS21C084
5417	15338	25591	1.62	1.0E-63	U78509.1	NT	Homo sapiens glucocorticoid receptor (GR) gene, intron D, exon 5, and intron E
5417	15338	25592	1.62	1.0E-63	U78509.1	NT	Homo sapiens glucocorticoid receptor (GR) gene, intron D, exon 5, and intron E
6007	15522	25904	0.15	1.0E-63	4657792	NT	Homo sapiens neurabinin 1 (neurabinin, von Recklinghausen disease, Watson disease) (NFI) mRNA
8067	16051	26197	2.06	1.0E-63	11431590	NT	Homo sapiens protein kinase C, beta 1 (PRKCB1), mRNA

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Table 4

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6299	18163	28320	4.09	1.0E-63	D42072.1	NT	Human mRNA for NF1 N1-isoform-exon11, complete cds
6807	16986	29876	2.04	1.0E-63	A6307832.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
6971	16848	27059	1.18	1.0E-63	Y10183.1	NT	H. sapiens mRNA for MEMO protein
7024	16901	27063	1.99	1.0E-63	AF103032.1	NT	Homo sapiens protein kinase inhibitor gamma (PKIG) mRNA, complete cds
7407	16460	26640	1.8	1.0E-63	A5010918.1	NT	Homo sapiens mRNA for KIAA1485 protein, partial cds
7407	16463	26643	1.22	1.0E-63	AF091395.1	NT	Homo sapiens Tris isoform mRNA, complete cds
7529	17380	27865	4.54	1.0E-63	X13474.1	NT	Human Prk44 gene for Alzheimer's disease A4 amyloid protein precursor (exon 9)
7529	17380	27866	4.54	1.0E-63	X13474.1	NT	Human Prk44 gene for Alzheimer's disease A4 amyloid protein precursor (exon 9)
9051	19494	28132	5.92	1.0E-63	A026292.1	EST_HUMAN	nc004123.x1 NC1_CGAP_Lu6 Homo sapiens cDNA clone IMAGE:1880768 3' similar to WFT-7984.4
9716	19257		2.33	1.0E-63	11417858	NT	CE13745
8025	17775		1.22	8.0E-94	AL163268.2	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2), mRNA
3880	13781	23579	1.74	6.0E-94	AF14262.1	NT	Homo sapiens chromosome 21 segment15821509
9830	16531		1.67	6.0E-94	11418351	NT	Homo sapiens transcription enhancer factor 5 mRNA, complete cds
6299	18217	26019	3.05	5.0E-94	AB014612.1	NT	Homo sapiens mRNA for KIAA0072 protein, partial cds
6299	18217	26020	3.05	5.0E-94	AB014612.1	NT	Homo sapiens mRNA for KIAA0072 protein, partial cds
6880	16599	26599	1.72	5.0E-64	A722384.1	EST_HUMAN	299706.61 Scores: final: 1.72, NC21fr: 394 Homo sapiens cDNA clone IMAGE:109894.3'
6183	16089	26218	1.83	5.0E-64	A722384.1	EST_HUMAN	063405.61 Scores: final: 1.83, NC21fr: 394 Homo sapiens cDNA clone IMAGE:109894.3'
9391	19736	24911	4.68	5.0E-64	A015900.1	EST_HUMAN	149804.41 Scores: final: 4.68, NC21fr: 394 Homo sapiens cDNA clone IMAGE:16239.3'
9391	19736	24911	1.27	5.0E-64	T89398.1	EST_HUMAN	Homo sapiens mRNA for KIAA0027 protein, partial cds
9907	19384		1.26	5.0E-94	D25217.2	NT	Homo sapiens cleavage and polyadenylation specific factor 1, 100KD subunit (CPSF1), mRNA
1799	11697		4.55	4.0E-94	L05094.1	NT	Homo sapiens ribosomal protein L27 mRNA, complete cds
2621	12489	22379	0.85	4.0E-94	4500008	NT	Homo sapiens protein phosphatase 1, regulatory subunit 10 (PPP1R10) mRNA
4618	14805	24295	3.02	4.0E-94	AI591312.1	EST_HUMAN	1w11f10.x1 NC1_CGAP_Bms52 Homo sapiens cDNA clone IMAGE:2265403 3' similar to TR-Q15265 Q15266
5892	15708	25921	1.84	4.0E-94	11440670	NT	PROTEIN TYROSINE PHOSPHATASE
5892	15708	25922	1.84	4.0E-94	11440670	NT	Homo sapiens solute carrier family 22 (organic cation transporter), member 1-like (SLC22A1L), mRNA
8749	17066	28142	1.72	4.0E-94	11545792	NT	Homo sapiens solute carrier family 22 (organic cation transporter), member 1-like (SLC22A1L), mRNA
595	10351	20539	1.17	3.0E-94	AB022785.1	NT	Homo sapiens ASH2L gene, complete cds, similar to Drecephila ash2 gene
704	10357	20482	1.17	3.0E-94	4502509	NT	Homo sapiens complement component 5 (C5) mRNA
1706	11907	21477	1.05	3.0E-94	AF167706.1	NT	Homo sapiens cyclase-rich repeat-containing protein S52 precursor, mRNA, complete cds
1706	11907	21478	1.05	3.0E-94	AF167706.1	NT	Homo sapiens cyclase-rich repeat-containing protein S52 precursor, mRNA, complete cds

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1735	11636	21504	3.46	3.0E-64	4597569	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA
4095	13065	23772	0.82	3.0E-64	AA049405.1	EST_HUMAN	znfxg30b1.1 Soares, fetal, N23/F6, 9w Homo sapiens cDNA clone IMAGE:774782 5'
5484	15403	25466	3.38	3.0E-64	11469269	EST	Homo sapiens zinc finger protein ZTF (ZNF271), mRNA
5681	15787	25900	4.16	3.0E-64	11520229	NT	Homo sapiens chromosome 21 open reading frame 18 (C21ORF18), mRNA
6771	16950	28538	1.16	3.0E-64	AF162309.1	NT	Homo sapiens proboscoidin alpha 13 (PCDH-alpha13) mRNA, complete cds
6902	16960	27992	3.79	3.0E-64	AB014579.1	NT	Homo sapiens mRNA for KIA02676 protein, partial cds
7533	17884	27595	4.36	3.0E-64	AF007942.1	NT	Homo sapiens glycophorin-L mRNA, complete cds
8448	18321	28580	1.75	3.0E-64	475782.1	NT	Homo sapiens axonal transport of synaptic vesicles (ATSV) mRNA
8628	18736	29025	2.27	3.0E-64	U28711.1	NT	Human cdkb truncated form 1 lacking leucine zipper mRNA, complete cds
143	19177	19937	2.24	1.0E-64	BE26571.1	EST_HUMAN	601175762F1 NHL/MGC, 17 Homo sapiens cDNA clone IMAGE:3531038 5'
3050	19277	22768	1.91	1.0E-64	BE263433.1	EST_HUMAN	601111896F1 NHL/MGC, 16 Homo sapiens cDNA clone IMAGE:3393569 5'
3060	19277	22770	1.91	1.0E-64	BE263433.1	EST_HUMAN	601111896F1 NHL/MGC, 16 Homo sapiens cDNA clone IMAGE:3393569 5'
4391	14160	23038	1.33	1.0E-64	6509629	NT	Homo sapiens brachyoligin protein (BL20746), mRNA
7331	17255	27430	1.93	1.0E-64	11482710	NT	Homo sapiens brachyoligin protein (BL20746), mRNA
7636	17487	27707	1.41	1.0E-64	BE789378.1	EST_HUMAN	Homo sapiens cyclin box gene 5 (B-cell lineage specific activator protein) (PAX5), mRNA
8418	18292	28546	2.49	1.0E-64	U65950.1	NT	Homo sapiens cyclin box gene 5 (B-cell lineage specific activator protein) (PAX5), mRNA
8535	18500	28775	2.19	1.0E-64	A027244.1	EST_HUMAN	Homo sapiens IL-1 receptor antagonist (IL-1Ra) (IL-1RN) gene, alternatively spliced forms, complete cds
9789	19177	19937	1.88	1.0E-64	BE26571.1	EST_HUMAN	601175762F1 NHL/MGC, 17 Homo sapiens cDNA clone IMAGE:1959722 3' similar to TRC08246
1461	11366	21260	1.95	0.0E-96	AF027902.1	NT	C026345 NEURAL CELL ADHESION PROTEIN BIG-2 PRECURSOR, ;
3118	13043	22859	1.13	0.0E-96	7692027	NT	Homo sapiens TNF-alpha stimulated ABC protein (ACSB0) mRNA, complete cds
3118	13043	22840	1.13	0.0E-96	7692027	NT	Homo sapiens TNF-alpha stimulated ABC protein (ACSB0) mRNA, complete cds
6801	16650	28669	1.87	0.0E-96	AF274753.1	NT	Homo sapiens KIA0295 gene product (KIA0295), mRNA
4436	14331	24119	1.59	8.0E-65	A1700998.1	EST_HUMAN	Homo sapiens KIA0295 gene product (KIA0295), mRNA
4436	14331	24119	1.59	8.0E-65	A1700998.1	EST_HUMAN	Homo sapiens KIA0295 gene product (KIA0295), mRNA
6294	16158	26314	1.83	8.0E-65	11426529	NT	W69604.L1 NOL_GCAP_L24 Homo sapiens cDNA clone IMAGE:2340606 3' similar to gbK00558
6294	16158	26315	1.83	8.0E-65	11426529	NT	W69604.L1 NOL_GCAP_L24 Homo sapiens cDNA clone IMAGE:2340606 3' similar to gbK00558
6770	16649	26837	2.05	8.0E-65	AF032897.1	NT	TUBULIN ALPHA-1 CHAIN (HUMAN);
7391	17309	27516	1.75	8.0E-65	11420944	NT	TUBULIN ALPHA-1 CHAIN (HUMAN);
7391	17309	27516	1.75	8.0E-65	11420944	NT	TUBULIN ALPHA-1 CHAIN (HUMAN);
7697	17517	27744	2.82	8.0E-65	5174644	NT	Homo sapiens profilin deshydrogenase (profilin oxidase) (PRODH) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF-SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7681	17631		2.83	8.0E-66	AB007816.1	NT	Homo sapiens mRNA for KIAA1385 protein, partial cds
8096	17987	28236	2.41	8.0E-65	AF112152.1	NT	Homo sapiens developmental arteries and neural crest EGF-like protein mRNA, complete cds
9686	16242		8.68	8.0E-65	AA020566.1	EST_HUMAN	zfx4001 s1 Source, testis_NHT Homo sapiens cDNA clone IMAGE:744640 3' similar to contains L11 L1 repetitive element
274	10240	20058	9.46	7.0E-65	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
274	10240	20059	9.46	7.0E-65	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4270	14169	23947	5.64	7.0E-65	N95705.1	NT	Homo sapiens Lys-like protein (CD59) mRNA, complete cds
4316	14213		1.93	7.0E-65	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21 D046
4982	14857	24623	1.03	7.0E-65	N95929.1	NT	Homo sapiens homeobox protein (PHOX1) mRNA, 3' end
5340	15291	25097	1.76	3.0E-65	BF526041.1	EST_HUMAN	9020711487-1 NCL CGAP_Emb4 Homo sapiens cDNA clone IMAGE:4214147 5'
922	10917	20694	0.96	2.0E-65	4604374	NT	Homo sapiens H factor 1 (complement) (HFI) mRNA
1625	11529	21397	1.6	2.0E-65	7662027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
1625	11529	21398	1.6	2.0E-65	7662027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
1897	11793	21672	7.79	2.0E-65	4507512	NT	Homo sapiens testis inhibitor of metalloproteinase 3 (Sorby/fundus dystrophy, pseudoinflammatory) (TIMP3) mRNA
1900	11766	21676	3.3	2.0E-65	EE363073.1	EST_HUMAN	601312167F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:5658862 5'
2376	12266	22147	1.3	2.0E-65	5453668	NT	Homo sapiens G protein-coupled receptor 19 (GPR19) mRNA
2376	12266	22148	1.3	2.0E-65	5453665	NT	Homo sapiens G protein-coupled receptor 19 (GPR19) mRNA
2417	12264	22161	16.55	2.0E-65	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
2466	12242	22235	2.45	2.0E-65	4789429	NT	Homo sapiens glycine cleavage system protein 2 (aminomethyl carrier) (GCSH) mRNA
2797	10946	20693	0.96	2.0E-65	4504374	NT	Homo sapiens H factor 1 (complement) (HFI) mRNA
3120	13045	23842	3.51	2.0E-65	AF015452.1	NT	Homo sapiens Usp29a-gamma mRNA, complete cds
3517	13453	23252	2.78	2.0E-65	7705900	NT	Homo sapiens uncoupling protein 15 (UCP15) mRNA
3517	13453	23253	2.78	2.0E-65	7705900	NT	Homo sapiens uncoupling protein 15 (UCP15) mRNA
3595	13479	23258	0.96	2.0E-65	AB037807.1	NT	Homo sapiens mRNA for KIAA1385 protein, partial cds
3600	13604	23300	1.02	2.0E-65	AA020294.1	EST_HUMAN	qnd102LX1 Source, NHMIPu_S1 Homo sapiens cDNA clone IMAGE:680546 3' similar to WP72037.4 (CG3705),
4294	14163	23940	2.3	2.0E-65	7657185	NT	Homo sapiens hypothetical gene product (KIAA2281A), mRNA
4671	14646	24615	2.57	2.0E-65	7697979	NT	Homo sapiens KIAA0187 gene product (KIAA0187), mRNA
5022	14655	24663	0.98	2.0E-65	AA447691.1	EST_HUMAN	zxt1407.r1 Source, total, fetus_N02HF8_3m Homo sapiens cDNA clone IMAGE:766157 5'
5022	14655	24664	0.98	2.0E-65	AA447691.1	EST_HUMAN	zxt1407.r1 Source, total, fetus_N02HF8_3m Homo sapiens cDNA clone IMAGE:766157 5'
5367	15287	25121	3.66	2.0E-65	7705764	NT	Homo sapiens CGI-48 protein (LOC51059), mRNA
5367	15287	25122	3.66	2.0E-65	7705764	NT	Homo sapiens CGI-48 protein (LOC51059), mRNA

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6734	19642	26748	4.34	2.0E-96	M9724.1	NT	Human muscle-type phosphofructokinase (PFK-M) gene, exon 7
6957	19662	26964	2.25	2.0E-96	AF297797.1	NT	Homo sapiens cullin4b heavy chain 9 (DNAH9) mRNA, complete cds
6045	18038	26179	1.62	2.0E-96	11435773	NT	Homo sapiens huntingtin (Huntington disease) (HD), mRNA
8106	17966	28245	2.38	2.0E-96	4757653	NT	Homo sapiens bone morphogenetic protein receptor, type IA (BMPRIA) mRNA
9462	19084	28285	1.98	2.0E-96	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
9840	19338	28211	4.34	2.0E-96	11418184	NT	Homo sapiens adenylosuccinate lyase (ADSL), mRNA
6480	15371	26427	7.73	1.0E-95	AA284681.1	EST_HUMAN	422914.1 Sources every tumor N6HOT; Homo sapiens cDNA clone IMAGE:714007 5' similar to TR-G:007084 G1057084 F5942.5;
6480	15371	26428	7.73	1.0E-95	AA284681.1	EST_HUMAN	422914.1 Sources every tumor N6HOT; Homo sapiens cDNA clone IMAGE:714007 5' similar to TR-G:007084 G1057084 F5942.5;
6437	16298	26440	4.85	1.0E-95	BF370000.1	EST_HUMAN	RC6-FN0016-20600.011-G31 FN0019 Homo sapiens cDNA
6437	16298	26441	4.85	1.0E-95	BF370000.1	EST_HUMAN	RC6-FN0016-20600.011-G31 FN0019 Homo sapiens cDNA
6767	18048	26835	1.67	9.0E-96	BE567259.1	EST_HUMAN	801437232.F1 NH_MGC_73 Homo sapiens cDNA clone IMAGE:3922423 5'
435	12694	26201	0.82	8.0E-96	BE507697.1	EST_HUMAN	801497638.F1 NH_MGC_70 Homo sapiens cDNA clone IMAGE:3899761 5'
435	12698	26202	0.82	8.0E-96	BE507697.1	EST_HUMAN	801497638.F1 NH_MGC_70 Homo sapiens cDNA clone IMAGE:3899761 5'
5393	18502	26202	2.66	8.0E-96	AV189047.1	EST_HUMAN	FN01-T0016-00300-002-006 L70019 Homo sapiens cDNA
3834	13746	23638	0.95	7.0E-96	AV231620.1	NT	Homo sapiens chromosome 21 unknown mRNA
2213	12029	22003	0.85	6.0E-96	BE171684.1	EST_HUMAN	M93-HT659-25020-002-407 HT659 Homo sapiens cDNA
3278	13197	22937	0.99	8.0E-96	BE171684.1	EST_HUMAN	M93-HT659-25020-002-407 HT659 Homo sapiens cDNA
3427	13354	23159	28.15	8.0E-96	M28973.1	NT	Homo sapiens chromosome 21 segment HS21C001
8831	18044	28627	1.98	8.0E-96	7622289	NT	Homo glyceraldehyde-3-phosphate dehydrogenase pseudogene 3 and
8831	18044	28628	1.98	8.0E-96	7622289	NT	Homo sapiens KIA00763 gene product (KIA00763), mRNA
8870	19552	28972	2.09	6.0E-96	8923939	NT	Homo sapiens myotub, heavy polypeptide 2, skeletal muscle, adult (MTH2), mRNA
317	10279	20566	2.7	5.0E-96	AB032968.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
824	10751	20569	3.06	5.0E-96	AB032968.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
624	10751	20569	3.06	5.0E-96	AB032968.1	NT	Homo sapiens phosphodiesterase 6A, cAMP-specific, rod, alpha (PDE6A), mRNA
2576	12447	22713	2.31	5.0E-96	11416767	NT	Homo sapiens phosphodiesterase 6A, cAMP-specific, rod, alpha (PDE6A), mRNA
2691	12919	22713	0.98	5.0E-96	6912735	NT	Homo sapiens transmembrane receptor subunit channel 5 (TRPC5), mRNA
4810	14394	22713	1.22	5.0E-96	X00812.1	NT	H. sapiens DNA for monomine oxidase type A (7) (partial)
9005	18048	28193	4.23	5.0E-96	11424999	NT	Homo sapiens A kinase (PKA) anchor protein 1 (AKAP1), mRNA
6045	18048	28194	4.23	5.0E-96	11424999	NT	Homo sapiens A kinase (PKA) anchor protein 1 (AKAP1), mRNA
9719	19599	28788	1.81	5.0E-96	M68347.1	NT	Human type IV collagenase (CLG4B) gene, exon 5
9719	19599	28789	1.81	5.0E-96	M68347.1	NT	Human type IV collagenase (CLG4B) gene, exon 5

Table 4

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession	Top Hit Database Source	Top Hit Descriptor
4057	13957		9.22	3.0E-99	H69556.1	EST_HUMAN	YbH12.11 Soares fetal liver cDNA clone IMAGE212327.6
4058	13958		3.49	2.0E-99	45903060	EST_HUMAN	Human sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
4059	10355		1.58	2.0E-99	AI163248.1	EST_HUMAN	Human sapiens chromosome 21 segment HS2100-8
4060	10356		1.58	2.0E-99	BE114047.4	EST_HUMAN	RGSH-H10230-040500*-110-902 HT0230 Homo sapiens cDNA
4851	14337		9.08	2.0E-99	AJ698491.1	EST_HUMAN	AJ698491 GJM6 NIH MGCC 7 Homo sapiens cDNA clone GKCFCMD07.5
7161	17602		2.05	2.0E-99	AW24940.1	EST_HUMAN	26103351, 5'UTR NIH MGCC 7 Homo sapiens cDNA clone IMAGE2819351.5
6551	10350		1.69	1.0E-99	Y18890.1	EST_HUMAN	Human endogenous retrovirus type K (HERV-K), gag, pol and env genes
17421	11643		2.03	1.0E-99	AF595564.1	EST_HUMAN	EST7697124 IMAGE sequences, MAGC Homo sapiens cDNA
17422	11643		2.03	1.0E-99	AF595564.1	EST_HUMAN	EST7697124 IMAGE sequences, MAGC Homo sapiens cDNA
17423	11643		2.03	1.0E-99	AF595564.1	EST_HUMAN	EST7697124 IMAGE sequences, MAGC Homo sapiens cDNA
1806	11703		0.94	1.0E-99	4493750	EST_HUMAN	Homo sapiens beta containing monooxygenase 2 (FMO2) mRNA
1806	11703		0.94	1.0E-99	4493750	EST_HUMAN	Homo sapiens beta containing monooxygenase 2 (FMO2) mRNA
2181	12068		1.99	1.0E-99	U75967.1	EST_HUMAN	Human hepatocyte growth factor gene, exon 1
2181	12068		1.99	1.0E-99	U75967.1	EST_HUMAN	Human hepatocyte growth factor gene, exon 1
2181	12068		1.99	1.0E-99	U75967.1	EST_HUMAN	Human hepatocyte growth factor gene, exon 1
2216	12850		2.20	1.0E-99	U61472.2	EST_HUMAN	Falls catus superficial myosin heavy chain (sMyHC) mRNA, complete cds
7059	19935		20.95	1.0E-99	U119428	EST_HUMAN	Homo sapiens similar to ectodermal pyrophosphatase 3 (H sapiens) (LOC63214), mRNA
7135	17015		1.94	1.0E-99	AF274893.1	EST_HUMAN	Homo sapiens secretory pathway component Sac3B1-4 mRNA, alternatively spliced, complete cds
7843	17993		1.84	1.0E-99	A3033116.1	EST_HUMAN	Homo sapiens mRNA for KIAA1250 protein, partial cds
7843	17993		1.84	1.0E-99	A3033116.1	EST_HUMAN	Homo sapiens mRNA for KIAA1250 protein, partial cds
7843	17993		1.84	1.0E-99	A3033116.1	EST_HUMAN	Homo sapiens mRNA for KIAA1250 protein, partial cds
3265	12700		0.95	1.0E-97	BF245240.1	EST_HUMAN	6018837125 NIH MGCC 57 Homo sapiens cDNA clone IMAGE:4051202.5
6459	16319		2.76	8.0E-97	BE11849.1	EST_HUMAN	DK-H1017-011059-0407 HT0117 Homo sapiens cDNA
8572	16832		1.76	5.0E-97	AL043314.2	EST_HUMAN	DK-H1017-011059-0407 HT0117 Homo sapiens cDNA clone DKF-Zk43A0329.6
6755	16514		10.79	5.0E-97	AA418003.1	EST_HUMAN	g676123.1 Soares, NPA3, mRNA
7758	17429		2.76	5.0E-97	BF164972.1	EST_HUMAN	RGH-ET0812-26990-033-098 BT0812 Homo sapiens cDNA
8832	18648		1.87	5.0E-97	BE168597.1	EST_HUMAN	MGH-H10211-15550-0104302 HT0241 Homo sapiens cDNA
8832	18648		1.87	5.0E-97	BE168597.1	EST_HUMAN	MGH-H10211-15550-0104302 HT0241 Homo sapiens cDNA
924	10849		2.08	4.0E-97	BC004466.1	EST_HUMAN	CHD-5N0108-17000-298-s08 ENO108 Homo sapiens cDNA
1688	11764		2.18	4.0E-97	BC004466.1	EST_HUMAN	CHD-5N0108-17000-298-s08 ENO108 Homo sapiens cDNA
1688	11764		2.18	4.0E-97	BC004466.1	EST_HUMAN	CHD-5N0108-17000-298-s08 ENO108 Homo sapiens cDNA
0082	16027		6.1	4.0E-97	Y11339.2	EST_HUMAN	Homo sapiens beta-tubulin, A1-tubulin guanine nucleotide-exchange protein 2 (BtG2), mRNA
0082	16027		6.1	4.0E-97	Y11339.2	EST_HUMAN	Homo sapiens beta-tubulin, A1-tubulin guanine nucleotide-exchange protein 2 (BtG2), mRNA
0082	16027		6.1	4.0E-97	Y11339.2	EST_HUMAN	Homo sapiens beta-tubulin, A1-tubulin guanine nucleotide-exchange protein 2 (BtG2), mRNA
0687	16848		1.41	4.0E-97	U1142760	EST_HUMAN	Homo sapiens mRNA for GANAc alpha-2, 6-sialyltransferase 1, long form
0687	16848		1.41	4.0E-97	U1142760	EST_HUMAN	Homo sapiens mRNA for GANAc alpha-2, 6-sialyltransferase 1, long form
7326	17342		2.74	4.0E-97	A5011100.1	EST_HUMAN	Homo sapiens v-src antigen (Schmidt-Ruppin A-1) vral oncogene homolog (SRC), mRNA
7326	17342		2.74	4.0E-97	A5011100.1	EST_HUMAN	Homo sapiens v-src antigen (Schmidt-Ruppin A-1) vral oncogene homolog (SRC), mRNA
7326	17342		2.74	4.0E-97	A5011100.1	EST_HUMAN	Homo sapiens v-src antigen (Schmidt-Ruppin A-1) vral oncogene homolog (SRC), mRNA

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon ID NO.	ORF-SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7328	17232	27434	1.17	4.0E-97	AB011166.1	NT	Homo sapiens mRNA for KIAA0954 protein, partial cds
8503	18376	28641	1.76	4.0E-97	11863122	NT	Homo sapiens AXL receptor tyrosine kinase (AXL), transcript variant 1, mRNA
8503	18376	28642	1.76	4.0E-97	11863122	NT	Homo sapiens AXL receptor tyrosine kinase (AXL), transcript variant 1, mRNA
8723	17682	28124	12.68	4.0E-97	AB042557.1	NT	Homo sapiens mRNA, similar to rat myomoglobin, complete cds
8726	17685	28128	2.31	4.0E-97	AB033116.1	NT	Homo sapiens mRNA for KIAA1260 protein, partial cds
8736	17695	28128	2.31	4.0E-97	AB033116.1	NT	Homo sapiens mRNA for KIAA1260 protein, partial cds
8531	18072	28026	3.83	4.0E-97	11418318	NT	Homo sapiens Q-2 and S-phase expressed 1 (Q2SE1), mRNA
243	10210	20026	1.17	3.0E-97	AB032983.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
898	10783	20553	10.96	3.0E-97	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
898	10783	20554	10.96	3.0E-97	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
1423	12664	21195	1.77	3.0E-97	4736513	NT	Homo sapiens X-ray crystallography (XRC) gene, exon 7
2386	12662	22181	1.92	3.0E-97	U92555.1	NT	Homo sapiens perlecanin (PCN) mRNA
3323	13147	22948	1.14	3.0E-97	5174478	NT	Homo sapiens alpha 1 (EEF1A1) mRNA
4870	14566	23449	12.65	1.0E-97	4503470	NT	Homo sapiens alpha 1 (EEF1A1) mRNA
8972	15778	25897	2.19	1.0E-97	BE069488.1	EST	Homo sapiens alpha 1 (EEF1A1) mRNA
8098	17678	28229	3.41	1.0E-97	11427757	NT	Homo sapiens alpha 1 (EEF1A1) mRNA
8098	17678	28230	3.41	1.0E-97	11427757	NT	Homo sapiens alpha 1 (EEF1A1) mRNA
8529	18464	28708	2.82	1.0E-97	AA553761.1	EST	Homo sapiens alpha 1 (EEF1A1) mRNA
8703	17812	28135	13.54	1.0E-97	11426272	NT	Homo sapiens alpha 1 (EEF1A1) mRNA
8703	17812	28137	13.54	1.0E-97	11426272	NT	Homo sapiens alpha 1 (EEF1A1) mRNA
8893	10069	20538	8	9.0E-98	BE069373.1	EST	Homo sapiens alpha 1 (EEF1A1) mRNA
1245	11162	21012	1.29	9.0E-98	63620022	NT	Homo sapiens alpha 1 (EEF1A1) mRNA
6623	15503	26591	4.74	9.0E-98	4758118	NT	Homo sapiens alpha 1 (EEF1A1) mRNA
6623	15503	26592	4.74	9.0E-98	4758118	NT	Homo sapiens alpha 1 (EEF1A1) mRNA
7271	17148	27342	2.77	9.0E-98	X00980.1	NT	Homo sapiens alpha 1 (EEF1A1) mRNA
7318	17195	27395	2.41	9.0E-98	11321890	NT	Homo sapiens alpha 1 (EEF1A1) mRNA
7355	17223	27423	1.39	9.0E-98	AB032322.1	NT	Homo sapiens alpha 1 (EEF1A1) mRNA
8399	18246	29469	2.24	9.0E-98	AB032322.1	NT	Homo sapiens alpha 1 (EEF1A1) mRNA
9345	10069	20558	4.97	9.0E-98	BE069373.1	EST	Homo sapiens alpha 1 (EEF1A1) mRNA
1300	11256	21112	0.89	8.0E-98	AB033768.1	NT	Homo sapiens alpha 1 (EEF1A1) mRNA
1540	11444	21803	1.04	8.0E-98	5031810	NT	Homo sapiens alpha 1 (EEF1A1) mRNA

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Probe NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Htt BLAST Value	Top Htt Accession No.	Top Htt Database Source	Top Htt Descriptor
1540	11444	21304	1.04	8.0E-96	5031810	NT	Homo sapiens L2-inducible T-cell kinase (ITK), mRNA
1541	11444	21304	0.98	8.0E-96	AB517007.1	NT	Homo sapiens PMS2, 16 mRNA, partial cds
1595	11971	21468	0.98	8.0E-96	AB517007.1	NT	Homo sapiens PMS2, 16 mRNA, partial cds
1695	13837	21468	0.98	8.0E-96	AB517007.1	NT	Homo sapiens PMS2, 16 mRNA, partial cds
3720	13823	23421	3.03	3.0E-96	JC41093.1	NT	Homo mitochondrial creatine kinase (CKMT) gene, complete cds
5049	14021		0.88	5.0E-96	AL163391.2	EST	Homo sapiens chromosome 21 segment 182120001
8711	16253	25220	1.28	4.0E-96	U5348727.1	EST	Homo sapiens chromosome 21 segment 182120001
12311	12919	21917	1.21	3.0E-96	AJ403124.1	EST	Homo sapiens cDNA clone IMAGE151829.3
2355	12313	23229	1.85	3.0E-96	AJ403124.1	EST	Homo sapiens cDNA clone 18
2955	12313	23229	1.85	3.0E-96	AJ403124.1	EST	Homo sapiens cDNA clone 18
2120	12982		2.09	3.0E-96	A4071408.1	EST	Homo sapiens cDNA clone 18
8147	16020	28169	1.7	3.0E-96	11419210	NT	Homo sapiens cDNA clone 18
8147	16020	28169	1.7	3.0E-96	11419210	NT	Homo sapiens cDNA clone 18
7083	16090	27153	3.31	3.0E-96	A46898.1	EST	Homo sapiens cDNA clone 18
7685	17535	27760	1.6	3.0E-96	AJ403124.1	EST	Homo sapiens cDNA clone 18
7685	17535	27760	1.6	3.0E-96	AJ403124.1	EST	Homo sapiens cDNA clone 18
8322	15196	29448	5.15	3.0E-96	U930309.1	NT	Human fumurate precursor (F4) mRNA, nuclear gene encoding mitochondrial protein, complete cds
9055	13873		2.47	3.0E-96	11418177	NT	Human fumurate precursor (F4) mRNA, nuclear gene encoding mitochondrial protein, complete cds
9055	13873		2.47	3.0E-96	11418177	NT	Human fumurate precursor (F4) mRNA, nuclear gene encoding mitochondrial protein, complete cds
2033	11924	21816	2.0E-96	B224281.1	EST	HUMAN	801172658P1 NH1.MGC.17 Homo sapiens cDNA clone IMAGE3328134.8
2191	12079	21983	1.45	2.0E-96	AL163292.1	NT	Homo sapiens chromosome 21 segment 182120002
4190	14009	23890	0.96	2.0E-96	AF232897.1	NT	Homo sapiens potassium channel subunit 1 (HERG.3) mRNA, complete cds
4244	14143	23916	4.94	2.0E-96	4798331	NT	Homo sapiens fatty-acid-Coenzyme A ligase, long-chain 1 (FACL4) mRNA
4720	14009	24390	1.51	2.0E-96	AF218902.1	NT	Homo sapiens atricetin precursor (ATRN) gene, exon 18
4720	14009	24391	1.51	2.0E-96	AF218902.1	NT	Homo sapiens atricetin precursor (ATRN) gene, exon 18
5069	14839	24711	8.39	2.0E-96	90450260	NT	Homo sapiens low density lipoprotein receptor related protein-deleted in tumor (LRPDI), mRNA
5069	14839	24711	8.39	2.0E-96	90450260	NT	Homo sapiens low density lipoprotein receptor related protein-deleted in tumor (LRPDI), mRNA
5163	15020	24716	1.09	2.0E-96	4798978	NT	Homo sapiens protein tyrosine kinase 2 beta (PTK2B) mRNA
5303	15224	25026	4.95	2.0E-96	17005912	NT	Homo sapiens PDZ domain-containing guanine nucleotide exchange factor 1 (GNEF1), mRNA
7004	16891	27073	3.87	2.0E-96	11422813	NT	Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), mRNA
7004	16891	27074	3.87	2.0E-96	11422813	NT	Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), mRNA
7497	17397	27572	1.5	2.0E-96	X12684.1	NT	Homo sapiens arginase gene exon 3 (EQ 3.5.3.1)
7591	17501		1.18	2.0E-96	17058938	NT	Homo sapiens arginase gene exon 3 (EQ 3.5.3.1)
9350	19028	25301	1.43	2.0E-96	11435947	NT	Homo sapiens AAK1, protein (LOC511161), mRNA
9350	19028	25301	1.43	2.0E-96	11435947	NT	Homo sapiens chromosome 12 open reading frame 3 (G2ORF3), mRNA
3991	10345	20172	19.93	1.0E-96	AB92007.1	EST	HUMAN
3991	10345	20172	19.93	1.0E-96	AB92007.1	EST	HUMAN
93604.01	NGI_OGAP_U1	Homo sapiens cDNA clone IMAGE2261743.3 similar to SW182_B_HUMAN					

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Disease Source	Top Hit Description
447	10391	20212	2.38	1.0E-68	AF098911.1	EST_HUMAN	FLU-BN065-10390-001-c06 BN065 Homo sapiens cDNA
1756	11655	21526	16.66	1.0E-68	AF06181.1	EST_HUMAN	2306961.1 Source: fetal liver spleen (NHL-S) Homo sapiens cDNA, clone IMAGE:245588 5' similar to PR-534094 Source: placental mucosal region L23 - human, 1
5256	15178	24953	8.36	1.0E-68	AA19384.1	EST_HUMAN	g268490.1 Striataganglion muscle 937209 Homo sapiens cDNA, clone IMAGE:526240 5' similar to TR:G060562
7203	17080	27266	1.36	1.0E-66	AF11346.1	NT	g268490.1 Striataganglion muscle 937209 Homo sapiens cDNA, clone IMAGE:526240 5' similar to TR:G060562
7203	17080	27267	1.36	1.0E-66	AF11346.1	NT	g268490.1 Striataganglion muscle 937209 Homo sapiens cDNA, clone IMAGE:526240 5' similar to TR:G060562
5681	15550	26862	4.26	9.0E-69	AF096835.1	EST_HUMAN	Homo sapiens beta-tubulin mRNA, complete cds
8465	18338	26822	2.6	9.0E-69	AF079829.1	EST_HUMAN	EST380711 IMAGE resequences, MAG3 Homo sapiens cDNA
8465	18338	26803	2.6	9.0E-69	AF079829.1	EST_HUMAN	EST380711 IMAGE resequences, MAG3 Homo sapiens cDNA
8716	18533	26817	1.84	9.0E-69	AA134604.1	EST_HUMAN	EST380711 IMAGE resequences, MAG3 Homo sapiens cDNA
7095	16522	27134	1.16	8.0E-69	AF035487.1	NT	EST380711 IMAGE resequences, MAG3 Homo sapiens cDNA
5951	15471	25550	9.2	7.0E-69	AF035608.1	NT	EST380711 IMAGE resequences, MAG3 Homo sapiens cDNA
6884	16976	26868	2.31	7.0E-69	AF007186.1	NT	EST380711 IMAGE resequences, MAG3 Homo sapiens cDNA
2080	11970	21863	0.83	6.0E-69	11430555	EST_HUMAN	EST380711 IMAGE resequences, MAG3 Homo sapiens cDNA
2380	11970	21864	0.83	6.0E-69	11430555	EST_HUMAN	EST380711 IMAGE resequences, MAG3 Homo sapiens cDNA
3814	13726	23817	1.87	8.0E-69	AF07694.1	EST_HUMAN	EST380711 IMAGE resequences, MAG3 Homo sapiens cDNA
4642	14520	24318	1.16	6.0E-69	4902090	NT	EST380711 IMAGE resequences, MAG3 Homo sapiens cDNA
6013	15517	25047	2.36	6.0E-69	LC3610.1	NT	EST380711 IMAGE resequences, MAG3 Homo sapiens cDNA
6013	15517	25048	2.36	6.0E-69	LC3610.1	NT	EST380711 IMAGE resequences, MAG3 Homo sapiens cDNA
6118	16558	26787	1.21	6.0E-69	X93910.1	NT	EST380711 IMAGE resequences, MAG3 Homo sapiens cDNA
7143	16926	27100	2.18	6.0E-69	AF090245.1	NT	EST380711 IMAGE resequences, MAG3 Homo sapiens cDNA
7143	17020	27213	3.57	6.0E-69	AF090245.1	NT	EST380711 IMAGE resequences, MAG3 Homo sapiens cDNA
8102	17952	28241	3.72	6.0E-69	AF090245.1	NT	EST380711 IMAGE resequences, MAG3 Homo sapiens cDNA
902	10827	20071	0.86	5.0E-69	U35464.1	NT	EST380711 IMAGE resequences, MAG3 Homo sapiens cDNA
902	10827	20072	0.86	5.0E-69	U35464.1	NT	EST380711 IMAGE resequences, MAG3 Homo sapiens cDNA
1922	11817	21996	2.36	5.0E-69	Y11395.1	NT	EST380711 IMAGE resequences, MAG3 Homo sapiens cDNA
4453	14636	24148	1.35	5.0E-69	AF006960.1	NT	EST380711 IMAGE resequences, MAG3 Homo sapiens cDNA
6096	14636	24709	2.46	5.0E-69	AF006960.1	NT	EST380711 IMAGE resequences, MAG3 Homo sapiens cDNA
9350	19032		2.1	5.0E-69	BE590177.1	EST_HUMAN	EST380711 IMAGE resequences, MAG3 Homo sapiens cDNA

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Mean Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6844	10723		6.37	3.0E-99	M66866.1	NT	Human E2AHLA fusion protein (E2AHLF) mRNA, complete cds
1219	11128		3.46	2.0E-99	AJ27492.1	EST_HUMAN	XP006030.1 NO1_OGAP_H99 Homo sapiens cDNA clone IMAGE:273674.3 similar to gb:M31212 MYOSIN LIGHT CHAIN ALKAL1, NON-MUSCLE ISOFORM (HUMAN);
3220	13144	22547	1.03	2.0E-99	M30936.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
4443	14337	24127	3.15	2.0E-99	AF06703.1	NT	Human sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene encoding mitochondrial protein, complete cds
7053	10630	27121	9.75	2.0E-99	W2307.1	EST_HUMAN	gb:46000.11 Soares_fell_d_jung_NHL19W Homo sapiens cDNA clone IMAGE:306635.5 similar to
8451	18324	28683	3.83	2.0E-99	AF247457.2	NT	gb:M16162 BETA-GLUCURONIDASE PRECURSOR (HUMAN);
312	10274	20093	1.53	1.0E-99	AF114467.1	NT	Homo sapiens myosin X (MYO10) mRNA, complete cds
375	10329	20162	1.04	1.0E-99	11529150	NT	Homo sapiens interaction hot isoform (TSN) mRNA, complete cds
1401	11306	21166	2.11	1.0E-99	M30936.1	NT	Homo sapiens G2-binding protein transcription factor, alpha subunit (G2BTPA), mRNA
1537	11441	21268	1.47	1.0E-99	AF19233.1	NT	Homo sapiens truncated Niemann-Pick C3 protein (NPC3) mRNA, complete cds
1537	11441	21268	1.47	1.0E-99	AF19233.1	NT	Homo sapiens truncated Niemann-Pick C3 protein (NPC3) mRNA, complete cds
1895	11781	21556	1.1	1.0E-99	4603730	NT	Homo sapiens FKBP-binding protein 6 (FKBP6) mRNA, complete cds
1895	11781	21557	1.1	1.0E-99	4603730	NT	Homo sapiens FKBP-binding protein 6 (FKBP6) mRNA, complete cds
3048	12273	22768	0.99	1.0E-99	103171.1	NT	Human hMafKron-alpha receptor (hMafKron-alpha-R) mRNA, and translated products
4283	14182	23080	2.74	1.0E-99	AF068018.1	NT	Homo sapiens fatty acid amide hydrolase (FAAH) gene, exon 14
4283	14182	23081	2.74	1.0E-99	AF068018.1	NT	Homo sapiens fatty acid amide hydrolase (FAAH) gene, exon 14
8200	15053		1.16	1.0E-99	AL183261.2	NT	Homo sapiens chromosome 21 segment HS21O381
7308	17181		1.16	1.0E-99	11419721	NT	Homo sapiens ALEX1 protein (LOC31339), mRNA
7483	17383	27857	1.88	1.0E-99	AW940174.1	EST_HUMAN	LOC2022.01 Soares_NFL_1_GBC_S1 Homo sapiens cDNA clone IMAGE:2608371.5 similar to TR:062711
8683	18571	28554	2.4	1.0E-99	AB023222.1	NT	OS27111 PRO-POUTPASE POLYPROTEIN;
9125	18884		3.76	1.0E-99	AF240786.1	NT	Homo sapiens guanine S-transferase theta 2 (GSTT2) and guanine S-transferase theta 1 (GSTT1) genes, complete cds
1	9889	19780	1.13	1.0E-100	AL183247.2	NT	Homo sapiens chromosome 21 segment HS21O347
2	9889	19780	1.53	1.0E-100	AL183247.2	NT	Homo sapiens chromosome 21 segment HS21O347
62	10048	19859	1.48	1.0E-100	11418230	NT	Homo sapiens Trefoil-specific XK-related protein on Y (XKRY), mRNA
62	10048	19860	1.48	1.0E-100	11418230	NT	Homo sapiens Trefoil-specific XK-related protein on Y (XKRY), mRNA
81	10095	19983	1.82	1.0E-100	AW76237.1	EST_HUMAN	XP78411.1 NO1_OGAP_Bn63 Homo sapiens cDNA clone IMAGE:282406.3
162	10135	19983	1.16	1.0E-100	AL183206.2	NT	Homo sapiens chromosome 21 segment HS21O306
314	10276	20065	1.01	1.0E-100	AL183249.2	NT	Homo sapiens chromosome 21 segment HS21O346
340	10299	20114	2.43	1.0E-100	T05087.1	EST_HUMAN	HS21O2975 Field brain, Stratagene (calf93620) Homo sapiens cDNA clone HFB0R32

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
430	10376		1.53	1.0E-100	AF003528.1	NT	Homo sapiens X-linked aniridial ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
481	10425		7.04	1.0E-100	X96931.1	NT	G gorilla DNA for ZNF80 gene homolog
500	10442	20255	4.17	1.0E-100	BE180609.1	EST_HUMAN	RC3-H10025-04000-022-509 HT0655 Homo sapiens cDNA
1002	10520	20763	2.43	1.0E-100	7691685	EST	Homo sapiens DKFZP569M0122 protein (DKFZP569M0122), mRNA
1002	10520	20764	2.43	1.0E-100	7691685	EST	Homo sapiens DKFZP569M0122 protein (DKFZP569M0122), mRNA
1528	11433		1.33	1.0E-100	AW207555.1	EST_HUMAN	U1H-B11-afic-c-07.0J.1 N1 CGAP_Sub3 Homo sapiens cDNA clone IMAGE:272184.3
1533	11437	21294	1.46	1.0E-100	AI200857.1	EST_HUMAN	qf20209.4 Soares, testis, NHT Homo sapiens cDNA clone IMAGE:1754833.3 similar to SW:CYT_COT1A
2105	12062		1.45	1.0E-100	D83349.1	NT	Rat mRNA for short type PB-cadherin, complete cds
2358	12367	22190	1.08	1.0E-100	X62488.1	NT	H sapiens mRNA for FN-gamma (PK-C-0)
2674	12599	22429	1.87	1.0E-100	11418876	NT	Homo sapiens KIAA0957 protein (KIAA0957), mRNA
2695	12613		2.45	1.0E-100	D11078.1	NT	Homo sapiens RG22 gene, retrovirus-like element
4116	14016	23799	1.49	1.0E-100	AF052354.1	NT	Homo sapiens cyclodextrin-related protein 1a mRNA, partial cds
4123	14043	23816	1.87	1.0E-100	4603762	NT	Homo sapiens follicle stimulating hormone receptor (FSHR) mRNA
5024	14897	24495	3.07	1.0E-100	5632104	NT	Homo sapiens small optic lobes (Drosophila) homolog (SOLH) mRNA
5024	14897	24496	3.07	1.0E-100	5632104	NT	Homo sapiens small optic lobes (Drosophila) homolog (SOLH) mRNA
5232	15150	24924	1.8	1.0E-100	BF244218.1	EST_HUMAN	U1101821HEMEX1 Homo sapiens cDNA clone HEMEX11003046.5
5406	15415	25478	1.4	1.0E-100	AU118182.1	EST_HUMAN	Homo sapiens NF-E2-related factor 3 gene, complete cds
5514	15432	25489	1.55	1.0E-100	AI135101.1	NT	Homo sapiens NF-E2-related factor 3 gene, complete cds
5915	15621	25948	5.1	1.0E-100	AU140244.1	EST_HUMAN	U1101821HEMEX1 Homo sapiens cDNA clone HEMEX11003046.5
6015	15918	26049	1.41	1.0E-100	RI0887.1	EST_HUMAN	Y56608.21 Soares fetal liver apoen TNFHS Homo sapiens cDNA clone PLACE2000137.5
6116	16010	26146	1.4	1.0E-100	BF376478.1	EST_HUMAN	MF1-TN0048-00000-004-065 TN0048 Homo sapiens cDNA
6116	16010	26147	1.4	1.0E-100	BF376478.1	EST_HUMAN	MF1-TN0048-00000-004-065 TN0048 Homo sapiens cDNA
6119	16013	26151	6.89	1.0E-100	X04671.1	NT	Human mRNA for kidney epithelial growth factor (EGF) precursor
6993	16841	27033	6.19	1.0E-100	BF103833.1	EST_HUMAN	901647357F1 NIH_JMCG_61 Homo sapiens cDNA clone IMAGE:3931310.5
6993	16890		5.44	1.0E-100	AL163203.2	NT	Human sapiens chromosome 21 segment -HS21C003
7322	17198	27398	3.2	1.0E-100	A0400918.1	NT	Homo sapiens mRNA for KIAA1485 protein, partial cds
7322	17198	27398	3.2	1.0E-100	A0400918.1	NT	W57709.x1 NCI_CGAP_P228 Homo sapiens cDNA clone IMAGE:2489920.3 similar to contains element MER22 repetitive element;
7399	17347		1.53	1.0E-100	A072388.1	EST_HUMAN	PMD-SN0005-100300-001-106 BN0055 Homo sapiens cDNA
7426	16439	26925	1.67	1.0E-100	AW696011.1	EST_HUMAN	Homo sapiens mRNA for KIAA1626 protein, partial cds
7527	17378	27587	1.73	1.0E-100	A0406846.1	NT	Homo sapiens mRNA for KIAA1626 protein, partial cds
7527	17378	27598	1.73	1.0E-100	A0406846.1	NT	Homo sapiens mRNA for KIAA1626 protein, partial cds
7654	17514	27740	1.69	1.0E-100	AW690487.1	EST_HUMAN	HH33c11.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2669396.5

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7962	17614	27741	1.69	1.0E-100	AW030487.1	EST_HUMAN	H43211.Y1.NQ1_CQAP_GU1 Homo sapiens cDNA clone IMAGE:266596 5'
8018	17668		1.20	1.0E-100	U03611.1	NT	Human endogenous retrovirus HERV-K, pol gene
8141	18029	28078	5.20	1.0E-100	BF22782.1	EST_HUMAN	MRO-EN0070-27030-003-111 BN0070 Homo sapiens cDNA
8608	15713	28749	2.14	1.0E-100	Y04633.1	NT	H.sapiens: C007 gene exon 4
8609	15473	28746	2.14	1.0E-100	Y04633.1	NT	H.sapiens: C007 gene exon 4
8600	15449	28851	4.66	1.0E-100	AF11170.3	NT	Homo sapiens 14332 Jgagp2 gene, complete cds; and unknown gene
8600	15449	28852	4.66	1.0E-100	AF11170.3	NT	Homo sapiens 14332 Jgagp2 gene, complete cds; and unknown gene
8688	9669	19780	1.96	1.0E-100	AL03247.2	NT	Homo sapiens galpin-illo protein (GLP) gene, complete cds
8830	18738		1.80	1.0E-100	AF230865.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) gene, complete cds
9048	19832	29714	5.56	1.0E-100	BF240788.1	NT	Homo sapiens S183 domain binding protein 1 (SH3BP1) mRNA
9551	19027	25302	2.21	1.0E-100	U1545732	NT	Homo sapiens S183 domain binding protein 1 (SH3BP1) mRNA
9540	19409	25181	3.38	1.0E-100	U147074.1	NT	Homo sapiens transcobalamin II, transcobalamin 2 (SEC14L2) mRNA
70	10055	19671	1.23	1.0E-101	U110714.1	NT	Homo sapiens SEC11 (S. cerevisiae) like 2 (SEC14L2) mRNA
71	10055	19672	1.23	1.0E-101	U110714.1	NT	Homo sapiens SEC11 (S. cerevisiae) like 2 (SEC14L2) mRNA
671	10805	20422	1.16	1.0E-101	AB007915.2	NT	Homo sapiens mRNA for KIA00446 protein (partial cds)
689	10821	20447	4.48	1.0E-101	U110734.1	NT	Homo sapiens ventral anterior homeobox 2 (VAX2) mRNA
689	10821	20448	4.48	1.0E-101	U110734.1	NT	Homo sapiens ventral anterior homeobox 2 (VAX2) mRNA
764	10884	20621	1.32	1.0E-101	7697454	NT	Homo sapiens peccadillo (peccadillo) homolog 1, containing BRCT domain (PES1) mRNA
838	10762	20612	1.28	1.0E-101	4603914	NT	Homo sapiens phosphoribosylglycylamide tautomyltransferase, phosphoribosylglycylamide synthetase, phosphoribosylglycylamide synthetase (GART) mRNA
905	10832	20679	3.44	1.0E-101	U22066.1	NT	Homo sapiens of cardiac alpha-myosin heavy chain gene
969	10892	20741	12.74	1.0E-101	BF081218.1	EST_HUMAN	60219647 AF11_NIGC-83 Homo sapiens cDNA clone IMAGE:427293 5'
1036	10854	20766	1.63	1.0E-101	AJ221878.1	EST_HUMAN	qg95000.x1 Soares, N.F., L. GBC, S11 Homo sapiens cDNA clone IMAGE:184538 5'
1712	11613	21483	0.87	1.0E-101	7692183	NT	Homo sapiens KIA00699 gene product (KIA00699) mRNA
1712	11613	21484	0.87	1.0E-101	7692183	NT	Homo sapiens KIA00699 gene product (KIA00699) mRNA
1901	11797	21677	1.62	1.0E-101	4502996	NT	Homo sapiens carboxypeptidase A1 (pericentric) (CPA1) mRNA
2010	11902	21762	1.63	1.0E-101	BE443070.1	EST_HUMAN	RC3-ST0281-140900-016-H09 ST0281 Homo sapiens cDNA
2301	12718	22380	1.66	1.0E-101	5728892	NT	Homo sapiens A kinase (PRKA) anchor protein 3 (ACAP3) mRNA
2572	12443	22335	4.4	1.0E-101	K72666.1	NT	H.sapiens EWS gene, exon 5
2714	12576	22468	2.56	1.0E-101	AJ23744.1	NT	Homo sapiens RIBLIR gene (partial), exon 12
2714	12576	22469	2.56	1.0E-101	AJ23744.1	NT	Homo sapiens RIBLIR gene (partial), exon 12
2925	12652		12.14	1.0E-101	J126512.1	NT	Homo sapiens goniotoc downstream Rhebus box
3167	13092	22987	2.51	1.0E-101	4686270	NT	Homo sapiens gamma-glutamyltransferase 1 (GGT1) mRNA

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3203	13127		2.16	1.0E-101	BF035327.1	EST_HUMAN	6014585317 NH_MGC_68 Homo sapiens cDNA clone IMAGE:3802086 5'
3334	13254	22059	1.97	1.0E-101	AW965556.1	EST_HUMAN	EST137025 IMAGE:rescues, MAGI Homo sapiens cDNA
3354	12276	22688	1.75	1.0E-101	AJ237744.1	NT	Homo sapiens REIIR gene (partial), exon 12
3354	12276	22659	1.75	1.0E-101	AJ237744.1	NT	Homo sapiens REIIR gene (partial), exon 12
3800	13712	23459	4.93	1.0E-101	AB022785.1	NT	Homo sapiens ASH2L gene, complete cds, similar to Drosophila ash2 gene
4955	14840	24009	1.97	1.0E-101	AB022785.1	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1) mRNA
4955	14840	24010	1.97	1.0E-101	5021460.1	EST_HUMAN	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1) mRNA
5257	15179	24554	1.97	1.0E-101	5021460.1	EST_HUMAN	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1) mRNA
5651	15563	24554	1.97	1.0E-101	AW965139.1	EST_HUMAN	Homo sapiens cyclophilin B (CYLN2) mRNA
5651	15563	24556	3.73	1.0E-101	7427512.1	NT	Homo sapiens cyclophilin B (CYLN2) mRNA
5333	16193	26566	3.73	1.0E-101	7427512.1	NT	Homo sapiens cyclophilin B (CYLN2) mRNA
8333	16196	26566	4.16	1.0E-101	AF208970.1	NT	Homo sapiens Kuppfer-type zinc finger protein (KEG3) mRNA, alternative splice form 4, partial cds
8333	16196	26567	4.16	1.0E-101	AF208970.1	NT	Homo sapiens Kuppfer-type zinc finger protein (KEG3) mRNA, alternative splice form 4, partial cds
8416	16278	26441	5.93	1.0E-101	AF208970.1	EST_HUMAN	hws542-11 NOLGAP_G44 Homo sapiens cDNA clone IMAGE:2633487 3'
8471	18330	26441	5.93	1.0E-101	BE257384.1	EST_HUMAN	hws542-11 NOLGAP_G44 Homo sapiens cDNA clone IMAGE:2633487 3'
8544	18402	26561	5.93	1.0E-101	BE257384.1	EST_HUMAN	hws542-11 NOLGAP_G44 Homo sapiens cDNA clone IMAGE:2633487 3'
8544	18402	26561	5.93	1.0E-101	BE257384.1	EST_HUMAN	hws542-11 NOLGAP_G44 Homo sapiens cDNA clone IMAGE:2633487 3'
8583	18573	26794	2.98	1.0E-101	BF028174.1	EST_HUMAN	NCI-47290821 NH_MGC_68 Homo sapiens cDNA clone IMAGE:395687 5'
7208	17065	27274	1.15	1.0E-101	AA038800.1	EST_HUMAN	203666 r1 Strep. pyogenes, NADPH Homo sapiens cDNA clone IMAGE:471908 5' similar to PKR3-5440 35440 ID5935.06 protein - yeast
7440	18458	26550	16.52	1.0E-101	X00066.1	NT	Human mRNA for pericardial gamma-glutamyltransferase
7440	18458	26551	16.52	1.0E-101	X00066.1	NT	Human mRNA for pericardial gamma-glutamyltransferase
7454	17263	27468	18.4	1.0E-101	9842492.1	NT	Human mRNA for pericardial gamma-glutamyltransferase
7623	17474	27694	5.94	1.0E-101	BE19697.1	EST_HUMAN	Homo sapiens gamma-glutamyltransferase 1 (GGT1), transcript variant 3, mRNA
7623	17474	27695	5.94	1.0E-101	BE19697.1	EST_HUMAN	Homo sapiens gamma-glutamyltransferase 1 (GGT1), transcript variant 3, mRNA
7623	17474	27695	5.94	1.0E-101	BE19697.1	EST_HUMAN	Homo sapiens gamma-glutamyltransferase 1 (GGT1), transcript variant 3, mRNA
7623	17474	27695	5.94	1.0E-101	BE19697.1	EST_HUMAN	Homo sapiens gamma-glutamyltransferase 1 (GGT1), transcript variant 3, mRNA
7950	17800	28040	1.76	1.0E-101	11429127.1	NT	Homo sapiens Jenus kinase 2 (protein tyrosine kinase) (JAK2), mRNA
8252	18132	28381	2.88	1.0E-101	S38327.1	NT	branched chain alpha keto acid dehydrogenase complex E1 alpha subunit (human, Genomic, 195 nt, segment 8 of 9)
8454	18327	28586	1.78	1.0E-101	AB020026.1	EST_HUMAN	Homo sapiens mRNA for KIAA0816 protein, partial cds
8454	18327	28586	1.78	1.0E-101	AB020026.1	EST_HUMAN	Homo sapiens mRNA for KIAA0816 protein, partial cds
8910	19189		11.62	1.0E-101	AW939051.1	NT	QVH-TD0068-240200-095-01 DT0098 Homo sapiens cDNA
338	10297	20111	3.24	1.0E-102	AI18303.2	NT	Homo sapiens chromosome 21 segment HS21C103
604	10540	20350	0.90	1.0E-102	BE252470.1	NT	8011082221 NH_MGC_16 Homo sapiens cDNA clone IMAGE:3344326 5'
798	10688	20126	1.46	1.0E-102	4557834.1	NT	Homo sapiens down-regulated in adenoma (DRA) mRNA
1101	11017	20859	1.95	1.0E-102	MT0676.1	NT	Human endogenous retrovirus (HENV) mRNA
1247	11154	21002	1.39	1.0E-102	11437146.1	NT	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA
1247	11154	21003	1.39	1.0E-102	11437146.1	NT	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar ELAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8424	18296	28853	1.99	1.0E-102	4507822	NT	Homo sapiens UDP glycosyltransferase 2 family, polypeptide B11 (UGT2B11) mRNA
8424	18298	28854	2.78	1.0E-102	4507822	NT	Homo sapiens UDP glycosyltransferase 2 family, polypeptide B11 (UGT2B11) mRNA
8708	18525	28807	1.59	1.0E-102	BF35243.1	EST_HUMAN	RC6-ET0072 - 50060-071-F01 ET0072 Homo sapiens cDNA
8847	18755	29051	4.04	1.0E-102	U41302.1	NT	Human chromosome 16 creatine transporter (SLC6A8) and (COM) paralogous genes, complete cds
9054	18837	29247	2.82	1.0E-102	AL18320.2	NT	Homo sapiens chromosome 21 segment HS21C030
9601	19183	29247	4.77	1.0E-102	AV13062.1	EST_HUMAN	h07612.x1 NC1_OGAP_Oc20 Homo sapiens cDNA clone IMAGE:396038.3
63	10049	19881	0.92	1.0E-103	BE608158.1	EST_HUMAN	h01500405F1 NIH.MGC.70 Homo sapiens cDNA clone IMAGE:3802305.5
63	10049	19882	0.82	1.0E-103	BE608158.1	EST_HUMAN	h01500405F1 NIH.MGC.70 Homo sapiens cDNA clone IMAGE:3802305.5
63	10078	19884	6.1	1.0E-103	D37078.2	NT	Homo sapiens mRNA for KIAA0235 protein, partial cds
201	10173	19989	0.83	1.0E-103	5453763	NT	Homo sapiens nuclear protein (KXED repeat) (NOP56) mRNA
965	10688	20744	1.01	1.0E-103	AL278348.1	NT	Homo sapiens mRNA for pregnancy-associated plasma oncin-E (PAPPE gene)
1223	11131	20865	7.28	1.0E-103	BE677841.1	EST_HUMAN	Homo sapiens phosphatidylinositol 4-kinase 230 (p44230) mRNA, complete cds
1578	11482	21342	2.32	1.0E-103	AF012872.1	NT	Homo sapiens GDS-ASSOCIATED PROTEIN (SMAP) mRNA
1872	11768	21843	1.04	1.0E-103	7697622	NT	Homo sapiens bone morphogenetic protein 8 (osteogenic protein 2) (BMP8) mRNA
1832	11827	21708	1.27	1.0E-103	4502428	NT	Homo sapiens bone morphogenetic protein 8 (osteogenic protein 2) (BMP8) mRNA
1832	11827	21708	1.27	1.0E-103	4502428	NT	Homo sapiens bone morphogenetic protein 8 (osteogenic protein 2) (BMP8) mRNA
2257	12141	22040	1.57	1.0E-103	AL134991.1	EST_HUMAN	AL134991 PLCE1 Homo sapiens cDNA clone IMAGE:380985.9
2401	12278	22175	2.22	1.0E-103	AF050588.1	NT	Homo sapiens promyelocyt leukemia zinc finger protein (PLZF) gene, complete cds
2578	12446	22340	0.86	1.0E-103	N82770.1	EST_HUMAN	h091008.x1 Scapeta, placenta, 2N4HP8u9V Homo sapiens cDNA clone IMAGE:259596.3
3030	12585	23454	2.43	1.0E-103	BE744722.1	EST_HUMAN	h0157313F1 NIH.MGC.3 Homo sapiens cDNA clone IMAGE:3854319.5
3333	13253	23058	3.44	1.0E-103	AW28246.1	EST_HUMAN	CHHBW-C4H-1T3-JU1.51 NC1_OGAP-5085 Homo sapiens cDNA clone IMAGE:273165.3
3383	13310	23108	1.06	1.0E-103	AB000692.1	NT	Homo sapiens mRNA for KMT4142 protein, partial cds
3695	13699		2.41	1.0E-103	AF023861.1	NT	Musca domestica cyclophilin A mRNA, complete cds
3725	13637	23423	1.16	1.0E-103	AA485983.1	EST_HUMAN	af00412.x1 Stralagene ling (85372) Homo sapiens cDNA clone IMAGE:840407.3 similar to contains element 1 (1-10) repetitive element
3757	13670	23454	1.99	1.0E-103	11430876	NT	Homo sapiens neurodin 1 (NRP1) mRNA
3922	13831	23811	3.02	1.0E-103	T23833.1	EST_HUMAN	seq3.00 DBHBMA-C0109-10 Bio Homo sapiens cDNA clone DBHBMA-C0109-10-Bio-7.3
9619	15584	25619	1.72	1.0E-103	AF176995.1	NT	Homo sapiens sapsin 2 (SEPF) mRNA, partial cds
5998	15603	26027	5.37	1.0E-103	AF053490.1	NT	Homo sapiens glycine receptor alpha 2 subunit (GLR2) gene, exon 4
8033	15938	26066	1.98	1.0E-103	AB000071.1	EST_HUMAN	h058005.x1 NC1_OGAP_Bmo25 Homo sapiens cDNA clone IMAGE:2162288.3 similar to TR:Q13769 Q13769 ANONYMOUS. ;

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Probe SEQ ID NO:	Exon NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6033	15536	26070	1.68	1.0E-103	AI500071.1	EST_HUMAN	tm58005.x1 NCL CGAP_Bn25 Homo sapiens cDNA clone IMAGE:2162289 3' similar to TRC13769 Q13769 ANONYMOUS. ;
6052	15102	24876	1.68	1.0E-103	5032282	NT	Homo sapiens dyshyph (muscular dyshyph, Duchenne and Becker types), includes DXS142, DXS164, DXS260, DXS230, DXS239, DXS268, DXS269, DXS270, DXS272 (DND), transcript variant Dp-427m, mRNA
6052	15102	24876	1.68	1.0E-103	5032282	NT	Homo sapiens dyshyph (muscular dyshyph, Duchenne and Becker types), includes DXS142, DXS164, DXS260, DXS230, DXS239, DXS268, DXS269, DXS270, DXS272 (DND), transcript variant Dp-427m, mRNA
6052	15102	24876	1.68	1.0E-103	5032282	NT	ES1377940 IMAGE sequences, IMAGE Homo sapiens cDNA
6265	16153	26310	1.64	1.0E-103	AIW65776.1	EST_HUMAN	601571537F1 NIH MGC_56 Homo sapiens cDNA clone IMAGE:3835545 5'
6338	16201	26391	3.21	1.0E-103	BE748158.1	EST_HUMAN	tm58005.x1 NCL CGAP_Bn25 Homo sapiens cDNA clone IMAGE:2162289 3' similar to TRC13769 Q13769 ANONYMOUS. ;
6568	16426	26607	3.28	1.0E-103	AI500071.1	EST_HUMAN	tm58005.x1 NCL CGAP_Bn25 Homo sapiens cDNA clone IMAGE:2162289 3' similar to TRC13769 Q13769 ANONYMOUS. ;
6568	16426	26606	3.28	1.0E-103	AI500071.1	EST_HUMAN	tm58005.x1 NCL CGAP_Bn25 Homo sapiens cDNA clone IMAGE:2162289 3' similar to TRC13769 Q13769 ANONYMOUS. ;
6623	16702	26656	2.95	1.0E-103	T31060.1	EST_HUMAN	ES1377163 Human Brain Homo sapiens cDNA 5' end similar to None
7010	19587	27076	1.17	1.0E-103	AIU140344.1	EST_HUMAN	AIU140344 PLAGE2 Homo sapiens cDNA clone PLACE200374.5
7010	19687	27060	1.17	1.0E-103	AIU140344.1	EST_HUMAN	AIU140344 PLAGE2 Homo sapiens cDNA clone PLACE200374.5
7050	19627	27116	1.43	1.0E-103	3F109244.1	EST_HUMAN	769403.x1 Scores, NSF_F8_9W_OT_PA_P_51 Homo sapiens cDNA clone IMAGE:3025994 3' similar to SV PTNF_HUMAN O16825 PROTEIN-TYROSINE PHOSPHATASE D1 ;
7267	17144	27337	3.08	1.0E-103	6005921	NT	Homo sapiens tripe functional domain (PTPRF interacting) (TRIO), mRNA
7267	17144	27338	3.08	1.0E-103	6005921	NT	Homo sapiens tripe functional domain (PTPRF interacting) (TRIO), mRNA
7767	17607	27670	2.02	1.0E-103	Z33976.1	NT	H. sapiens mRNA for latent transforming growth factor-beta binding protein (LTBP-2)
7815	17665	27659	2.98	1.0E-103	AW63576.1	EST_HUMAN	ES1307549 IMAGE sequences, VU31 Homo sapiens cDNA
7878	17728	27972	9.93	1.0E-103	AI87866.1	EST_HUMAN	91044.y1 Schistosoma falciparum brain 00004 Homo sapiens cDNA clone IMAGE:2516326 5' similar to TRC13046 O16046 KIAA0339 ;
8115	18004	28250	3.08	1.0E-103	AI782759.1	EST_HUMAN	60260.y1 NCL CGAP_Luo Homo sapiens cDNA clone IMAGE:1522283 5' similar to TRC62684 Q62084 PHOSPHOLIPASE C NIGEBORING ;
8218	18101	28353	2.74	1.0E-103	AF149793.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
8718	18101	28354	2.74	1.0E-103	AF149793.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
8661	18066	28652	2.96	1.0E-103	AIU136283.1	EST_HUMAN	AIU136283 PLACE1 Homo sapiens cDNA clone PLACE1006923 5'
8743	17652	28136	6.48	1.0E-103	436010.1	NT	Homo sapiens polyoma kidney disease (PKD1) gene, exons 27-30
8673	18778	26070	3.42	1.0E-103	BE644611.1	EST_HUMAN	769404.x1 Scores, NSF_F8_9W_OT_PA_P_51 Homo sapiens cDNA clone IMAGE:3287610 3' similar to contains MER26 b MER26 repetitive element ;

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9049	18833		1.72	1.0E-03	AF224689.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D) genes, complete cds
9079	18855		2.65	1.0E-03	11526291	NT	Homo sapiens hypothetical protein FL204547 (FL20454), mRNA
9275	18879	25323	2.21	1.0E-03	AB011360.1	NT	Homo sapiens gene for AF-4, complete cds
233	12022	20016	2.6	1.0E-04	AL037549.3	EST_HUMAN	DKFZ2654H1072.11 864 (synonym: hibr2) Homo sapiens cDNA clone DKFZ2654H1072.5'
233	12022	20017	2.6	1.0E-04	AL037549.3	EST_HUMAN	DKFZ2654H1072.11 864 (synonym: hibr2) Homo sapiens cDNA clone DKFZ2654H1072.5'
1845	11741	21617	1.81	1.0E-04	4802428	NT	Homo sapiens bone morphogenetic protein 3 (osteogenic protein 2) (BMP3) mRNA
2147	12035	21632	7.16	1.0E-04	AA132075.1	EST_HUMAN	gb220653 Striatagene cdon (863704) Homo sapiens cDNA clone IMAGE 587626 3' similar to
2157	12044	21644	1.91	1.0E-04	BE744628.1	EST_HUMAN	gb214118, natl CG96 GL YOOPTRO TEN PRECURSOR (HUMAN);
2318	12199	22007	1.15	1.0E-04	BE334221.1	EST_HUMAN	RC101574907.1 natl MGC. 9 Homo sapiens cDNA clone IMAGE 3828438 5'
2318	12199	22008	1.15	1.0E-04	BE334221.1	EST_HUMAN	RC101574907.1 natl MGC. 9 Homo sapiens cDNA clone IMAGE 3828438 5'
2387	12255	22199	1.55	1.0E-04	BC344271.1	EST_HUMAN	RG1-C10246-110000-214472 C10246 Homo sapiens cDNA
2842	12770	22598	7.64	1.0E-04	MS4671.1	NT	RG1-C10246-110000-214472 C10246 Homo sapiens cDNA
2888	12813		2.82	1.0E-04	Y11181.1	NT	Homo sapiens ARP2 (actin-related protein 2, yeast) homolog (AOTR2), mRNA
3345	13285		1.54	1.0E-04	AA316438.1	EST_HUMAN	Homo sapiens hypoxanthine phosphoribosyl transferase II
3550	13465	23280	0.99	1.0E-04	AB039102.1	NT	EST121658 Adrenal gland and Homo sapiens cDNA 5' and
3550	13465	23281	0.99	1.0E-04	AB039102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
3661	13772	23564	0.91	1.0E-04	AB032998.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
4280	14176	23957	4.28	1.0E-04	X02761.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
4504	14397	24182	0.9	1.0E-04	AF231620.1	NT	Human mRNA for fibronectin (FN precursor)
4504	14397	24183	0.9	1.0E-04	AF231620.1	NT	Homo sapiens chromosome 21 unknown mRNA
5617	15532	25615	1.33	1.0E-04	U43376.1	NT	Homo sapiens chromosome 21 unknown mRNA
5617	15532	25616	1.33	1.0E-04	U43376.1	NT	Human Down Syndrome region of chromosome 21 DNA
5891	15797	25919	8.46	1.0E-04	A1789797.1	EST_HUMAN	Human Down Syndrome region of chromosome 21 DNA
5891	15797	25920	8.46	1.0E-04	A1789797.1	EST_HUMAN	Human Down Syndrome region of chromosome 21 DNA
6073	16056	26204	1.52	1.0E-04	BE314182.1	EST_HUMAN	Y03812.1 NCI CGAP K2412 Homo sapiens cDNA clone IMAGE 2401727 3' similar to TR-Q14148 Q14148
6073	16056	26205	1.52	1.0E-04	BE314182.1	EST_HUMAN	KIAA0132 PROTEIN, contains element LTR repetitive element
6298	18182	26309	2.38	1.0E-04	11425672	NT	KIAA0132 PROTEIN, contains element LTR repetitive element
7298	18182	26309	2.38	1.0E-04	BF448220.1	EST_HUMAN	KIAA0132 PROTEIN, contains element LTR repetitive element
7298	18182	26309	2.38	1.0E-04	BF448220.1	EST_HUMAN	KIAA0132 PROTEIN, contains element LTR repetitive element
7370	17239	27442	4.68	1.0E-04	A17091395.1	NT	801150451 F1 NH. MGC. 19 Homo sapiens cDNA clone IMAGE 3503220 5'
7370	17239	27443	4.68	1.0E-04	A17091395.1	NT	801150451 F1 NH. MGC. 19 Homo sapiens cDNA clone IMAGE 3503220 5'
7370	17239	27443	4.68	1.0E-04	A17091395.1	NT	Homo sapiens adaptor-related protein complex 2, beta 1 subunit (AP2B1), mRNA
7370	17239	27443	4.68	1.0E-04	A17091395.1	NT	naid16911.1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE 3365648 3'
7370	17239	27443	4.68	1.0E-04	A17091395.1	NT	Homo sapiens Tiro isoform mRNA, complete cds
7370	17239	27443	4.68	1.0E-04	A17091395.1	NT	Homo sapiens Tiro isoform mRNA, complete cds

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7430	16443	26630	3.84	1.0E-104	BF322941.1	EST_HUMAN	L3-HT0019-060900-246-F07 HT0019 Homo sapiens cDNA
7430	16443	26631	3.84	1.0E-104	BF322941.1	EST_HUMAN	L3-HT0019-060900-246-F07 HT0019 Homo sapiens cDNA
7809	17659	27868	3.14	1.0E-104	BE791713.1	EST_HUMAN	001581503F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE 393897 5'
7809	17659	27869	3.14	1.0E-104	BE791713.1	EST_HUMAN	001581503F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE 393897 5'
7947	17797	28037	3.42	1.0E-104	AV128070.1	EST_HUMAN	AV128070 HTC Homo sapiens cDNA clone HTCBY407 5'
7965	18057	28057	4.51	1.0E-104	AV130705.1	EST_HUMAN	AL130705 HT28P3 Homo sapiens cDNA clone NT28P3001308 5'
8014	17864	28110	4.24	1.0E-104	U06835.1	NT	Human beta2-integrin (ITGB4) gene, exon 19, 20, 21, 22, 23, 24 and 25
8617	18484	28755	1.84	1.0E-104	BE720191.1	EST_HUMAN	RQ4-HT0895-310700-021-1509 HT0895 Homo sapiens cDNA
8617	18484	28756	1.84	1.0E-104	BE720191.1	EST_HUMAN	RQ4-HT0895-310700-021-1509 HT0895 Homo sapiens cDNA
8641	18505	28783	4.49	1.0E-104	BF694288.1	EST_HUMAN	00211212F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE 3302597 5'
8642	18540		1.37	1.0E-104	BE393892.1	EST_HUMAN	00131218F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE 393897 5'
277	12037	20062	2.85	1.0E-105	4592189	NT	Homo sapiens amyloid beta (A4) precursor protein (protease resistant), Alzheimer disease (APP), mRNA
419	9886	19777	10.85	1.0E-103	4595150	NT	Homo sapiens Mas1 (mesol) homolog (MEIS1) mRNA
576	10517	20323	3.22	1.0E-103	AF023897.1	NT	Homo sapiens potassium channel subunit (KERG-3) cDNA, complete cds
579	10517	20324	3.22	1.0E-103	AF023897.1	NT	Homo sapiens potassium channel subunit (KERG-3) cDNA, complete cds
1777	11700	21850	1.16	1.0E-105	AL103280.2	NT	Homo sapiens chromosome 21 segment HS21C030
1834	11760	21855	1.75	1.0E-105	D30078.1	NT	Homo sapiens chromosome 21 segment HS21C030
2142	12330	21828	1.34	1.0E-103	AF031839.1	EST_HUMAN	Human mRNA for KIAA0123 gene, partial cds
2039	12654		0.87	1.0E-103	AF031839.1	EST_HUMAN	Human mRNA for KIAA0123 gene, partial cds
2075	12502		2.87	1.0E-103	AF031839.1	EST_HUMAN	Human mRNA for KIAA0123 gene, partial cds
3307	13228	23022	0.83	1.0E-103	AJ229041.1	NT	Homo sapiens 5S9 to coding between AML1 and GBR1 on chromosome 21q22, segment 1/3
3307	13228	23033	0.83	1.0E-103	AJ229041.1	NT	Homo sapiens bromodomain adjacent to zinc finger domain, 28 (BAZ2B), mRNA
3992	13506		1.26	1.0E-105	11425332	NT	Homo sapiens bromodomain adjacent to zinc finger domain, 28 (BAZ2B), mRNA
3992	13506		1.26	1.0E-105	11425332	NT	Homo sapiens bromodomain adjacent to zinc finger domain, 28 (BAZ2B), mRNA
4008	13974	22689	2.15	1.0E-103	AW091688.1	EST_HUMAN	EST1373761 IMAGE, resequences, MACG Homo sapiens cDNA
4038	14526	24313	0.84	1.0E-103	BC598881.1	EST_HUMAN	EST145923F1 NIH_MGC_05 Homo sapiens cDNA clone IMAGE 3880150 5'
4038	14526	24314	0.84	1.0E-103	BC598881.1	EST_HUMAN	EST145923F1 NIH_MGC_05 Homo sapiens cDNA clone IMAGE 3880150 5'
4855	14735		3.74	1.0E-105	AL103280.2	NT	Homo sapiens chromosome 21 segment HS21C008
5044	14916	24690	0.86	1.0E-105	AS018339.1	NT	Homo sapiens mRNA for KIAA0796 protein, complete cds
5065	14865		2.23	1.0E-105	AS020073.1	NT	Homo sapiens mRNA for KIAA0796 protein, complete cds
5161	14916	24690	1.3	1.0E-105	AS018339.1	NT	Homo sapiens mRNA for KIAA0796 protein, complete cds
5167	15124	24840	3.06	1.0E-105	11419193	NT	Homo sapiens GTPase activating protein-like (GAPL), mRNA
5167	15124	24841	3.06	1.0E-105	11419193	NT	Homo sapiens GTPase activating protein-like (GAPL), mRNA
6979	19559	28754	6.43	1.0E-105	T05037.1	EST_HUMAN	EST020975 Trk brain, Stralagene (cmt595205) Homo sapiens cDNA clone HFB032

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
686-4	16773	26967	1.8	1.0E-106	AW007164.1	EST_HUMAN	w50c10.x1 NC1 CGAP_Bn25 Homo sapiens cDNA clone IMAGE:2500536 3' similar to
7234	17111	27304	2.96	1.0E-106	AW016879.1	EST_HUMAN	UHFACSA, PINCH P86933 ACETYL-COENZYME A SYNTHETASE ;
8303	18181	28428	5.44	1.0E-105	AF248822.1	NT	UHF-B10p-abh-124-U1 3' NC1 CGAP_S102 Homo sapiens cDNA clone IMAGE:2711782 3'
8590	18430	28656	1.8	1.0E-105	D63548.1	NT	Homo sapiens SMARCA4 Iszfam (SMARCA4) gene, complete cds, alternatively spliced
8602	18460	28740	2.06	1.0E-105	7705569	NT	Homo sapiens COL4A3 gene for $\alpha 1(V)$ collagen, exon 31
8867	18679	28668	2.01	1.0E-105	AW027554.1	EST_HUMAN	Homo sapiens Ran binding protein 11 (LOC61194), mRNA
145	10119	19657	0.96	1.0E-106	AW027554.1	EST_HUMAN	w74702.x1 Soares, Hymus, NHFTh Homo sapiens cDNA clone IMAGE:2535301 3' similar to TRP87892
131	10770	19657	1.54	1.0E-106	AW503038.1	EST_HUMAN	P87802 PROTEASE ;
531	10473	20296	1.77	1.0E-106	AW503038.1	EST_HUMAN	UHF-BN0-alky-07-047-U1 NH_MGC_50 Homo sapiens cDNA clone IMAGE:3078348 5'
599	10527	20334	0.79	1.0E-106	AW56556.1	EST_HUMAN	w73c01.x1 NC1 CGAP_U1 Homo sapiens cDNA clone IMAGE:2216008 3'
590	10527	20334	1.21	1.0E-106	J00146.1	NT	EST1377629 IMAGE ressequens, MAGI Homo sapiens cDNA
1508	11413	21272	2.66	1.0E-106	AF115712.1	NT	Human dihydrolipoate reductase pseudogene (ps-hd1)
1674	11576	21444	4.81	1.0E-106	U48724.1	NT	Human scutellin neuronic-1 mRNA, complete cds
1762	11691	21533	5.12	1.0E-106	AA527446.1	EST_HUMAN	Homo sapiens colubine neurokinin-1 receptor (EGFR) precursor-mRNA, exon 4, partial cds
1782	11681	21534	5.12	1.0E-106	AA527446.1	EST_HUMAN	Human epidermal growth factor receptor (EGFR) precursor-mRNA, exon 4, partial cds
2075	11965	21858	1.08	1.0E-106	BE142398.1	EST_HUMAN	LTR3 repetitive element ;
2268	12183	22062	8.95	1.0E-106	4504184	NT	LTR3 repetitive element ;
2456	12333	22220	1.68	1.0E-106	AF063528.1	NT	HTF0-TT0185-140200-008-210 LTR105 Homo sapiens cDNA
2507	12428	22322	1.26	1.0E-106	U94675.2	NT	Homo sapiens Kikvid anti-tetotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
2598	12431	22344	1.94	1.0E-106	AF250201.1	EST_HUMAN	Homo sapiens sperm membrane protein BS-43 mRNA, complete cds
2728	12591	22487	4.23	1.0E-106	AF250201.1	EST_HUMAN	S01146733T1 NH_MGC_19 Homo sapiens cDNA clone IMAGE:3502481 5'
2795	13151	21183	2.97	1.0E-106	4904184	NT	HTF0-TT0185-140200-008-210 LTR105 Homo sapiens cDNA clone IMAGE:1878307 3'
2795	13151	21184	2.97	1.0E-106	4904184	NT	Homo sapiens glutathione S-transferase theta 1 (GSTT1), mRNA
2911	12837	22635	5.01	1.0E-106	AB037747.1	NT	Homo sapiens glutathione S-transferase theta 1 (GSTT1), mRNA
2911	12837	22636	5.01	1.0E-106	AB037747.1	NT	Homo sapiens mRNA for KIAA1326 protein, partial cds
3143	13068	22667	2.36	1.0E-106	8622965	NT	Homo sapiens mRNA for KIAA1326 protein, partial cds
3143	13068	22668	2.36	1.0E-106	8622965	NT	Homo sapiens hypothetical protein FLJ11272 (FLJ11273), mRNA
3328	13248	23063	0.8	1.0E-106	AB006681.1	NT	Homo sapiens hypothetical protein FLJ11272 (FLJ11273), mRNA
3354	13311	23109	0.98	1.0E-106	AB006681.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
						NT	Homo sapiens mRNA for KIAA1276 protein, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Distance Source	Top Hit Description
3394	13311	23110	0.98	1.0E-108 A60303.04.1	NT		Homo sapiens mRNA for KIAA1278 protein, partial cds
3395	13660	23934	7.22	1.0E-106 A197474650.1	EST - HUMAN		EST T308935 MAGS (resequenced), MAGN Homo sapiens cDNA
3395	13660	23936	7.22	1.0E-106 A197466.1	EST - HUMAN		EST T308935 MAGS (resequenced), MAGN Homo sapiens cDNA
4487	14391	24116	1.21	1.0E-105 SE144268.1	EST - HUMAN		MFQ-HYD65-14620-008-010, HMO185 Homo sapiens cDNA
5183	13047		1.21	1.0E-105 A161444.1	NT		Homo sapiens cytochrome gene, clone 41
5298	15219	25022	2.98	1.0E-106 A4781155.1	EST - HUMAN		g34605.x1 Soares, Islets_NHT Homo sapiens cDNA, clone 1381225 5' similar to gp:12433 PROTEIN
5711	15619	25723	6.76	1.0E-103 SF79574.1	EST - HUMAN		PHS-12 (HUMAN)
5868	15712	25991	16.4	1.0E-105 11549319.1	EST - HUMAN		002120407251 NH1_MGC_93 Homo sapiens cDNA, clone IMAGE:5265097 5'
5986	15712	25992	16.4	1.0E-105 11549319.1	NT		Homo sapiens xycoglycyltransferase II (X2T), mRNA
6081	16224	26365	5.59	1.0E-106 A4693779.1	EST - HUMAN		Homo sapiens xycoglycyltransferase II (X2T), mRNA
6590	16252	26413	4.33	1.0E-105 11429817.1	NT		nc7207.x1 Strabagene schizo brain S111 Homo sapiens cDNA, clone IMAGE:5909732 3' similar to gp:108673
6431	16392	26438	1.50	1.0E-105 SE232722.1	EST - HUMAN		KINESIN HEAVY CHAIN (HUMAN);
6460	16348	26517	7.6	1.0E-106 11429503.1	NT		00110057981 NH1_MGC_10 Homo sapiens cDNA, clone IMAGE:2665346 5'
6460	16348	26518	7.6	1.0E-106 11429503.1	NT		00110057981 NH1_MGC_10 Homo sapiens cDNA, clone IMAGE:2665346 5'
6460	16348	26518	7.6	1.0E-106 11429503.1	EST - HUMAN		Homo sapiens sorting nexin 11 (SNX11), mRNA
6657	16837	26733	5.33	1.0E-105 SE741103.1	EST - HUMAN		0015043351F1 NH1_MGC_9 Homo sapiens cDNA, clone IMAGE:3948493 5'
6657	16837	26734	5.33	1.0E-105 SE741103.1	EST - HUMAN		0015043351F1 NH1_MGC_9 Homo sapiens cDNA, clone IMAGE:3948493 5'
6764	16833	26821	1.48	1.0E-106 A623068.1	EST - HUMAN		ar0807.x1 Barlested cortex HPLR186 Homo sapiens cDNA, clone IMAGE:2177732 3' similar to gp:306233
7052	16929	27120	3.16	1.0E-106 A694123.1	EST - HUMAN		102405.x1 NCL_GGAP_KH11 Homo sapiens cDNA, clone IMAGE:2293632 3' similar to SW:ICAG_HUMAN
7261	17166	27363	1.86	1.0E-106 A623307.1	EST - HUMAN		000604.99 NO ISLET CELL AUTOANTIGEN 1
7261	17166	27364	1.86	1.0E-106 A623307.1	EST - HUMAN		000604.99 NO ISLET CELL AUTOANTIGEN 1
7351	17219	27419	2.79	1.0E-106 A1750447.1	EST - HUMAN		00577008.x1 NCL_GGAP_GCBT1 Homo sapiens cDNA, clone IMAGE:1354790 3'
7424	17291	27501	1.86	1.0E-106 A479599.1	EST - HUMAN		00577008.x1 NCL_GGAP_GCBT1 Homo sapiens cDNA, clone IMAGE:1354790 3'
7424	17291	27502	1.86	1.0E-106 A479599.1	EST - HUMAN		00577008.x1 NCL_GGAP_GCBT1 Homo sapiens cDNA, clone IMAGE:1354790 3'
7603	17653	27891	1.32	1.0E-106 BF027310.1	EST - HUMAN		0003004.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA, clone NHTBC_003a04, random
7603	17653	27891	1.32	1.0E-106 BF027310.1	EST - HUMAN		Im111002.x1 NH1_MGC_20 Homo sapiens cDNA, clone IMAGE:3954403 5'
7680	17730	27976	5.63	1.0E-106 A6054417.1	EST - HUMAN		Im111002.x1 NCL_GGAP_KH11 Homo sapiens cDNA, clone IMAGE:2190099 3' similar to contains MSR1.13
7680	17730	27976	5.63	1.0E-106 A6054417.1	EST - HUMAN		Im111002.x1 NCL_GGAP_KH11 Homo sapiens cDNA, clone IMAGE:2190099 3' similar to contains MSR1.13
7680	17730	27976	5.63	1.0E-106 A6054417.1	EST - HUMAN		Im111002.x1 NCL_GGAP_KH11 Homo sapiens cDNA, clone IMAGE:2190099 3' similar to contains MSR1.13
7680	17730	27976	5.63	1.0E-106 A6054417.1	EST - HUMAN		Im111002.x1 NCL_GGAP_KH11 Homo sapiens cDNA, clone IMAGE:2190099 3' similar to contains MSR1.13

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7901	17751	27860	1.86	1.0E-106	AW363269.1	EST_HUMAN	ROD-CTD3.16-201189-01-411 CT0318 Homo sapiens cDNA
8219	17869	28113	3.61	1.0E-106	AL103202.2	NT	Homo sapiens chromosome 21 segment HS21C02
8269	18089	28386	6.21	1.0E-106	BF032755.1	EST_HUMAN	601453461F1 NIH_MGC_98 Homo sapiens cDNA clone IMAGE:3857366 5'
8269	18149	28390	6.21	1.0E-106	BF032755.1	EST_HUMAN	601453461F1 NIH_MGC_98 Homo sapiens cDNA clone IMAGE:3857366 5'
8415	18260	28544	2.28	1.0E-106	J05300.1	NT	Human yamada receptor mRNA, complete cds
8415	18260	28545	2.28	1.0E-106	J05300.1	NT	Human yamada receptor mRNA, complete cds
9121	18260	28545	2.28	1.0E-106	J05300.1	NT	Human yamada receptor mRNA, complete cds
9342	19022	25298	2.31	1.0E-106	BE694488.1	EST_HUMAN	601453067F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918524 5'
9342	19022	25298	2.31	1.0E-106	BE694488.1	EST_HUMAN	601453067F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918524 5'
9554	19153	26590	5.35	1.0E-106	BE695905.1	EST_HUMAN	RC1-CTD249-000300-024-005 CT0249 Homo sapiens cDNA
234	10293		3.48	1.0E-107	A2171735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
264	10229		1.05	1.0E-107	X80459.1	NT	Human FNAR gene for fibronectin alpha5beta1 receptor
606	10543		1.07	1.0E-107	4626983	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
814	10550	20381	1.7	1.0E-107	AF155103.1	NT	Homo sapiens IV-REN.25 antigen mRNA, partial cds
796	10725	20565	0.86	1.0E-107	X80459.1	NT	Human FNAR gene for fibronectin alpha5beta1 receptor
868	10794	20644	1.16	1.0E-107	X80459.1	NT	Human FNAR gene for fibronectin alpha5beta1 receptor
953	10877	20724	10.67	1.0E-107	AF154121.1	NT	Homo sapiens sodium-dependent high-affinity dicarboxylate transporter (NALDC3) mRNA, complete cds
1257	11164	21075	0.78	1.0E-107	AB032253.1	NT	Homo sapiens BAX1B mRNA for bromodomain adjacent to zinc finger domain 1B, complete cds
1551	11468	21314	2.13	1.0E-107	BF037405.1	EST_HUMAN	CT2-H10540-120300-395-405 HT0540 Homo sapiens cDNA
1718	11619	21488	1.47	1.0E-107	AF186275.1	NT	Homo sapiens cathepsin Z precursor (CTSZ) gene, exon 3
1797	11695	21571	0.95	1.0E-107	AB007022.2	NT	Homo sapiens mRNA for KIAA0453 protein, partial cds
1797	11695	21572	0.95	1.0E-107	AB007022.2	NT	Homo sapiens mRNA for KIAA0453 protein, partial cds
2161	12048	21949	1.26	1.0E-107	U13729.1	NT	Homo sapiens diaphanous phosphatase IV (CD20) gene, exon 20
2487	12362	22257	0.86	1.0E-107	BE732490.1	EST_HUMAN	601607619F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3942306 5'
2487	12362	22258	0.86	1.0E-107	BE732490.1	EST_HUMAN	601607619F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3942306 5'
2976	12603	22701	1.94	1.0E-107	AW642451.1	EST_HUMAN	PM1-CH00031-190100-001-403 CH0031 Homo sapiens cDNA
2976	12603	22702	1.94	1.0E-107	AW642451.1	EST_HUMAN	PM1-CH00031-190100-001-403 CH0031 Homo sapiens cDNA
3061	12688	22719	2.82	1.0E-107	5902097	NT	Homo sapiens SMY3 (suppressor of mit two 3, yeast) homolog 2 (SMY3H2), mRNA
3764	13687	23450	3.92	1.0E-107	AF020077.1	NT	Homo sapiens myoblastin (MTM1) gene, exon 9
5575	15490	25957	3.26	1.0E-107	BE697099.1	EST_HUMAN	601452595F1 NIH_MGC_98 Homo sapiens cDNA clone IMAGE:3846464 5'
6356	16219	26390	1.52	1.0E-107	AW803913.1	EST_HUMAN	UHFH-BND-alf-cb-04-U17 NH_MGC_30 Homo sapiens cDNA clone IMAGE:3076510 5'
6356	16219	26391	1.52	1.0E-107	AW803913.1	EST_HUMAN	UHFH-BND-alf-cb-04-U17 NH_MGC_30 Homo sapiens cDNA clone IMAGE:3076510 5'
6445	16306	26471	1.63	1.0E-107	AF169078.1	EST_HUMAN	wh56904X1 NCL CGAP_Kd11 Homo sapiens cDNA clone IMAGE:2844791 3'

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Prote SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Acce- sion No.	Top Hit Database Source
8097	17678	26028	2.73	1.0E-107 A032850.1	EST_HUMAN	bc006v.1 NCJ_CGAP_G1.1 Homo sapiens cDNA clone IMAGE:2210303 3' similar to SW-ANCT_DICD1
8316	18153	29443	1.82	1.0E-107 L49141.1	NT	P00095 ALPHA-ACTININ-3, NON-MUSCULAR:
8337	18254	29453	1.98	1.0E-107 BF-095911.1	EST_HUMAN	Homo sapiens alpha-actinin-3 muscle-specific protein (NESP) gene, exon 4
8638	18683	28776	9.12	1.0E-107 BE540690.1	EST_HUMAN	X02223.6321 NH_MGC_66 Homo sapiens cDNA clone IMAGE:4291039 5'
8697	17681	28776	9.12	1.0E-107 BE540690.1	EST_HUMAN	X01036631.F1 NH_MGC_10 Homo sapiens cDNA clone IMAGE:3452629 5'
8697	17681	28122	4.21	1.1H19701	NT	Homo sapiens RPS-Cas protein (RSP-Cas), mRNA
8697	17681	28123	4.21	1.1H19701	NT	Homo sapiens RPS-Cas protein (RSP-Cas), mRNA
9167	19673		3.84	1.0E-107 AA001415.1	EST_HUMAN	bc04601.1 Soares retina N24b-HR. Homo sapiens cDNA clone IMAGE:351944 3' similar to contains THR.b1
938	10864	20711	1.46	1.0E-108 BE256042.1	EST_HUMAN	THK repetitive element.
1244	11151	20986	1.95	1.0E-108 Y18000.1	NT	BT01770187.NH_MGC_17 Homo sapiens cDNA clone IMAGE:3532346 5'
2282	12166	22063	7.41	1.0E-108 AG69040.1	EST_HUMAN	Bt016701.X1 NCJ_CGAP_P28 Homo sapiens cDNA clone IMAGE:2248938 3' similar to gbM14219 BONE
2282	12166	22064	7.41	1.0E-108 AG69040.1	EST_HUMAN	BT016701.X1 NCJ_CGAP_P28 Homo sapiens cDNA clone IMAGE:2248938 3' similar to gbM14219 BONE
2378	12256	22150	7.2	1.0E-108 BE200694.1	EST_HUMAN	R015810A10.1 NH_MGC_138 (HUMAN); db_J05727 Mouse thiodiazine mRNA, complete cds (MOUSE);
3305	13220	20028	0.84	1.0E-108 AFQ32897.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
3395	13220	20029	0.84	1.0E-108 AFQ32897.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
3742	13654	23437	0.92	1.0E-108 FA033955	NT	Homo sapiens pericardial material 1 (PCMT1) cDNA
4065	13967	23744	1.33	1.0E-108 AVI064438.1	EST_HUMAN	Mt2art1.x1 NCJ_CGAP_GUT Homo sapiens cDNA clone IMAGE:370060 3' similar to SW-3EP1_MOUSE
4425	14320	24166	1.59	1.0E-108 U72961.1	NT	P56194 SHS-BINDING PROTEIN SBP-1;
4425	14320	24167	1.89	1.0E-108 U72961.1	NT	Human hepatocyte nuclear factor 4-alpha gene, exon 2
4659	14825	24167	1.89	1.0E-108 U72961.1	NT	Human hepatocyte nuclear factor 4-alpha gene, exon 2
4659	14825	24376	2.85	1.0E-108 7661978	NT	Homo sapiens PSN1 gene, alternative transcript
4838	14748	24528	2.19	1.0E-108 AJ000005.1	NT	Homo sapiens PSN1 gene, alternative transcript
5395	15286	25120	1.33	1.0E-108 AVI3840494.1	EST_HUMAN	R001HT.0372-241199-031-d03 HT0372 Homo sapiens cDNA
5395	15312	25167	2.77	1.0E-108 BE589016.1	EST_HUMAN	R01444622.F1 NH_MGC_66 Homo sapiens cDNA clone IMAGE:3840950 5'
5395	15312	25167	2.77	1.0E-108 BE589016.1	EST_HUMAN	R01444622.F1 NH_MGC_66 Homo sapiens cDNA clone IMAGE:3840950 5'
5732	15540	25745	5.06	1.0E-108 AF264717.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP2 mRNA, complete cds
5732	15540	25746	5.06	1.0E-108 AF264717.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP2 mRNA, complete cds

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Probe SEQ ID NO.	Exon NO.	ORF SEQ ID NO.	Expression Signal	Meat Similar (Top Hit BLAST E Value)	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5789	16695	28804	1.37	1.0E-108	AJ133288.1	NT	Homo sapiens cawdwin-11/2 locus, Contig1_ D78522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
5247	16713	26265	5.35	1.0E-108	11431857	NT	Homo sapiens G protein-coupled receptor, family C, group E, member B (GPCR5B), mRNA
8369	16280	28421	3.34	1.0E-108	4759333	NT	Homo sapiens delta-9 fatty acid desaturase (FADS6), mRNA
6068	16678		1.33	1.0E-108	AF093500.1	NT	Homo sapiens cell-to-cell growth factor-like protein, precursor, mRNA, complete cds
8202	15059	24891	2.77	1.0E-108	Y12400.1	NT	Homo sapiens mRNA for Gdgl-associated microtubule-binding protein (GMAP-210)
8503	18461	28731	4.26	1.0E-108	AW966185.1	EST_HUMAN	EST1378258 IMAGE resequences, VAGI Homo sapiens cDNA
8577	18555		2.03	1.0E-108	11441465	NT	Homo sapiens G protein-coupled receptor 48 (GPCR48), mRNA
8706	12166	22063	4.14	1.0E-108	A1899040.1	EST_HUMAN	187410.4 NCI CGAP P28 Homo sapiens cDNA clone IMAGE:2248638 3' similar to gp34.1219 BONE PROTEOGLYCAN II PRECURSOR (HUMAN);
8708	12166	22064	4.14	1.0E-108	A1899040.1	EST_HUMAN	187410.4 NCI CGAP P28 Homo sapiens cDNA clone IMAGE:2248638 3' similar to gp34.1219 BONE PROTEOGLYCAN II PRECURSOR (HUMAN);
8709	16030	23503	2.79	1.0E-108	AK024447.1	NT	Homo sapiens mRNA for FLJ09037 protein, partial cds
8736	19270		5.99	1.0E-108	BF246356.1	EST_HUMAN	602018571F1 NCI CGAP FL067 Homo sapiens cDNA clone IMAGE:4154297 5'
98	10044	10856	0.9	1.0E-108	C96674.1	NT	Human mRNA for KIAA0229 gene, partial cds
212	10163	19937	0.92	1.0E-108	11422485	NT	Homo sapiens lipophilin protein FLJ1316 (FLJ1316), mRNA
222	10163	20033	1.51	1.0E-108	11438591	NT	Homo sapiens reticulocalbin 1, EF-hand calcium binding domain (RCN1), mRNA
486	10403	20219	3.84	1.0E-108	4507172	NT	Homo sapiens tetrahydrocysteine repeat domain 2 (TTC2) mRNA
583	10821	20326	14.94	1.0E-108	A3023216.1	NT	Homo sapiens mRNA for KIAA0959 protein, partial cds
583	10821	20326	14.94	1.0E-108	A3023216.1	NT	Homo sapiens mRNA for KIAA0959 protein, partial cds
1194	11065	20911	0.33	1.0E-109	A3023216.1	NT	Homo sapiens mRNA for KIAA0959 protein, partial cds
1195	11065	20911	0.33	1.0E-109	IJ26669.1	NT	Homo sapiens nuclear phosphoprotein S27 (NPM1) mRNA, complete cds
1831	11728	21602	1.48	1.0E-109	D13643.2	NT	Homo sapiens nuclear phosphoprotein S27 (NPM1) mRNA, complete cds
2194	12081	21993	2.03	1.0E-109	A183254.2	NT	Homo sapiens mRNA for KIAA0016 protein, partial cds
2204	12091	21993	1.97	1.0E-109	Y117123.1	NT	Homo sapiens chromosome 21 segment HS210084
2581	12452	22344	3.88	1.0E-109	A022328.1	EST_HUMAN	Homo sapiens SNUFUNK1 gene, exon 6
2581	12452	22344	3.88	1.0E-109	A022328.1	EST_HUMAN	TRC002197 002197 CIRCULATING CATHODIC ANTIGEN ;
2582	12453	22346	2.75	1.0E-109	4904206	NT	tw65601 x1 Scores, fetal, liver, spleen, INFLS, S1 Homo sapiens cDNA clone IMAGE:1654356 3' similar to TRC002197 002197 CIRCULATING CATHODIC ANTIGEN ;
3020	12848	22740	1.88	1.0E-109	N8190.1	EST_HUMAN	tw65601 x1 Scores, fetal, liver, spleen, INFLS, S1 Homo sapiens cDNA clone IMAGE:1654356 3' similar to TRC002197 002197 CIRCULATING CATHODIC ANTIGEN ;
3342	13292	23098	1.45	1.0E-109	A1693192.1	EST_HUMAN	J2816F Human fetal heart, Lenticle ZAP Express Homo sapiens cDNA clone J2816 5' similar to ZINC FINGER PROTEIN ZNF43
3342	13292	23098	1.45	1.0E-109	A1693192.1	EST_HUMAN	CNG-NN0009-190400-150-T10 NN0009 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3474	13390	23165	1.2	1.0E-103 AF240698.1	NT	EST_HUMAN	Homo sapiens retinol dehydrogenase homolog isoform-1 (RDH) mRNA, complete cds
3757	13380	23165	1.83	1.0E-103 BE146144.1	EST_HUMAN	EST_HUMAN	MRO-HT10200-110400-108-act1 HT0200 Homo sapiens cDNA
3911	13821	23907	1.54	1.0E-106 AB011181.2	NT	EST_HUMAN	Homo sapiens mRNA for KIAA0609 protein, partial cds
3911	13821	23902	1.54	1.0E-103 AB011181.2	NT	EST_HUMAN	Homo sapiens mRNA for KIAA0609 protein, partial cds
4054	13956	23732	3.67	1.0E-105 A1665417.1	EST_HUMAN	EST_HUMAN	ts6606.x1 NQ1_OGAP_Q06 Homo sapiens cDNA clone IMAGE:2293930 3' similar to WP-F83A.2.8 CE:16106
4070	13972	23749	1.02	1.0E-105 AA692274.1	EST_HUMAN	EST_HUMAN	nu8342.1s1 NQ1_OGAP_P122 Homo sapiens cDNA clone IMAGE:1218202 3' similar to SW:G172_HUMAN
4070	13972	23750	1.02	1.0E-105 AA692274.1	EST_HUMAN	EST_HUMAN	P90712 GLUTATHIONE S-TRANSFERASE THETA 2;
4304	14202	23969	2.26	1.0E-103 49042038	NT	EST_HUMAN	P90712 GLUTATHIONE S-TRANSFERASE THETA 2;
4466	14390	24175	1.19	1.0E-103 76620393	NT	EST_HUMAN	Homo sapiens guanylate cyclase activator 1A (ralph) (GUCA1A) mRNA
4830	14720	24503	1.04	1.0E-103 RI1400.1	EST_HUMAN	EST_HUMAN	ye48406.r1 S22es infant brain 1N1B Homo sapiens cDNA clone IMAGE:53057 5'
4884	14850	24503	0.66	1.0E-103 BE239373.1	EST_HUMAN	EST_HUMAN	6011962232 NH1_MGC.16 Homo sapiens cDNA clone IMAGE:2566535 5'
4884	14850	24527	0.66	1.0E-103 BE239373.1	EST_HUMAN	EST_HUMAN	6011962232 NH1_MGC.16 Homo sapiens cDNA clone IMAGE:2566535 5'
5264	15170	24560	2.31	1.0E-103 5174622	NT	EST_HUMAN	Homo sapiens chemical protein 11 (serpine trypsinase) (P11) mRNA
5548	15594	24560	1.48	1.0E-103 BE173556.1	EST_HUMAN	EST_HUMAN	RC1-110515.20340.022-20.1 HT0515 Homo sapiens cDNA
6465	16025	25491	3.66	1.0E-103 11432574	NT	EST_HUMAN	Homo sapiens AT-binding transcription factor 1 (ATBF1) mRNA
6465	16025	25492	5.01	1.0E-103 BE182707.1	EST_HUMAN	EST_HUMAN	601839465F1 NH1_MGC.18 Homo sapiens cDNA clone IMAGE:4040279 5'
6465	16025	25493	5.01	1.0E-103 BE182707.1	EST_HUMAN	EST_HUMAN	601839465F1 NH1_MGC.18 Homo sapiens cDNA clone IMAGE:4040279 5'
6753	16832	26620	1.36	1.0E-103 AL049784.1	NT	EST_HUMAN	Next human gene mapping to chromosome 13
6820	16969	26625	1.23	1.0E-103 AL049784.1	NT	EST_HUMAN	Next human gene mapping to chromosome 13
7030	16907	27199	1.72	1.0E-103 AA071668.1	EST_HUMAN	EST_HUMAN	R940-ET10340-091256-027-025 BT0340 Homo sapiens cDNA
7071	16949	27199	5.71	1.0E-103 BE17540.1	EST_HUMAN	EST_HUMAN	BT0340 Homo sapiens cDNA library Homo sapiens cDNA clone 7B18-01
7071	16949	27140	5.71	1.0E-103 BE17540.1	EST_HUMAN	EST_HUMAN	BT0340 Homo sapiens cDNA library Homo sapiens cDNA clone IMAGE:5302124 5'
7326	17322	27402	2	1.0E-103 M84690.1	EST_HUMAN	EST_HUMAN	ye49481.1 Sources retina N26SHRT Homo sapiens cDNA clone IMAGE:122110 5' similar to SP-A53491
7462	17523	27528	1.41	1.0E-103 F00804.1	EST_HUMAN	EST_HUMAN	AS4461 BUEM1TANDE-SENSITIVE NAK-C1 COT-TRANSPORTER - SPIN17;
8155	18043	28294	2.93	1.0E-103 BE540009.1	EST_HUMAN	EST_HUMAN	HSC1C12 normalized infant brain cDNA Homo sapiens cDNA clone c-1c12
8155	18043	28295	2.93	1.0E-103 BE540009.1	EST_HUMAN	EST_HUMAN	1001030300F1 NH1_MGC.10 Homo sapiens cDNA clone IMAGE:3446569 5'
8183	18069	28318	14.2	1.0E-103 BF064831.1	EST_HUMAN	EST_HUMAN	020020724F2 NH1_MGC.81 Homo sapiens cDNA clone IMAGE:4240341 5'
8335	18212	28464	2.12	1.0E-105 7862276	NT	EST_HUMAN	Homo sapiens KIA00744 gene product; histone deacetylase 7 (KIA00744), mRNA
8335	18212	28465	2.12	1.0E-105 7862276	NT	EST_HUMAN	Homo sapiens KIA00744 gene product; histone deacetylase 7 (KIA00744), mRNA
8408	18341	28606	1.88	1.0E-103 AU121370.1	EST_HUMAN	EST_HUMAN	AU121370 HEMBB1 Homo sapiens cDNA clone HEMBB1002960 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF-SEQ ID NO:	Expression Signal	Most Similar (199) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8076	18504	28848	2.19	1.0E-109	4502338	NT	Homo sapiens Chondak-Higashi syndrome 1 (CHS1) mRNA
8710	18527	28810	4.83	1.0E-109	W16510.1	EST_HUMAN	2408712.11 heart, fetal_lung_NRH, 15W Homo sapiens cDNA clone IMAGE307439 5' similar to PIF3-43569 S-9369 p51-bola stress-activated protein kinase - rat;
9299	12001	21963	1.65	1.0E-109	Y17123.1	NT	Homo sapiens SNF-5/NT1 gene, exon 6
8954	19176	26275	2.6	1.0E-109	A301139.1	NT	Homo sapiens gene for A1-3, complete cds
3	9920	19751	1.46	1.0E-110	7548904	NT	Homo sapiens diolchase, loddhyronine, type II (DIO2), transcript variant 2. mRNA
34	10021	19817	3.89	1.0E-110	5503073	NT	Homo sapiens luteinizing hormone-releasing hormone receptor-like transcriptional regulator, 1 (LZTR1), mRNA
34	10021	19818	3.89	1.0E-110	5503073	NT	Homo sapiens luteinizing hormone-releasing hormone receptor-like transcriptional regulator, 1 (LZTR1), mRNA
75	10059	19876	30.63	1.0E-110	CO4498.1	EST_HUMAN	CO4488 Human heart cDNA (YNAKamura) Homo sapiens cDNA clone 3NHCS-487
104	9950	19781	1.67	1.0E-110	7548904	NT	Homo sapiens diolchase, loddhyronine, type II (DIO2), transcript variant 2. mRNA
297	10255	20076	0.91	1.0E-110	U67291.1	NT	Human mRNA for inward rectifier potassium channel, complete cds
516	10498	20289	1.16	1.0E-110	U64550.1	NT	Human dyshidrotic (DTH) gene, exon 2b
1163	11076	20521	1.09	1.0E-110	5301620	NT	Homo sapiens alpha-actinin-1 (ACTN1) for transcription, adjacent to 5' end finger domain 1B, complete cds
1258	11165	21076	1.01	1.0E-110	A5032283.1	NT	Homo sapiens 932746.1 mRNA for transcription, adjacent to 5' end finger domain 1B, complete cds
1879	11775	21650	1.5	1.0E-110	BC379477.1	EST_HUMAN	8012376457 NIH_MGC_341 Homo sapiens cDNA clone IMAGE309563 5'
2012	11904		1.98	1.0E-110	BF506866.1	EST_HUMAN	UHF044-acc-3-55-0-131 NCLC03P_3348 Homo sapiens cDNA clone IMAGE308574 3'
2810	12739		1.02	1.0E-110	4950358	NT	Homo sapiens choroidrich sulfite proteoglycan 4 (melanin-associated) (CSFGL) mRNA
3048	12975		1.07	1.0E-110	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L4-like ribosomal protein (L4L), and F1P2 (F1P2) genes, complete cds
3158	13083	22895	1.87	1.0E-110	11493041	NT	Homo sapiens pregnancy-zone protein (PZP), mRNA
3158	13083	22896	1.87	1.0E-110	11493041	NT	Homo sapiens pregnancy-zone protein (PZP), mRNA
3596	13873	25650	0.62	1.0E-110	BC018536.1	EST_HUMAN	b652005.Y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE304848 5' similar to TR-053312 068312 KIA00668 PROTEIN ;
4533	14426	24207	2.06	1.0E-110	A017213.1	EST_HUMAN	cd22b10.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627563 3' similar to SW-N121_RAT_P2591 NUCLEAR ENVELOPE PORE MEMBRANE PROTEIN POM 121 ;
4555	14447	24232	2.08	1.0E-110	AU177812.1	EST_HUMAN	AU117812 HEMBA1 Homo sapiens cDNA clone HEMBA1002241 5'
4638	14718		2.34	1.0E-110	7662441	NT	Homo sapiens KIAA1002 protein (KIAA1002), mRNA
5237	15161	24929	1.9	1.0E-110	BC254065.1	EST_HUMAN	9011187701 NIH_MGC_17 Homo sapiens cDNA clone IMAGE309538 5'
5511	15426	25402	7.34	1.0E-110	11416233	NT	Homo sapiens hypodermal protein FLJ10300 (FLJ10300), mRNA
5511	15426	25403	7.34	1.0E-110	11416233	NT	Homo sapiens hypodermal protein FLJ10300 (FLJ10300), mRNA
6032	16456	26068	4.36	1.0E-110	M5511.1	NT	Human cystic fibrosis transmembrane conductance regulator (CFTR) gene, exon 7
6391	16293	26413	10.04	1.0E-110	A1714276.1	EST_HUMAN	A1714276 DBR Homo sapiens cDNA clone DBO36501 5'
6391	16293	26414	10.04	1.0E-110	A1714276.1	EST_HUMAN	A1714276 DBR Homo sapiens cDNA clone DBO36501 5'
8409	16270	26422	2.7	1.0E-110	A5020675.1	NT	Homo sapiens mRNA for KIAA0668 protein, partial cds

Table 4

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Probe SEQ ID NO.	Exon NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7623	17374	27693	2.91	1.0E-110	AW68394.1	EST_HUMAN	QV2.LT0053.020-000-119-001.LT0053 Homo sapiens cDNA
7915	17795	29004	4.27	1.0E-110	11432732	NT	Homo sapiens galactinolase 2 (GALK2) mRNA
8130	18018	28295	3.7	1.0E-110	Y12337.1	NT	H sapiens mRNA for myotonic dystrophy protein kinase like protein
8334	18211	29432	3.49	1.0E-110	BE734357.1	EST_HUMAN	00156560AF1 NH1.MGC. 21 Homo sapiens cDNA clone IMAGE3840433 5'
8354	18211	29432	3.49	1.0E-110	BE734357.1	EST_HUMAN	00156560AF1 NH1.MGC. 21 Homo sapiens cDNA clone IMAGE3840433 5'
8740	17969	28133	2.43	1.0E-110	AA445523.1	EST_HUMAN	zw57022.1 Scores, testis_NHT Homo sapiens cDNA clone IMAGE:781286 5' similar to TR.G1145816
9091	18637	29685	4.15	1.0E-110	BE867218.1	EST_HUMAN	00143379AF1 NH1.MGC. 72 Homo sapiens cDNA clone IMAGE3324548 5'
9204	18635	29685	5.78	1.0E-110	AW062558.1	EST_HUMAN	L0-BT0763-040509-064-070.BT0763 Homo sapiens cDNA
9444	19080	29432	1.63	1.0E-110	AF911339.1	NT	Homo sapiens gene for AF 4, complete cds
9578	19594	29760	5.07	1.0E-110	BF334545.1	EST_HUMAN	PK8.NT0082.140500-006-012.NT0082 Homo sapiens cDNA
109	10140	19978	16.65	1.0E-111	U43701.1	NT	Human fibronectin protein L23a mRNA, complete cds
189	10151	19978	1.02	1.0E-111	4758007	NT	Homo sapiens ras GTPase activating protein-like (NGAP) mRNA
748	10350	19978	1.87	1.0E-111	BF033271.1	EST_HUMAN	001458531F1 NH1.MGC. 96 Homo sapiens cDNA clone IMAGE3362086 5'
728	10358	23489	3.68	1.0E-111	63593923	NT	Homo sapiens cat eye syndrome critical region gene 1 (CECR1) mRNA
911	10633	23594	73.62	1.0E-111	M25142.1	NT	Homo sapiens alpha-myosin heavy chain (MYH6) gene, exons 32 to 34
3842	13558	23542	1.17	1.0E-111	6612541	NT	Homo sapiens act core on midline homolog 1 (SCML1) mRNA
3842	13558	23543	1.17	1.0E-111	6612541	NT	Homo sapiens act core on midline homolog 1 (SCML1) mRNA
4080	13662	23760	1.09	1.0E-111	7851550	NT	Homo sapiens DKF2-434D150 protein (DKF2-434D150) mRNA
4235	14133	23969	4.45	1.0E-111	K02258.1	NT	Human enkephalin B (enb) gene, exon 4 and 3' flank and complete cds
5394	15294	25117	2.82	1.0E-111	AA151017.1	EST_HUMAN	247607.1 Scores, pregnant, uterus_NbHPU Homo sapiens cDNA clone IMAGE508045 5' similar to gh.M25575 PREGNANCY-SPECIFIC BETA-1 GLYCOPROTEIN C PRECURSOR (HUMAN);
5394	15294	25118	2.82	1.0E-111	AA151017.1	EST_HUMAN	247607.1 Scores, pregnant, uterus_NbHPU Homo sapiens cDNA clone IMAGE508045 5' similar to gh.M25575 PREGNANCY-SPECIFIC BETA-1 GLYCOPROTEIN C PRECURSOR (HUMAN);
5075	15594	26985	1.71	1.0E-111	A0344670.1	EST_HUMAN	g90ag12.x1 NOI_OGAP K05 Homo sapiens cDNA clone IMAGE:1917574 3' similar to gh.M25983 RAS-RELATED PROTEIN RAL A (HUMAN);
9402	16293	29423	3.03	1.0E-111	BF306228.1	EST_HUMAN	L2-NT0101-0280700-114-E03.NT0101 Homo sapiens cDNA
6579	16437	26922	2.28	1.0E-111	AA183814.1	EST_HUMAN	2762612.1 Stratiotes muscled 937209 Homo sapiens cDNA clone IMAGE 592774 5' similar to gh.X03740
6795	16974	29996	3.13	1.0E-111	AA183814.1	EST_HUMAN	MYOSIN HEAVY CHAIN, SKELETAL, MUSCLE (HUMAN);
7113	19500	27221	10.8	1.0E-111	BF214602.1	NT	Human beta-2 integrin (ITGB4) gene, exon 13
7149	17026	27221	13.75	1.0E-111	X177033.1	NT	001847132F1 NH1.MGC. 55 Homo sapiens cDNA clone IMAGE 4078303 5'
7149	17026	27222	13.75	1.0E-111	X177033.1	NT	Human mRNA for integrin alpha-2 subunit
7251	17128	27321	3.26	1.0E-111	AF061395.1	NT	Homo sapiens T19 isoform mRNA, complete cds

Table 4

Single Exon Probes Expressed in Heart

[illegible]

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8445	18319	28578	1.72	1.0E-112	BC284779.1	EST_HUMAN	g142408.y6 NOL_OGAP_K03 Homo sapiens cDNA clone IMAGE:3139899 5'
8500	18373	28637	1.75	1.0E-112	AI162003.1	EST_HUMAN	FUSED TOES: g142408.y6 NOL_OGAP_K03 Homo sapiens cDNA clone IMAGE:1869902 5' similar to TR-Q64362 Q64362
8600	18373	28638	1.75	1.0E-112	AI162003.1	EST_HUMAN	FUSED TOES: g142408.y6 NOL_OGAP_K03 Homo sapiens cDNA clone IMAGE:1869902 5' similar to TR-Q64362 Q64362
8621	18393	28637	5	1.0E-112	AI162003.1	EST_HUMAN	FUSED TOES: g142408.y6 NOL_OGAP_K03 Homo sapiens cDNA clone IMAGE:1869902 5' similar to TR-Q64362 Q64362
725	10657	20487	3.71	1.0E-113	AI162598.1	EST_HUMAN	cd5601.1 x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:195825 3'
725	10657	20488	3.71	1.0E-113	AI162598.1	EST_HUMAN	cd5601.1 x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:195825 3'
927	10652	20700	6.32	1.0E-113	MT1895.1	NT	Human X-linked phosphotyrosine kinase gene, exon 8
1523	11428	21286	2.94	1.0E-113	AI162598.1	EST_HUMAN	cd5601.1 x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:195825 3'
2048	11939	21833	1.18	1.0E-113	BF518218.1	EST_HUMAN	UHFH3W1-ant-403-0UI.11 NOL_OGAP_SUG7 Homo sapiens cDNA clone IMAGE:3982879 3'
2405	12292	22170	0.99	1.0E-113	AJ006976.1	NT	Homo sapiens PTP gene
3001	13018	22613	2.34	1.0E-113	AJ223948.1	NT	Homo sapiens mRNA for putative RNA helicase, 3' end
5035	14907	24677	0.65	1.0E-113	7657065	NT	Homo sapiens vels avian erythroblastosis virus E26 oncogene related (ERG), mRNA
5035	14907	24678	0.65	1.0E-113	7657065	NT	Homo sapiens vels avian erythroblastosis virus E26 oncogene related (ERG), mRNA
5211	18524	28144	16.27	1.0E-113	BE760838.1	EST_HUMAN	g142408.y6 NOL_OGAP_K03 Homo sapiens cDNA clone IMAGE:3872556 5'
5377	15307	25144	6.33	1.0E-113	AI172724.1	EST_HUMAN	AI172724.1 N2R22 Homo sapiens cDNA clone IMAGE:3872556 5'
5608	15523	25605	3.92	1.0E-113	AU140291.1	EST_HUMAN	AI140291.1 N2R22 Homo sapiens cDNA clone IMAGE:3872556 5'
5609	15608	25710	2.05	1.0E-113	11525737	NT	Homo sapiens LDR-N-acyl-L-glutamate-D-galactosamine polypeptide N-acyl-L-glutamate synthetase 8 (GALNT8) (GALNT8), mRNA
7237	17134	27326	2.65	1.0E-113	BE382842.1	EST_HUMAN	g142408.y6 NOL_OGAP_K03 Homo sapiens cDNA clone IMAGE:3872556 5'
7237	17134	27327	2.65	1.0E-113	BE382842.1	EST_HUMAN	g142408.y6 NOL_OGAP_K03 Homo sapiens cDNA clone IMAGE:3872556 5'
7658	17508	27751	1.29	1.0E-113	11428387	NT	Homo sapiens transmembrane protein 2 (TMEM2), mRNA
8458	15339	28604	1.73	1.0E-113	AI1500519.1	EST_HUMAN	UHFH3W1-ant-403-0UI.11 NOL_OGAP_SUG7 Homo sapiens cDNA clone IMAGE:3077326 5'
8550	15719	29582	2.07	1.0E-113	6009002	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA
8550	15719	29583	2.07	1.0E-113	6009002	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA
8554	18452	28721	3.44	1.0E-113	BE232968.1	EST_HUMAN	g142408.y6 NOL_OGAP_K03 Homo sapiens cDNA clone IMAGE:3872556 5'
629	10566	20379	7.66	1.0E-114	T70551.1	EST_HUMAN	yH1501.51 Sphaera fletii liver sphen 1NFLS Homo sapiens cDNA clone IMAGE:108288 3' similar to g142408.y6 NOL_OGAP_K03 Homo sapiens cDNA clone IMAGE:108288 3' similar to
1055	10972	20815	1.31	1.0E-114	8822087	NT	g142408.y6 NOL_OGAP_K03 Homo sapiens cDNA clone IMAGE:108288 3' similar to
1291	11198	21053	3.47	1.0E-114	7957529	NT	Homo sapiens hypoxanthine phosphoribosyl transferase 1 (HGPRT), mRNA
1648	11552	21413	5.53	1.0E-114	6079073	NT	Homo sapiens nucleophosin-like protein 1 (NLP-1), mRNA
2773	10025	18823	0.82	1.0E-114	AI1035102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Seq SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E	Top Hit Accession No.	Top Hit Source	Top Hit Description
2773	10325	18524	0.62	1.0E-114	AB03102.1	NT	Human sapiens mRNA for KIAA1278 protein, partial cds
3032	13519	22874	2.28	1.0E-114	X04036.1	NT	Human gene for cathepsin (EC 1.11.1.8) exon 2 mapping to chromosome 11, band p13
3135	13300	23851	1.2	1.0E-114	BF-20174.1	EST_HUMAN	BC185852P.NIH_MGC_19 Homo sapiens cDNA clone IMAGE:410024 5'
3834	13843	22821	1.85	1.0E-114	AF14973.1	EST_HUMAN	Human sapiens NOD1_MGC_19 Homo sapiens cDNA clone IMAGE:410024 5'
5120	14688	24762	1.2	1.0E-114	AA164468.1	EST_HUMAN	AF06065.1 Stenotrophomonas 387/239 Homo sapiens cDNA clone IMAGE:626832 5' similar to cathepsin
5121	14689	24763	2.31	1.0E-114	AF004349.1	EST_HUMAN	NC_022.8 MGC22 repetitive element
5316	15237	25040	1.37	1.0E-114	AF068930	NT	Human sapiens PRY protein kinase mRNA, complete cds
5316	15237	25041	1.37	1.0E-114	AF068980	NT	Human sapiens alpha domain, seven thrombospondin repeats (Type 1 and Type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 3A (SEMA3A) mRNA
6316	16717	26338	7.08	1.0E-114	Y18000.1	NT	(TM) and short cytoplasmic domain, (semaphorin) 3A (SEMA3A) mRNA
6316	16719	26339	7.08	1.0E-114	Y18000.1	NT	(TM) and short cytoplasmic domain, (semaphorin) 3A (SEMA3A) mRNA
6906	16466	26673	1.86	1.0E-114	4557603	EST_HUMAN	Human sapiens NP2 gene
6748	16627	26814	1.73	1.0E-114	AF934139.1	EST_HUMAN	Human sapiens gamma-aminobutyric acid (GABA) A receptor, alpha 2 (GABRA2) mRNA
6748	16627	26815	1.73	1.0E-114	AF934139.1	EST_HUMAN	9160306.1 NC1_OGAP_Bnc25 Homo sapiens cDNA clone IMAGE:2017463 3'
7048	16625	27161	3.39	1.0E-114	U63041.1	NT	Human neural cell adhesion molecule CD56 mRNA, complete cds
7048	16625	27162	3.39	1.0E-114	U63041.1	NT	Human neural cell adhesion molecule CD56 mRNA, complete cds
7090	16697	27162	0.35	1.0E-114	AB011133.1	NT	Human sapiens mRNA for KIAA0861 protein, partial cds
7418	17281	28753	3.78	1.0E-114	AF037458.1	EST_HUMAN	AF0805.1 NIH_MGC_2 Homo sapiens cDNA clone IMAGE:284744 5'
7447	16459	26652	3.13	1.0E-114	AF077794.1	EST_HUMAN	Human sapiens Glycine kinase ppbco-arc (HSC) gene, exon 12 and partial cds
7844	17684	27942	1.31	1.0E-114	AF116327.2	NT	Human sapiens Chromosome 21 segment HS21C027
8167	18355		7.14	1.0E-114	BE302688.1	EST_HUMAN	3a7g12.1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2606036 5' similar to p12709 40S
8527	18369	26666	4.38	1.0E-114	AF073454.1	EST_HUMAN	RIBOSOMAL PROTEIN 24 (HUMAN), gb-M20632 Mouse L9p63 protein mRNA from a repetitive element, complete (MOUSE);
8527	18369	26667	4.38	1.0E-114	AF073454.1	EST_HUMAN	AV733454r cDNA Homo sapiens cDNA clone cGABAO8 5'
8534	18367	26863	2.86	1.0E-114	AF073454.1	EST_HUMAN	AV733454r cDNA Homo sapiens cDNA clone cGABAO8 5'
8534	18367	26863	2.86	1.0E-114	AF073454.1	EST_HUMAN	AV733454r cDNA Homo sapiens cDNA clone cGABAO8 5'
8834	18447	28933	2.86	1.0E-114	AF073454.1	EST_HUMAN	Human sapiens TNF-inhibable protein CG12.1 (CG12.1), mRNA
9470	19748		3.21	1.0E-114	11418041	NT	Human sapiens hypophosphorylated protein (Q1042K10.2), mRNA
9729	19266	25222	3.06	1.0E-114	11034950	NT	Human sapiens hypophosphorylated protein (Q1042K10.2), mRNA
9729	19266	25223	3.06	1.0E-114	11034950	NT	Human sapiens hypophosphorylated protein (Q1042K10.2), mRNA
21	10059	18601	3.36	1.0E-114	4726111	NT	Human sapiens FLA-B associated transcript 1 (DMSB1E) mRNA
125	10059	18620	0.95	1.0E-115	4505938	NT	Human sapiens polyoma virus (RNA1) (DNA derived), polyprotein A (220D) mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
129	10103		1.99	1.0E-115	4357/82/NT	EST	Homo sapiens brain, 16 (K01118) mRNA
289	10253	20273	2.17	1.0E-115	AW94775.1	EST_HUMAN	QV4-UM0058-350635-59-508 UM00584 Homo sapiens cDNA clone IMAGE: 594083 3' similar to TR000535 000536
528	10467	20278	1.08	1.0E-115	A333208.1	EST_HUMAN	q06001.X1 NQ1 CGAR_CGH.Homo sapiens cDNA, clone IMAGE: 594083 3' similar to TR000535 000536
525	10467	20279	1.08	1.0E-115	A333208.1	EST_HUMAN	q06001.X1 NQ1 CGAR_CGH.Homo sapiens cDNA, clone IMAGE: 594083 3' similar to TR000535 000536
769	10659	20537	1.83	1.0E-115	5174702/NT	EST_HUMAN	Homo sapiens Transforming growth factor beta-activated kinase-binding protein (TAB1), mRNA
769	10660	20538	1.83	1.0E-115	5174702/NT	EST_HUMAN	Homo sapiens Transforming growth factor beta-activated kinase-binding protein (TAB1), mRNA
771	10701	20540	49.32	1.0E-115	4830394/NT	EST_HUMAN	Homo sapiens keratin, heavy polypeptide 1 (P1H1) mRNA
1539	11443	21301	0.92	1.0E-115	AZ29180.1	EST_HUMAN	Homo sapiens alpha-antitrypsin semialdehyde synthase mRNA, complete cds
1539	11443	21302	0.92	1.0E-115	AZ29180.1	EST_HUMAN	Homo sapiens alpha-antitrypsin semialdehyde synthase mRNA, complete cds
1786	11683	21591	3.14	1.0E-115	AJ27862.1	NT	Homo sapiens partial TTN gene for titin
1789	11689	21973	1.42	1.0E-118	U796027.1	NT	Homo sapiens Tyrosine kinase (BTK), alpha-D-glucosylase A (GLA), L44-like ribosomal protein (L44L) and PTPs (PTP) genes, complete cds
2034	11925	21818	0.97	1.0E-115	B574469.1	EST_HUMAN	6017/9535F1 NH1 MGC_9 Homo sapiens cDNA clone IMAGE:392832 5'
2034	11925	21818	0.97	1.0E-115	B574469.1	EST_HUMAN	6017/9535F1 NH1 MGC_9 Homo sapiens cDNA clone IMAGE:392832 5'
2820	12749		1.78	1.0E-118	AW94776.1	EST_HUMAN	QV4-UM0054-300300-186-108 UM00544 Homo sapiens cDNA
3077	13004	22795	2.1	1.0E-115	AJ245922.1	NT	Homo sapiens mRNA for alpha-tubulin 8 (TUBA8 gene)
3077	13004	22796	2.1	1.0E-115	AJ245922.1	NT	Homo sapiens mRNA for alpha-tubulin 8 (TUBA8 gene)
3427	13344	23149	4.03	1.0E-116	AJ27692.1	NT	Homo sapiens partial TTN gene for titin
3956	13984	23894	4.04	1.0E-115	AB002348.2	NT	Homo sapiens mRNA for KIAA0350 protein, perlecan
4169	14059	23844	1.09	1.0E-115	AL137103.1	NT	Novel human gene mapping to chromosome X
4301	14169	23844	1.09	1.0E-115	AL137103.1	NT	Novel human gene mapping to chromosome X
4335	14232	24014	3.81	1.0E-115	6912856/NT	EST_HUMAN	Homo sapiens si:2-like 3 (SIRT3), mRNA
4335	14232	24014	3.81	1.0E-115	6912856/NT	EST_HUMAN	Homo sapiens si:2-like 3 (SIRT3), mRNA
4578	14468	24254	2.98	1.0E-115	AL086957.1	EST_HUMAN	Homo sapiens EphA4 (EPHA4), mRNA
4578	14468	24255	2.98	1.0E-115	AL086957.1	EST_HUMAN	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
4813	14936	24462	2.96	1.0E-115	AL103286.2	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
4813	14936	24463	2.96	1.0E-115	AL103286.2	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
5279	15071	24977	1.75	1.0E-118	AW97035.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C008
5330	15250	25055	7.22	1.0E-115	BF861387.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C008
5402	15321	25250	2.05	1.0E-115	1142512/NT	EST_HUMAN	60211934JF1 NH1 MGC_59 Homo sapiens cDNA clone IMAGE:4270738 5'
5402	15321	25250	2.05	1.0E-115	1142512/NT	EST_HUMAN	60211934JF1 NH1 MGC_59 Homo sapiens cDNA clone IMAGE:4270738 5'
5562	15726	26575	12.92	1.0E-115	11420303/NT	EST_HUMAN	Homo sapiens similar to ER to nucleus signalling (H1), sapiens (LOC093433), mRNA
5562	15726	26575	12.92	1.0E-115	11420303/NT	EST_HUMAN	Homo sapiens similar to ER to nucleus signalling (H1), sapiens (LOC093433), mRNA
5593	15838	26590	1.93	1.0E-115	7081883/NT	EST_HUMAN	Homo sapiens similar to ribosomal protein S20 (H), sapiens (LOC38439), mRNA
5593	15838	26590	1.93	1.0E-115	7081883/NT	EST_HUMAN	Homo sapiens similar to ribosomal protein S20 (H), sapiens (LOC38439), mRNA

Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5653	15538	25691	1.03	1.0E-116	7061693	NT	Homo sapiens KIAA0054 gene product; Helicase (KIAA0054), mRNA
6313	16176	26533	1.25	1.0E-116	A079558.1	EST_HUMAN	oz21.605.x1 Soares, fetal, fetus, N22HF8, Sw Homo sapiens cDNA clone IMAGE:1676914 3'
6313	16176	26534	1.25	1.0E-116	A079558.1	EST_HUMAN	oz21.605.x1 Soares, fetal, fetus, N22HF8, Sw Homo sapiens cDNA clone IMAGE:1676914 3'
6376	16241	26401	7.41	1.0E-116	A802321.2	NT	Homo sapiens mRNA for KIAA0695 protein, partial cds
6744	16523	26811	12.78	1.0E-116	BE630187.1	EST_HUMAN	RC6-ET0081-130700-011-C01 ET0081 Homo sapiens cDNA
6744	16523	26812	12.78	1.0E-116	BE630187.1	EST_HUMAN	RC6-ET0081-130700-011-C01 ET0081 Homo sapiens cDNA
7145	16963	27184	2.2	1.0E-116	11434772	NT	Homo sapiens ankyrin-like translation initiation factor 4B (EIF4B), mRNA
7745	17595	27016	1.92	1.0E-116	A8002336.1	NT	Homo sapiens mRNA for KIAA0338 gene, partial cds
7745	17595	27017	1.92	1.0E-116	A8002336.1	NT	Homo sapiens mRNA for KIAA0338 gene, partial cds
8100	17599	28259	3.5	1.0E-116	AW157154.1	EST_HUMAN	932269.x1 NC CGAP LH Homo sapiens cDNA clone IMAGE:2852339 3' similar to SW_CAYP_CANFA
8701	18119	28301	2.26	1.0E-116	4902528	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1E subunit (CAVNA1E) mRNA
9501	19200	20366	1.42	1.0E-116	BE27592.1	EST_HUMAN	601121337F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2868775 5'
783	10713	20552	1.26	1.0E-116	4507334	NT	Homo sapiens synaptophysin 1 (SYN1), mRNA
841	10768	21733	6.98	1.0E-116	4507335	NT	Homo sapiens synaptophysin 1 (SYN1), mRNA
1652	11673	21733	2.38	1.0E-116	5174479	NT	Homo sapiens perlecanin (PGC1), mRNA
1980	11673	21734	2.38	1.0E-116	AU153060.1	EST_HUMAN	AU153060 NT2674 Homo sapiens cDNA clone NT2674-001228 5'
2050	12711	21834	1.01	1.0E-116	MT19824.1	NT	Human apolipoprotein B-100 (apoB) gene, exons 17 and 18
2050	12711	21835	1.01	1.0E-116	MT19824.1	NT	Human apolipoprotein B-100 (apoB) gene, exons 17 and 18
2256	12143	22042	1.88	1.0E-116	5463941	NT	Homo sapiens protein phosphatase, EF hand calcium-binding domain 1 (PPEF1) mRNA
2263	12176	22181	1.46	1.0E-116	UT83008.1	NT	Human efficacy receptor olf17-201-1 (OLF17-201-1) gene, olfactory receptor cDNA 1732 (OLF17-32) gene and efficacy receptor pseudo_cdf17-01 (OLF17-01) pseudogene, complete cds
2407	12284	22181	4.48	1.0E-116	A9018333.1	NT	Homo sapiens mRNA for KIAA0790 protein, partial cds
2704	12650	22458	2.19	1.0E-116	BE689256.1	EST_HUMAN	601153337F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3914900 5'
3137	13092	22860	4.73	1.0E-116	LT7570.1	NT	Homo sapiens DiGeorge syndrome critical region, centromeric end
3137	13092	22861	4.73	1.0E-116	LT7570.1	NT	Homo sapiens DiGeorge syndrome critical region, centromeric end
4281	14180	23568	2.01	1.0E-116	5031654	NT	Homo sapiens sodium phosphate transporter 3 (NPT3), mRNA
4747	14632	24118	1.17	1.0E-116	A1907096.1	EST_HUMAN	PW-BT135-070499-016 BT135 Homo sapiens cDNA
5122	14890	24784	2.12	1.0E-116	AJ243213.1	NT	Homo sapiens partial 5-HT ₂ receptor gene, exons 2 to 5
5657	15550	25941	5.88	1.0E-116	W42822.1	EST_HUMAN	zc2407.r1 Soares, senescent, fibroblasts, NHHSF Homo sapiens cDNA clone IMAGE:323245 5' similar to SW_ADMJM_MOUSE P08249 MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR ;
5768	15676	25781	1.95	1.0E-116	A164656.1	NT	Homo sapiens mRNA for KIAA1636 protein, partial cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5768	15675	25742	1.65	1.0E-116	AB046955.1	NT	Homo sapiens mRNA for KIAA1335 protein, partial cds
5833	15759	25877	72.79	1.0E-116	BF577910.1	EST_HUMAN	002084730F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:426087 5'
5924	15820		1.8	1.0E-116	BE159133.1	EST_HUMAN	MF2-110379-210200-102.84 HT0379 Homo sapiens cDNA
6145	16016	26156	3.99	1.0E-116	CO3944.1	EST_HUMAN	CO2944 Human heart cDNA (YNAKamura) Homo sapiens cDNA clone 3NH0597
6175	16199	26225	2.97	1.0E-116	AV176814	EST_HUMAN	AV176814 DCR Homo sapiens cDNA clone DCRBC098 5'
6274	16753	26949	1.99	1.0E-116	AA342356.1	EST_HUMAN	EST02885 Jurkat T-cells V Homo sapiens cDNA 5' and similar to keratin 2
6374	16753	26950	1.99	1.0E-116	AA342356.1	EST_HUMAN	EST02885 Jurkat T-cells V Homo sapiens cDNA 5' and similar to keratin 2
7173	17090	27239	1.43	1.0E-116	BE555507.1	EST_HUMAN	001336268F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:360050 5'
7290	17137	27330	1.96	1.0E-116	AL215352.1	EST_HUMAN	009005.51 Source_NFL_T_GBC_ST Homo sapiens cDNA clone IMAGE:1844168 3' similar to
7577	17428	27642	1.77	1.0E-116	11418946	NT	Homo sapiens lamin, alpha 2 (lamin, congothal muscular overabundant) (LAMA2), mRNA
8074	17895	28216	3.88	1.0E-116	BF335848.1	EST_HUMAN	00553741.1 Source_NFL_T_GBC_ST Homo sapiens cDNA clone IMAGE:1935102 3' similar to WP50465.7
8477	18350	28615	3.23	1.0E-116	AA367140.1	EST_HUMAN	0011644.X1 Source_NHNPu_S1 Homo sapiens cDNA clone IMAGE:3344590 5'
8591	19741		2.08	1.0E-116	BE258599.1	EST_HUMAN	00116350F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3344590 5'
8776	19814		2.88	1.0E-116	AL134889.1	EST_HUMAN	DHFZP703271110.1 T1702 (synonym: hinc2) Homo sapiens cDNA clone DCFZP703271110 5'
8971	10487	20206	1.18	1.0E-117	4282630	NT	Homo sapiens acyl-Coenzyme A carboxylase alpha (ACACA), mRNA
1081	12094	20321	1.59	1.0E-117	AF124933.1	NT	Miss musculi fragile-X-related protein 1 (Frt10) gene, exons 1-6 through 15
1719	11620	21489	6.25	1.0E-117	AF123320.1	NT	Homo sapiens lymphocyte activation-associated protein mRNA, complete cds
1790	11688	21564	2.3	1.0E-117	AF16816.1	NT	Human apolipoprotein B-100 (apoB) gene, exon 10
2194	12051	21962	2.99	1.0E-117	AF095709.1	EST_HUMAN	EST3369769 MAGE resequencing, MAGE Homo sapiens cDNA
3230	13154	22953	1.75	1.0E-117	AA978114.1	EST_HUMAN	0032511.1 Source_NFL_T_GBC_ST Homo sapiens cDNA clone IMAGE:1979548 3'
3908	13818	23569	3.92	1.0E-117	AA316723.1	EST_HUMAN	EST1180414 HCC cell line (metastatic to liver in mouse) Homo sapiens cDNA 5' and similar to ribosomal protein L26
4247	14146	23620	1.96	1.0E-117	8059564	NT	Homo sapiens collagen, type IV, alpha 5 (Aport syndrome) (COL4A5), mRNA
4475	14359	24158	1.88	1.0E-117	AL042120.1	EST_HUMAN	DFZFZ454C1120.1 T1434 (synonym: hinc3) Homo sapiens cDNA clone DCFZP454C1120 5'
4622	14510	24256	1.35	1.0E-117	X98970.1	NT	H sapiens mRNA for TFCR16 protein
4622	14510	24260	1.35	1.0E-117	X98970.1	NT	H sapiens mRNA for TFCR16 protein
4705	14591	24382	9.22	1.0E-117	AF143304.2	NT	Homo sapiens Scar2 (SCAR2) gene, partial cds
4705	14591	24383	9.22	1.0E-117	AF143304.2	NT	Homo sapiens Scar2 (SCAR2) gene, partial cds
4856	14736	24516	3.96	1.0E-117	AB020673.1	NT	Homo sapiens mRNA for KIAA0899 protein, complete cds
5280	15202	24978	2.15	1.0E-117	BE790508.1	EST_HUMAN	001563057F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3832214 5'
6404	16256	28426	4.99	1.0E-117	U76571.1	NT	Homo sapiens nuclear hormone receptor (nhr) gene, 3' end of cds
6404	16255	28427	4.89	1.0E-117	U76571.1	NT	Homo sapiens nuclear hormone receptor (nhr) gene, 3' end of cds

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6185	18316	26482	3.77	1.0E-117	AV171788.1	EST_HUMAN	AV171788.D88 Homo sapiens cDNA clone DQ8BAE01.5
6185	18316	26483	3.77	1.0E-117	AV171788.1	EST_HUMAN	AV171788.D88 Homo sapiens cDNA clone DQ8BAE01.5
6651	19531	26725	6.58	1.0E-117	AI1950146.1	EST_HUMAN	W59607.X1 NC1 CGAP Bn23 Homo sapiens cDNA clone IMAGE.2469929.3 similar to TR076095
6837	19716	26908	1.7	1.0E-117	10834390	NT	Human gene for very low density lipoprotein receptor, exon 11
6837	19716	26909	1.7	1.0E-117	10834390	NT	Human gene for very low density lipoprotein receptor, exon 11
7351	17228	27428	2.28	1.0E-117	BT19524.1	NT	Human gene for very low density lipoprotein receptor, exon 11
7635	17496	27706	1.51	1.0E-117	BE73922.1	EST_HUMAN	283811.1 Soares fetal heart NH419W Homo sapiens cDNA clone IMAGE.3943748.5
8395	18262	28512	10.31	1.0E-117	W80605.1	EST_HUMAN	gbM14210 BONE PROTEOGLYCAN II PRECURSOR (HUMAN);
8595	19422	28732	3.96	1.0E-117	AB011541.1	NT	Homo sapiens mRNA for MECPG, partial cds
8595	19422	28733	3.96	1.0E-117	AB011541.1	NT	Homo sapiens mRNA for MECPG, partial cds
8698	19516	28974	15.63	1.0E-117	BE268663.1	EST_HUMAN	901185305F1 NH MSC 3 Homo sapiens cDNA clone IMAGE.3544093.5
8872	19854	28974	2.22	1.0E-117	4501848	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
8872	19854	28975	2.22	1.0E-117	4501848	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
64	10050	19893	6.64	1.0E-118	AF16501.1	NT	Homo sapiens RSP-C151 mRNA, complete cds
80	10074	19890	2.59	1.0E-118	AF16501.1	NT	Homo sapiens RSP-C151 mRNA, complete cds
803	10448	20251	5.09	1.0E-118	767016	EST_HUMAN	DK-29454065.1 434 (synonym: hns3) Homo sapiens cDNA clone DK724941068.5
858	12350	20567	2.99	1.0E-118	767016	EST_HUMAN	Homo sapiens hypothetical protein (D33281.9 C1), mRNA
2195	12073	21975	2.39	1.0E-118	BE39705.1	EST_HUMAN	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
2198	12073	21976	2.39	1.0E-118	BE39705.1	EST_HUMAN	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
2198	12073	21977	2.39	1.0E-118	BE39705.1	EST_HUMAN	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
2281	12195	22465	3.77	1.0E-118	AV1951728.1	EST_HUMAN	901281947F1 NH MSC 44 Homo sapiens cDNA clone IMAGE.3904019.5
2711	12574	22465	2.38	1.0E-118	U07000.1	NT	901281947F1 NH MSC 44 Homo sapiens cDNA clone IMAGE.3904019.5
2711	12574	22466	2.38	1.0E-118	U07000.1	NT	EST1533759 IMAGE resequence, IMAGE3 Homo sapiens cDNA
3095	12993	22897	3.73	1.0E-118	Y19392.1	NT	Human breakpoint cluster region (BCR) gene, complete cds
3169	13094	22897	4.51	1.0E-118	AI847894.1	NT	Human breakpoint cluster region (BCR) gene, complete cds
3169	13094	22898	4.51	1.0E-118	AI847894.1	EST_HUMAN	Homo sapiens PRKY exon 7
3998	13904	23979	7.97	1.0E-118	D29900.1	NT	gb01105.X1 NC1 CGAP XG5 Homo sapiens cDNA clone IMAGE.1916769.3
5329	18249	25063	2.02	1.0E-118	AF142624.1	NT	Human mRNA for ribosomal protein, complete cds
5329	18249	25064	2.02	1.0E-118	AF142624.1	NT	Human calcium channel gamma 4 subunit (CACNG4) gene, exon 3
5920	18535	25620	1.89	1.0E-118	11420704	NT	Homo sapiens calcium channel gamma 4 subunit (CACNG4) gene, exon 3
6020	18524	26054	1.87	1.0E-118	455732	NT	Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA
6020	18524	26055	1.87	1.0E-118	455732	NT	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2), mRNA

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6462	16341	26509	4.13	1.0E-118	11431050	NT	Homo sapiens chromosome 2 open reading frame 3 (CZORF3), mRNA
6646	16328	26722	2.23	1.0E-118	BE71223.1	EST_HUMAN	H01480166F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3872247 5'
6647	16763	26960	2.89	1.0E-118	BE06285.1	EST_HUMAN	Q10410253-090200-097-103 BT0293 Homo sapiens cDNA
6654	16763	25991	7.61	1.0E-118	BE003285.1	EST_HUMAN	Q10410253-090200-097-103 BT0293 Homo sapiens cDNA
6656	16767	26963	2.69	1.0E-118	AA443024.1	EST_HUMAN	z98407.1 Sources_NHMFPU_S1 Homo sapiens cDNA clone IMAGE:811769 5'
6656	16767	26964	1.34	1.0E-118	AA443024.1	EST_HUMAN	z98407.1 Sources_NHMFPU_S1 Homo sapiens cDNA clone IMAGE:811769 5'
7035	16912	27100	1.16	1.0E-118	AB002381.1	NT	Human mRNA for KIA0383 gene, partial cds
7035	16912	27101	1.16	1.0E-118	AB002381.1	NT	Human mRNA for KIA0383 gene, partial cds
7062	16639	27129	1.28	1.0E-118	465732	NT	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA
7062	16639	27130	1.28	1.0E-118	465732	NT	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA
7223	17100	27266	5.71	1.0E-118	BE203134.1	EST_HUMAN	801144868F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:316902 5'
7656	17766	28027	1.16	1.0E-118	BF195407.1	EST_HUMAN	7617409.1 NCL_GGAP_Bn33 Homo sapiens cDNA clone IMAGE:3864765 3' similar to SW_ZP3A_HUMAN
8566	16465	26737	3.06	1.0E-118	AA315007.1	EST_HUMAN	P21754 ZONA PELLUCIDA SPERM-BINDING PROTEIN 3A PRECURSOR
8647	16659	26847	1.75	1.0E-118	BF036897.1	EST_HUMAN	EST1169514 HCC cell line (metastasis to liver in mouse) H Homo sapiens cDNA 5' end similar to dynactin light chain 1, cytoplasmic
8647	16659	26848	1.75	1.0E-118	BF036897.1	EST_HUMAN	Q10410059-126000-385-512 UM0091 Homo sapiens cDNA
7441	10672	20508	0.51	1.0E-119	AF170402.1	NT	Homo sapiens chloride channel CLCA3 (CLCA3) mRNA, complete cds
1021	12683	20781	1.85	1.0E-119	7705407	NT	Homo sapiens CGL-195 protein (LOC51011), mRNA
1691	11766	21653	2.59	1.0E-119	AB023147.1	NT	Homo sapiens mRNA for KIA0350 protein, partial cds
3064	12691	22783	1.61	1.0E-119	662203	NT	Homo sapiens hypothetical protein FLN10052 (FLN10052), mRNA
3322	13126		1.08	1.0E-119	AA916780.1	EST_HUMAN	en00463.1 NO_GOP_L105 Homo sapiens cDNA clone IMAGE:1566241 3' similar to WP_044F8.2
3670	13761	23573	1.15	1.0E-119	4504119	NT	CS01214.1
6111	14679	24753	0.98	1.0E-119	AA073984.1	EST_HUMAN	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
5272	16194	24969	2.48	1.0E-119	AU133300.1	EST_HUMAN	7914403 Chromosome 7 Fetal Brain cDNA Library/Homo sapiens cDNA clone 79144F03
5282	15204	24960	14.93	1.0E-119	U69914.1	NT	AU133309 NT12944 Homo sapiens cDNA clone NT2934001691 5'
5285	15207	24964	3.32	1.0E-119	BF036121.1	EST_HUMAN	Human neurotrophin (NFI) gene, complete cds
5336	15266	25079	2.24	1.0E-119	AV60373.1	EST_HUMAN	RC1-NN0075-250600-018-005 NN0073 Homo sapiens cDNA clone GDC0803 5'
6726	15633	25736	7.19	1.0E-119	AF1510703.1	EST_HUMAN	q677080.x1 Sources_Heart_NH9119W Homo sapiens cDNA clone IMAGE:1706128 3' similar to
5687	16793	25914	2.79	1.0E-119	X65592.1	NT	SW_K1C1 MOUSE P02535 KERATIN, TYPE I OYTGSKLEFAL.10 ;
6695	16801	26925	1.42	1.0E-119	AV074193.1	EST_HUMAN	EST1360296 IMAGE reassessances, MAGM Homo sapiens cDNA
8361	16243	28403	1.42	1.0E-119	BE709514.1	EST_HUMAN	001562000F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3840801 5'

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NC:	Exon SEQ ID NC:	ORF SEQ ID NO:	Expression Signal	Mean Similar Top Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8914	18722	25013	2.07	1.0E-120	U84774.1	NT	Human muscle glycogen phosphorylase (PYGM) gene, 5'UTR and exon 1
9495	19111	26288	1.36	1.0E-120	11417852	NT	Homo sapiens calcineurin binding protein 1 (KIA00330), mRNA
67	10032	19897	1.04	1.0E-121	Y18000.1	NT	Homo sapiens NF2 gene
374	10328	20151	0.98	1.0E-121	AU124603.1	EST_HUMAN	AL134903 PLACE1 Homo sapiens cDNA clone PLACE1000890 5'
707	12074	20465	1.23	1.0E-121	5032182	NT	Homo sapiens TNF receptor-associated factor 1 (TRAF1) mRNA
1556	11491	21319	0.99	1.0E-121	AB011153.1	NT	Homo sapiens mRNA for KIA00561 protein, partial cds
1923	11918	21627	0.99	1.0E-121	4755139	NT	Homo sapiens inositol polyphosphate-4-phosphatase, type I, 107KD (INPP4A), splice variant a, mRNA
1923	11918	21658	0.99	1.0E-121	4755139	NT	Homo sapiens inositol polyphosphate-4-phosphatase, type I, 107KD (INPP4A), splice variant a, mRNA
2055	11945	21841	1.17	1.0E-121	L76931.1	NT	Homo sapiens metabotropic glutamate receptor 1 beta (mGluR1b) mRNA, complete cds
2630	12043	22258	1.05	1.0E-121	BF043378.1	EST_HUMAN	90214756F1 NGL CGAP Brn44 Homo sapiens cDNA clone IMAGE:4180285 5'
2630	12043	22258	1.05	1.0E-121	BF043378.1	EST_HUMAN	90214756F1 NGL CGAP Brn44 Homo sapiens cDNA clone IMAGE:4180285 5'
3042	12868	22763	3.99	1.0E-121	Y10268.1	NT	Homo sapiens HH33 gene for hair keratin, exons 1 to 9
3042	12868	22764	3.99	1.0E-121	Y10268.1	NT	Homo sapiens HH33 gene for hair keratin, exons 1 to 9
3421	13408	23213	1.09	1.0E-121	AF037183.1	NT	Homo sapiens mRNA for KIA01337 protein, partial cds
3421	13408	23214	1.09	1.0E-121	AF037183.1	NT	Homo sapiens mRNA for KIA01337 protein, partial cds
3624	13538	23228	6.61	1.0E-121	AF153195.2	NT	Homo sapiens adiponectin-related protein complex AP-1, splice subunit mRNA, complete cds
4236	14134	23910	1.21	1.0E-121	A063294.1	EST_HUMAN	9557001.X1 NGL CGAP Part1 Homo sapiens cDNA clone IMAGE:2035417 3'
4901	14781	24556	2.55	1.0E-121	X91937.1	NT	CH-81043-000235-075 B1043 Homo sapiens cDNA
5050	14822	24955	1.03	1.0E-121	A0904181.1	EST_HUMAN	Homo sapiens DNA for prostacyclin synthase, exon 6
6632	16812	26701	2.48	1.0E-121	D84122.1	NT	Homo sapiens COX1T (yeast) homolog, cytochrome c oxidase assembly protein (COX1T), mRNA
6632	16812	26702	2.48	1.0E-121	D84122.1	NT	Homo sapiens COX1T (yeast) homolog, cytochrome c oxidase assembly protein (COX1T), mRNA
8157	18045	28297	4.44	1.0E-121	11427789	NT	Homo sapiens UDP-glucuronosyltransferase 2B4 precursor (UGT2B4) mRNA, UGT2B4*E485 allele, complete cds
8163	18051	28303	2.28	1.0E-121	AF04200.1	NT	Homo sapiens chloride intracellular channel 4 like (CLIC4), mRNA
8335	18213	28460	4.91	1.0E-121	7303034	NT	YJ74031.1 Soares fetal liver spleen TNF- α Homo sapiens cDNA clone IMAGE:248448 3'
8363	18240	28489	3.48	1.0E-121	N06824.1	EST_HUMAN	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
287	10322	20047	3.99	1.0E-122	11526176	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
333	10322	20107	2.22	1.0E-122	AF114488.1	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
335	10312	20132	1.54	1.0E-122	11526176	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
864	10760	20841	2.85	1.0E-122	AF114488.1	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
1201	11111	20957	3.41	1.0E-122	N020707.1	NT	Human kappa-immunoglobulin germline pseudogene (Chr22.4) variable region (subgroup V kappa II)

Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
7471	17341	27537	12.28	1.0E-124	U09623.1	NT	Oryzodorus curticulus New Zealand white elongation factor 1 alpha (RibofL2) mRNA, complete cds
8658	18765	26057	5	1.0E-123	BF077282.1	EST_HUMAN	63089279HF NIH_MGC_83 Homo sapiens cDNA, clone IMAGE:350878 5'
8658	18765	26057	5	1.0E-123	BF077282.1	EST_HUMAN	63089279HF NIH_MGC_83 Homo sapiens cDNA, clone IMAGE:350878 5'
268	10233	20045	1.1	1.0E-124	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
268	10233	20049	1.1	1.0E-124	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
273	10249		1.88	1.0E-124	DR1675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4771	10421	20228	2.11	1.0E-124	AL193449.2	NT	Homo sapiens chromosome 21 segment HS21C046
676	10809	20429	2.03	1.0E-124	AA397591.1	EST_HUMAN	261004.71 Stratagene scabin brain ST1 Homo sapiens cDNA, clone IMAGE:726710 5' similar to TRG300482 G000482 POL-REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT);
676	10809	20430	2.03	1.0E-124	AA397591.1	EST_HUMAN	261004.71 Stratagene scabin brain ST1 Homo sapiens cDNA, clone IMAGE:726710 5' similar to TRG300482 G000482 POL-REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT);
7421	10773	20509	3.07	1.0E-124	AF159654.1	NT	Human putative ribosomal protein S1 mRNA
797	10720	20581	1.96	1.0E-124	4507500	NT	Homo sapiens hypophyseal protein (RNP), mRNA
8881	11021	20960	1.81	1.0E-124	7705448	NT	Homo sapiens finger protein (RNP), mRNA
1263	11200	21050	2.59	1.0E-124	11419052	NT	Homo sapiens glucose transporter 3 gene, exons 9, 10, and complete cds
1334	11231	21066	5.54	1.0E-124	AF274892.1	NT	Homo sapiens glucose transporter 3 gene, exons 9, 10, and complete cds
4324	11231	21067	5.54	1.0E-124	AF274892.1	NT	Homo sapiens glucose transporter 3 gene, exons 9, 10, and complete cds
1773	11072	21070	2.35	1.0E-124	AB170524.1	EST_HUMAN	80149719F NIH_MGC_60 Homo sapiens cDNA, clone IMAGE:3893954 5'
2076	11071	21077	2.19	1.0E-124	BE870679.1	EST_HUMAN	80149719F NIH_MGC_60 Homo sapiens cDNA, clone IMAGE:3893954 5'
2408	12285	22162	0.85	1.0E-124	AB024069.1	NT	Homo sapiens gene for B120, exon 11
3319	13240	22045	0.95	1.0E-124	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
3446	13363	23189	0.96	1.0E-124	S76984.1	NT	Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJBBR1) gene, exon
3446	13363	23189	0.96	1.0E-124	S76984.1	NT	Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJBBR1) gene, exon
3598	13512	23300	2.05	1.0E-124	X13794.1	NT	H. sapiens lactate dehydrogenase B gene exon 1 and 2 (EG 1.1.2.7) (and joined CDS)
3825	13737	23528	1.00	1.0E-124	4507500	NT	H. sapiens lactate dehydrogenase B gene exon 1 and 2 (EG 1.1.2.7) (and joined CDS)
3983	13890	23666	1.19	1.0E-124	4504116	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
4639	14527	23415	1.98	1.0E-124	AB024069.1	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
4850	14731		1.12	1.0E-124	MT187.1	NT	Homo sapiens gene for B120, exon 11
4850	14731		1.12	1.0E-124	MT187.1	NT	Homo sapiens gene for B120, exon 11
5039	14911	24685	1.72	1.0E-124	A1204535.1	EST_HUMAN	Human fibronectin gene splice type III repeat (EDII), exon x+1
5240	15504	24634	8.07	1.0E-124	BF006135.1	EST_HUMAN	gR60K3.1 Soares, Jettis, NHT Homo sapiens cDNA, clone IMAGE:1754069 3'
5500	15065	25560	6.43	1.0E-124	BF006135.1	EST_HUMAN	gR60K3.1 Soares, Jettis, NHT Homo sapiens cDNA, clone IMAGE:1754069 3'
5500	15065	25560	6.43	1.0E-124	BF006135.1	EST_HUMAN	gR60K3.1 Soares, Jettis, NHT Homo sapiens cDNA, clone IMAGE:1754069 3'
8165	10070	29820	3.31	1.0E-124	Y1117.1	NT	Mmusculus mRNA for hoxa3 gene
8851	16884	28974	5.96	1.0E-124	4508954.1	NT	Homo sapiens ribosomal protein L5 (RPL5) mRNA

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Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6930	16908	27002	1.35	1.0E-124	AW612106.1	EST_HUMAN	np4406.x1 NCI_GCAP_Kd11 Homo sapiens cDNA clone IMAGE:295320 3' similar to TR-058162
6930	16908	27003	1.35	1.0E-124	AW612106.1	EST_HUMAN	OS162 PEROXISOMAL SHORT-CHAIN ALCOHOL DEHYDROGENASE ;
7466	17326	27532	2.44	1.0E-124	AV645833.1	EST_HUMAN	np4406.x1 NCI_GCAP_Kd11 Homo sapiens cDNA clone IMAGE:295320 3' similar to TR-058162
7466	17326	27533	2.44	1.0E-124	AV645833.1	EST_HUMAN	OS162 PEROXISOMAL SHORT-CHAIN ALCOHOL DEHYDROGENASE ;
7542	17393	27804	7.8	1.0E-124	AT67183.1	EST_HUMAN	AY645633 GLC Homo sapiens cDNA clone GLCAGE04.3'
7542	17393	27805	7.8	1.0E-124	AT67183.1	EST_HUMAN	w63102.x1 NCI_GCAP_Kd12 Homo sapiens cDNA clone IMAGE:2400391 3'
7676	17390	27792	1.25	1.0E-124	AW603766.1	EST_HUMAN	w63102.x1 NCI_GCAP_Kd12 Homo sapiens cDNA clone IMAGE:2400391 3'
8404	18290	28532	2.25	1.0E-124	UB4776.1	NT	UHF-BNO-sic-04-04-04-11T NH_145C 50 Homo sapiens cDNA clone IMAGE:3078846 5'
8645	18509	28788	2.25	1.0E-124	AW66565.1	EST_HUMAN	Human muscle glycogen phosphorylase (PYGM) gene, exons 6 through 17
8787	17918	28182	1.87	1.0E-124	AA446455.1	EST_HUMAN	NP6503.x1 NCI_GCAP_G44 Homo sapiens cDNA clone IMAGE:2960906 3'
8787	17918	28183	1.87	1.0E-124	AA446455.1	EST_HUMAN	YFRS PROTEIN ; _G44 Homo sapiens cDNA clone IMAGE:211980 3' similar to TR-C31682 C31682
9173	10909	20420	3.98	1.0E-124	AA307551.1	EST_HUMAN	YFRS PROTEIN ; _G44 Homo sapiens cDNA clone IMAGE:211980 3' similar to TR-C31682 C31682
9173	10909	20420	3.98	1.0E-124	AA307551.1	EST_HUMAN	481104.1 Strikingly soluble beta S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR-G300462
9846	19028	25005	1.90	1.0E-124	AA307551.1	EST_HUMAN	G300462 POL-REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT) ;
9846	19028	25006	1.90	1.0E-124	11417863	NT	481104.1 Strikingly soluble beta S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR-G300462
310	10278	19779	5.41	1.0E-123	AB52356.1	NT	G300462 POL-REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT) ;
420	8987	19779	3.82	1.0E-123	BE743622.1	NT	Homo sapiens calcium binding protein 1 (KIA0330) mRNA
628	10355	20377	1.83	1.0E-123	AT110565.1	EST_HUMAN	Homo sapiens mRNA for KIA01172 protein, partial cds
628	10355	20378	1.83	1.0E-123	AT110565.1	EST_HUMAN	50157395F1 NH_145C 3' Homo sapiens cDNA clone IMAGE:382685 5'
711	10433	20469	1.24	1.0E-123	AF264750.1	NT	H40086 Human fetal liver cDNA library Homo sapiens cDNA
							Homo sapiens ALX-like protein mRNA, partial cds
842	10769	20619	2.13	1.0E-123	AA042813.1	EST_HUMAN	2630307.1 Soeren_pregnant_Uterus_NH4PU Homo sapiens cDNA clone IMAGE:466540 3' similar to
982	11005	20750	1.33	1.0E-123	AL163210.2	NT	gbX69587_c481.01 FACTORY RECEPTOR-LIKE PROTEIN HOMPOTE (HUMAN)
1136	11050	20800	1.63	1.0E-123	7682279.1	NT	Homo sapiens chromosome 21 segment HS21C010
1649	12700	21414	1.08	1.0E-123	7661807.1	NT	Homo sapiens KIA04744 gene product; histone deacetylase 7 (KIA04744), mRNA
1769	11668	21545	3.81	1.0E-123	AF016490.1	NT	Homo sapiens KIA04022 gene product (KIA04022), mRNA
1769	11668	21546	3.81	1.0E-123	AF016490.1	NT	Homo sapiens Ucarphin-alpha mRNA, complete cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2455	12342	22228	1.15	1.0E-126	AA02813.1	EST_HUMAN	255307 at Soares_pregant_Letus_NHIFU Homo sapiens cDNA clone IMAGE:485540 3' similar to gpX69957_ccl1 OULFACTORY RECEPTOR-LIKE PROTEIN HOMPOTE (HUMAN);
2551	12424	22315	1.95	1.0E-126	4504660	NT	Homo sapiens inhibin, alpha (INH) mRNA
2551	12424	22316	1.95	1.0E-126	4504660	NT	Homo sapiens inhibin, alpha (INH) mRNA
2555	12427	22320	2.45	1.0E-126	A1732966.1	EST_HUMAN	0164402.35 NC_ CGAP Kid5 Homo sapiens cDNA clone IMAGE:1471719 3'
2555	14344	24136	1.98	1.0E-126	11425114	NT	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
4450	14344	24137	1.98	1.0E-126	11425114	NT	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
4518	14409	24195	0.84	1.0E-126	BE315412.1	EST_HUMAN	01141162F1 NIH_MGC 9 Homo sapiens cDNA clone IMAGE:3140796 5'
5551	15493	25573	1.41	1.0E-126	11436448	NT	Homo sapiens KIA0096 protein (KIA0096), mRNA
5512	15527	25510	3.44	1.0E-126	BE382960.1	EST_HUMAN	0114347.2F1 NIH_MGC 72 Homo sapiens cDNA clone IMAGE:3910932 5'
5955	15570	25503	1.48	1.0E-126	BE562526.1	EST_HUMAN	01135526F1 NIH_MGC 44 Homo sapiens cDNA clone IMAGE:3389790 5'
5955	15570	25504	1.48	1.0E-126	BE562526.1	EST_HUMAN	01135526F1 NIH_MGC 44 Homo sapiens cDNA clone IMAGE:3389790 5'
8201	15981	26903	8.36	1.0E-126	X03427.1	NT	Homo sapiens GFI-II gene, exon 5
8201	15981	26904	8.38	1.0E-126	X03427.1	NT	Homo sapiens GFI-II gene, exon 5
8974	18851	27043	1.22	1.0E-126	U90283.1	NT	Human chromosome 10 duplicated atretic/duoduphry(4LD) gene segment containing exons 8-10
8974	18851	27044	1.22	1.0E-126	U90283.1	NT	Human chromosome 10 duplicated atretic/duoduphry(4LD) gene segment containing exons 8-10
7272	17148	27343	4.31	1.0E-126	BE161640.1	EST_HUMAN	Q17H10338-07030-191-012 HT0638 Homo sapiens cDNA
7272	17148	27343	4.31	1.0E-126	BE161640.1	EST_HUMAN	Q17H10338-07030-191-012 HT0638 Homo sapiens cDNA
5059	17960	28211	3.15	1.0E-126	AF043468.1	NT	Homo sapiens IREL gene, exon 5
8152	18040	28289	1.88	1.0E-126	AW131202.1	EST_HUMAN	X59032.1 NC_ CGAP Gsa4 Homo sapiens cDNA clone IMAGE:2022363 3' similar to TR-Q13284 Q13284
8152	18040	28290	1.88	1.0E-126	AW131202.1	EST_HUMAN	LAMBDA107A PROTEIN KINASE C-INTERACTING PROTEIN (1) ;
8152	18351	28916	5.13	1.0E-126	AB074667.1	NT	X59032.1 NC_ CGAP Gsa4 Homo sapiens cDNA clone IMAGE:2022363 3' similar to TR-Q13284 Q13284
8619	18476	28748	2.92	1.0E-126	7698905	NT	LAMBDA107A PROTEIN KINASE C-INTERACTING PROTEIN (1) ;
8619	18476	28748	2.92	1.0E-126	7698905	NT	Homo sapiens myosin, heavy polypeptide 1, skeletal muscle, adult (MYH1), mRNA
8704	18522	28804	2.49	1.0E-126	AF028020.1	NT	Homo sapiens p53(A) binding protein II (PABP2) gene, complete cds
8793	18607	28806	4.38	1.0E-126	BE074287.1	EST_HUMAN	RQ3-ST0186-26020-018-cl1 ST0186 Homo sapiens cDNA
8793	18607	28807	4.38	1.0E-126	BE074287.1	EST_HUMAN	RQ3-ST0186-26020-076-g09 ST0186 Homo sapiens cDNA
8941	18749	29044	1.96	1.0E-126	AB074667.1	NT	Q13-B10569-02020-076-g09 BT0569 Homo sapiens cDNA
757	10697	29525	0.85	1.0E-126	4758807	NT	Homo sapiens mRNA for KIAA0667 protein, partial cds
760	10690	29528	1.2	1.0E-126	M51636.1	NT	Homo sapiens CDC-like kinase (CLK) mRNA
760	10690	29528	1.2	1.0E-126	M51636.1	NT	Human laminin B1 chain gene, exon 20

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (10p) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
901	10826	20670	2.03	1.0E-126	X03735.1	NT	H.sapiens gene for alpha1-antichymotrypsin, exon 3
2552	12426	22317	2.24	1.0E-126	6382076	EST_HUMAN	Human sapiens KIAA binding protein 2 (KIABP2), mRNA
3035	12943	22757	6.07	1.0E-126	AA160709.1	EST_HUMAN	207203.r1 Striatagene pancreas (3637208) Homo sapiens cDNA clone IMAGE:592420 5'
3035	12943	22758	6.07	1.0E-126	AA160709.1	EST_HUMAN	207203.r1 Striatagene pancreas (3637208) Homo sapiens cDNA clone IMAGE:592420 5'
3577	13491	23281	1.21	1.0E-126	X53941.1	EST_HUMAN	H.sapiens DNA for liver cytochrome B5 pseudogene
3605	13519	23307	2.04	1.0E-126	7657038	NT	Homo sapiens death receptor 6 (DR6), mRNA
4677	14593	24356	0.96	1.0E-126	AF101193.1	NT	Homo sapiens collagen type XI alpha-1 (COL11A1) gene, exon 63
4677	14593	24357	0.96	1.0E-126	AF101193.1	NT	Homo sapiens collagen type XI alpha-1 (COL11A1) gene, exon 63
4728	14614	24400	1.57	1.0E-126	N24078.1	EST_HUMAN	y27506.r1 Soares melanocyte 2NRM Homo sapiens cDNA clone IMAGE:287850 5'
5779	15686	25795	3.68	1.0E-126	AA46075.1	EST_HUMAN	TRSG1145980.G114690 TITN
5797	15703	25813	3.82	1.0E-126	AB040688.1	NT	Homo sapiens mRNA for KIAA1825 protein, partial cds
5797	15703	25814	3.82	1.0E-126	AB040688.1	NT	Homo sapiens mRNA for KIAA1825 protein, partial cds
6860	16540	26737	2.77	1.0E-125	X16936.1	NT	Homo sapiens mRNA for alpha-IP (isolet 2.1)
8233	18114	25398	1.95	1.0E-126	BF-68375.1	EST_HUMAN	6071933BF1 NH1.WGC_48 Homo sapiens cDNA clone IMAGE:598240 5'
8006	18620	28970	2.41	1.0E-126	BE261660.1	EST_HUMAN	50714640.r1 NH1.WGC_19 Homo sapiens cDNA clone IMAGE:3502139 5'
9635	19068	24860	4.38	1.0E-126	BE743922.1	EST_HUMAN	60157763.r1 NH1.WGC_9 Homo sapiens cDNA clone IMAGE:3929885 5'
165	10138	19954	3.59	1.0E-127	AB024697.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
165	10138	19955	3.59	1.0E-127	AB024697.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
166	10138	19954	2.31	1.0E-127	AB024697.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
166	10138	19955	2.31	1.0E-127	AB024697.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
272	10238	20056	2.35	1.0E-127	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
272	10238	20057	2.35	1.0E-127	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
863	10780	20640	1.32	1.0E-127	AF114488.1	NT	Homo sapiens interseclin short isoform (ITSN) mRNA, complete cds
868	10823	20689	1.28	1.0E-127	U72621.2	NT	Homo sapiens bat on transformation LOT1 mRNA, complete cds
1605	11567	21433	0.98	1.0E-127	4827055	NT	Homo sapiens ubiquitin specific protease 8 (USP8) mRNA
2020	11911	21800	1.59	1.0E-127	5903068	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 1 (LILRA1), mRNA
2020	11911	21801	1.59	1.0E-127	5903068	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 1 (LILRA1), mRNA
2153	12041	21839	7.45	1.0E-127	4500620	NT	Homo sapiens titinonin protein, L26 (RFL_25) mRNA
2294	12176	22075	4.01	1.0E-127	AF2456505.1	NT	Homo sapiens sulfonin mRNA, complete cds
2596	12437	22340	2.78	1.0E-127	X12881.1	NT	Human mRNA for cytochrome 18
2579	12450	22341	0.96	1.0E-127	AA480131.1	EST_HUMAN	y26202.r1 Soares_tetral_N23HF8_Sw Homo sapiens cDNA clone IMAGE:789008 5'

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Probe SEQ ID NO.	Exon NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Htt BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2676	12450	22342	0.86	1.0E-127	AA460131.1	EST_HUMAN	2x4262.1 Soares, total testis N26HF6, 6w Homo sapiens cDNA clone IMAGE:780698 5'
3740	13652	22435	0.88	1.0E-127	AV161297.1	EST_HUMAN	au004006.Y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782904 5' similar to TRQ15170 Q15170 TRANSCRIPTION FACTOR S-HRELATED PROTEIN contains element MER22 repetitive element
4028	13029	23706	1.00	1.0E-127	AF183168.1	NT	Homo sapiens delayed rectifier potassium channel subunit Isk mRNA, complete cds
4128	14026	23802	0.86	1.0E-127	AF183472.2	NT	Homo sapiens chromosome 21 segment HS27D047
4180	14050	23833	21.46	1.0E-127	7706238	NT	Homo sapiens neuroblastoma amplified protein (LOC351894), mRNA
4190	14080	23834	21.46	1.0E-127	7706238	NT	Homo sapiens neuroblastoma-amplified protein (LOC351894), mRNA
4395	14291	24075	0.92	1.0E-127	AF252297.1	NT	Homo sapiens cytochrome P450 reductase metabolizing protein P450RAL-2 mRNA, complete cds
4499	14533	24178	4.16	1.0E-127	4606384	NT	Homo sapiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products
4521	14428	24178	4.16	1.0E-127	4606384	NT	Homo sapiens chromosome 21 segment HS21C038
4575	14466	24252	0.88	1.0E-127	AL162968.2	NT	Homo sapiens Rng1p and Y11 binding protein (RYBP), mRNA
5548	15462	25533	3.72	1.0E-127	X85704.1	NT	H. sapiens NGS2 gene, exon 6
5742	16650	25571	2.87	1.0E-127	X64004.1	NT	H. sapiens TGF11 gene, exon 3-6
5916	16722	25835	5.76	1.0E-127	450478	NT	Homo sapiens Integrin beta 8 (ITGB8) mRNA
6578	16436	26620	1.38	1.0E-127	11421914	NT	Homo sapiens Pericardial syndrome (POS), mRNA
6578	16436	26621	1.38	1.0E-127	11421914	NT	Homo sapiens Pericardial syndrome (POS), mRNA
7698	17406	27024	4.87	1.0E-127	AF274863.1	NT	Homo sapiens secretory pathway component Sec31B-1 mRNA, alternatively spliced, complete cds
7698	17406	27026	4.87	1.0E-127	AF274863.1	NT	Homo sapiens secretory pathway component Sec31B-1 mRNA, alternatively spliced, complete cds
7923	17773	28012	1.17	1.0E-127	11427339	NT	Homo sapiens Cholesteryl-Higher fatty acid synthase (CHS-1), mRNA
8498	18371	28634	6.74	1.0E-127	11417339	NT	Homo sapiens similar to heat shock 700D protein 88 (hsc70-2) [H. sapiens] (LOC83164), mRNA
8498	18371	28635	6.74	1.0E-127	11417339	NT	Homo sapiens similar to heat shock 700D protein 88 (hsc70-2) [H. sapiens] (LOC83164), mRNA
8898	18707	29001	2.46	1.0E-127	BE865415.1	EST_HUMAN	601434764.F1 NH1_MGC_72 Homo sapiens cDNA clone IMAGE:3910817 5'
8898	18707	29002	2.46	1.0E-127	BE865415.1	EST_HUMAN	601434764.F1 NH1_MGC_72 Homo sapiens cDNA clone IMAGE:3910817 5'
9397	10138	19854	1.96	1.0E-127	AB024587.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
9397	10138	19855	1.96	1.0E-127	AB024587.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
9395	19177	25276	2.1	1.0E-127	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
452	10569	20214	4.46	1.0E-128	BE385617.1	EST_HUMAN	601276127.F1 NH1_MGC_20 Homo sapiens cDNA clone IMAGE:3618622 5'
1138	11032	20652	1.48	1.0E-128	4758005	NT	Homo sapiens chondrocalcin sulfate proteoglycan 2 (version) (CSPG2) mRNA
1138	11032	20653	1.48	1.0E-128	4758005	NT	Homo sapiens chondrocalcin sulfate proteoglycan 2 (version) (CSPG2) mRNA
2025	11816	21805	12.19	1.0E-128	U02623.1	NT	Human FAU1P pseudogene, trinucleotide repeat regions
2025	11816	21806	12.19	1.0E-128	U02623.1	NT	Human FAU1P pseudogene, trinucleotide repeat regions

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2102	12049	21960	13.3	1.0E-128	4506718	NT	Homo sapiens fibronectin protein S2 (FN2) mRNA
2395	12273		0.65	1.0E-128	11437465	NT	Homo sapiens chromatin-specific transcription elongation factor, 140 kDa subunit (FACTP140), mRNA
3348	13208	23071	1.13	1.0E-128	AEO03073.1	NT	Homo sapiens mRNA for KIAA1247 protein, partial cds
4595	14457	24245	3.48	1.0E-128	11428973	NT	Homo sapiens prospero-related homeobox 1 (PROX1), mRNA
8905	15771	29800	2.07	1.0E-128	11420965	NT	Homo sapiens phosphodiesterase 1C, calmodulin-dependent (PDE1C), mRNA
8140	15988	29123	7.23	1.0E-128	BF224345.1	EST_HUMAN	Tg98510.01 NC1_OGAP_Lu24 Homo sapiens cDNA clone IMAGE:37
8976	16653	27046	3.28	1.0E-128	AEO07923.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
8978	16653	27047	3.28	1.0E-128	AEO07923.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
7834	17684	27929	1.25	1.0E-128	AA639188.1	EST_HUMAN	nc0441.1 NC1_OGAP_Ew1 Homo sapiens cDNA clone IMAGE:1182620 similar to TR-G651338 G651338
8502	17963	28232	5.94	1.0E-128	11423254	NT	CHROMOSOME SEGREGATION GENE HNOLOG CAS :
8101	17991	28240	3.87	1.0E-128	AA026959.1	EST_HUMAN	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2D (GRIN2D), mRNA
8320	18111	28334	1.79	1.0E-128	BE384475.1	EST_HUMAN	en58903a1 NC1_OGAP_GC4 Homo sapiens cDNA clone IMAGE:1652383 3' similar to gb:254641 CYCLIN-
9283	18948		3.03	1.0E-128	AV1965390.1	EST_HUMAN	61277650.1 NH1_MGC_20 Homo sapiens cDNA clone IMAGE:3618750 5'
116	10353	20182	2.19	1.0E-128	S07722.1	NT	EST357560 MAGE sequences, MAGE Homo sapiens cDNA
407	10353	20182	1.35	1.0E-128	S07722.1	NT	putative growth factor binding protein-2 [human, placenta, Genomic, 1019 nt, segment 2 of 4]
1869	11591	21431	2.86	1.0E-128	AL395660.1	NT	putative growth factor binding protein-2 [human, placenta, Genomic, 1019 nt, segment 2 of 4]
							Novel human mRNA containing Zinc finger CSD2 type domains
1863	11595	21465	2.29	1.0E-128	AF240783.1	NT	Homo sapiens glutathione S-transferase beta 2 (GSTT2) and glutathione S-transferase beta 1 (GSTT1)
1863	11595	21466	2.29	1.0E-128	AF240783.1	NT	genes, complete cds
1802	11699	21575	2.43	1.0E-128	11418522	NT	Homo sapiens zinc finger protein 76 (expressed in testis) (ZNF76), mRNA
2751	12613	22503	1.19	1.0E-128	4505952	NT	Homo sapiens placental-derived growth factor receptor, beta polypeptide (PDGFRB) mRNA
2751	12613	22504	1.19	1.0E-128	4505952	NT	Homo sapiens placental-derived growth factor receptor, beta polypeptide (PDGFRB) mRNA
3089	13016	22608	1.35	1.0E-128	Q14595	SWISSPROT	ZINC FINGER PROTEIN HZF10
3089	13016	22609	1.35	1.0E-128	Q14595	SWISSPROT	ZINC FINGER PROTEIN HZF10
3089	13016	22610	1.35	1.0E-128	Q14595	SWISSPROT	ZINC FINGER PROTEIN HZF10
3089	13016	22611	1.35	1.0E-128	Q14595	SWISSPROT	ZINC FINGER PROTEIN HZF10
4073	13975	23754	2.2	1.0E-128	AB040892.1	NT	Homo sapiens mRNA for KIAA1459 protein, partial cds
4183	14083	23845	9.7	1.0E-128	AW755254.1	EST_HUMAN	CNVAS Human cardiac muscle expression library Homo sapiens cDNA clone #151935 similar to CNVA5
4183	14083	23847	9.7	1.0E-128	AW755254.1	EST_HUMAN	Cardiomyopathy associated gene 5
4183	14083	23847	9.7	1.0E-128	AW755254.1	EST_HUMAN	CNVAS Human cardiac muscle expression library Homo sapiens cDNA clone #151935 similar to CNVA5
4183	14083	23847	9.7	1.0E-128	AW755254.1	EST_HUMAN	Cardiomyopathy associated gene 5

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Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Mean Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5700	16614	25715	2.89	1.0E-128	AJ00345.1	NT	Homo sapiens KVL011 gene
6220	16055	26245	6.17	1.0E-128	AJ00346.1	NT	Homo sapiens KVL011 gene
6287	16132	26286	7.59	1.0E-129	11420950	NT	Homo sapiens similar to ribosomal protein S28 (H. sapiens) (LOC303894), mRNA
6641	16720		3.58	1.0E-129	A301434.1	NT	Homo sapiens mRNA for KIAA0534 protein, partial cds
8554	18424	28093	3.62	1.0E-129	AAG2023.1	EST_HUMAN	af2507.1 Soares NHRMP1. S1 Homo sapiens cDNA clone IMAGE1047590 5'
8518	15132	28265	9.4	1.0E-129	11420950	NT	Homo sapiens similar to ribosomal protein S28 (H. sapiens) (LOC303894), mRNA
8885	18599	28595	2.04	1.0E-128	AJ143115.1	EST_HUMAN	AU133115 Y78AA1 Homo sapiens cDNA clone Y78AA1001410 5'
8888	18595	28594	2.04	1.0E-128	AJ143115.1	EST_HUMAN	AU133115 Y78AA1 Homo sapiens cDNA clone Y78AA1001410 5'
8250	18660		1.87	1.0E-128	H83155.1	EST_HUMAN	Y8455.1 Soares fetal liver sapien NFKLS Homo sapiens cDNA clone IMAGE109112 5' similar to SP-849150 B48160 P0-25-HIBERNATION-RELATED PROTEIN - TAMIAS ASIATICUS-ASIAN ;
9620	18203		1.99	1.0E-128	AL120739.1	EST_HUMAN	DKFZ6762K171.11 RP2 (yeast/human) Homo sapiens cDNA clone XE27675K171 5'
1643	11547	21408	6.81	1.0E-130	BE776192.1	EST_HUMAN	60111895F1 NHLJMG.20 Homo sapiens cDNA clone IMAGE3346368 5'
1643	11547	21408	6.81	1.0E-130	BE776192.1	EST_HUMAN	60111895F1 NHLJMG.20 Homo sapiens cDNA clone IMAGE3346368 5'
1940	11835		2.09	1.0E-130	X04923.1	NT	Homo sapiens beta globin (BC1111.1) exon 9 mapping to chromosome 11, band p13
2743	12065		7.7	1.0E-130	AJ010230.1	NT	Homo sapiens beta globin (BC1111.1) exon 9 mapping to chromosome 11, band p13
2649	12777	22564	4.11	1.0E-130	BE564219.1	EST_HUMAN	601343016F1 NHLJMG.53 Homo sapiens cDNA clone IMAGE3365468 5'
2649	12777	22565	4.11	1.0E-130	BE564219.1	EST_HUMAN	601343016F1 NHLJMG.53 Homo sapiens cDNA clone IMAGE3365468 5'
3503	13148	23243	1.97	1.0E-130	AF240383.1	NT	Homo sapiens neural dephosphatase homolog isoform1 (ROH) mRNA, complete cds
3703	12777	22564	4.77	1.0E-130	BE564219.1	EST_HUMAN	601343016F1 NHLJMG.53 Homo sapiens cDNA clone IMAGE3365468 5'
3703	12777	22565	4.77	1.0E-130	BE564219.1	EST_HUMAN	601343016F1 NHLJMG.53 Homo sapiens cDNA clone IMAGE3365468 5'
3857	13768	23560	1.09	1.0E-130	AW303501.1	EST_HUMAN	UHP-BNO-4kyg 05-0-0-UT NF1.MGC.60 Homo sapiens cDNA clone IMAGE3078731 5'
4458	14333	24722	7.48	1.0E-130	AW343953.1	EST_HUMAN	CH44-00045-16020-011-02 C00045 Homo sapiens cDNA
5028	14602	24673	1.09	1.0E-130	AW103295.1	EST_HUMAN	R04-CT0318-201169-031-411 C10318 Homo sapiens cDNA
5028	14602	24674	1.09	1.0E-130	AW353295.1	EST_HUMAN	R04-CT0318-201169-031-411 C10318 Homo sapiens cDNA
6301	16165	26022	2.04	1.0E-130	11416777	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, L-proline), member 7 (SLC6A7), mRNA
7119	10959	27187	2.45	1.0E-130	AW565242.1	EST_HUMAN	HS198312 IMAGE resources, MAGD Homo sapiens cDNA
7314	17150	27352	1.57	1.0E-130	AB097196.1	EST_HUMAN	Homo sapiens mRNA for KIAA1335 protein, partial cds
8513	18385	28550	32.43	1.0E-130	M02140.1	NT	Human cardiac alpha-myosin heavy chain (MYH6) gene, exons 2 and 4
4	9991	19782	2.49	0.0E+00	AA228126.1	EST_HUMAN	ZF8604.1 Soares, NHRMP1. S1 Homo sapiens cDNA clone IMAGE367590 5' similar to TR.G222811
4	9991	19783	2.49	0.0E+00	AA228126.1	EST_HUMAN	G222811 ALPHA 1 CHAIN OF TYPE XII COLLAGEN. ;
7	9991	19783	2.49	0.0E+00	AA228126.1	EST_HUMAN	ZF8604.1 Soares, NHRMP1. S1 Homo sapiens cDNA clone IMAGE367590 5' similar to TR.G222811
7	9991	19786	1.44	0.0E+00	4886138	NT	G222811 ALPHA 1 CHAIN OF TYPE XII COLLAGEN. ;
7	9991	19786	1.44	0.0E+00	4886138	NT	Homo sapiens checkpoint suppressor 1 (CHEST1), mRNA

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Probe SEQ ID NC:	Exon SEQ ID NC:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
15	10001	19762	1.34	0.0E+00	8023946	NT	Homo sapiens tyrosylated protein ELJ20371 (FLJ20371), mRNA
15	10001	19763	1.34	0.0E+00	8023946	NT	Homo sapiens tyrosylated protein ELJ20371 (FLJ20371), mRNA
20	10007	19769	2.46	0.0E+00	D83327.1	NT	Homo sapiens DORR1 mRNA, partial cds
20	10007	19860	2.46	0.0E+00	D83327.1	NT	Homo sapiens DORR1 mRNA, partial cds
24	10011	19804	3.97	0.0E+00	AT14348.1	NT	Homo sapiens beta-actin mRNA, complete cds
23	10011	19816	0.97	0.0E+00	M63800.1	NT	Homo sapiens beta-actin mRNA, complete cds
35	10022	19819	2.41	0.0E+00	6857929	NT	Homo sapiens RNA-binding protein S1, serine-rich domain (RNP-S1), mRNA
51	10038	19845	1.4	0.0E+00	U17151.2	NT	Homo sapiens RNA-binding protein S1, serine-rich domain (RNP-S1), mRNA
51	10038	19846	1.4	0.0E+00	U17151.2	NT	Homo sapiens RNA-binding protein S1, serine-rich domain (RNP-S1), mRNA
52	10039	19847	1.22	0.0E+00	U78004.1	EST_HUMAN	Homo sapiens mRNA for multicopy resistance protein 3 (ABCQ3)
52	10039	19848	1.22	0.0E+00	U78004.1	EST_HUMAN	Homo sapiens mRNA for multicopy resistance protein 3 (ABCQ3)
63	10040	19849	4.14	0.0E+00	U65958.1	NT	Homo sapiens Human placenta poly(A) (H1498a) Homo sapiens cDNA clone GEN516H08 5'
65	10042	19852	8.1	0.0E+00	AW069834.1	EST_HUMAN	Homo sapiens Human placenta poly(A) (H1498a) Homo sapiens cDNA clone GEN516H08 5'
55	10042	19853	8.1	0.0E+00	AW069834.1	EST_HUMAN	Homo sapiens Human placenta poly(A) (H1498a) Homo sapiens cDNA clone GEN516H08 5'
55	10042	19853	8.1	0.0E+00	AW069834.1	EST_HUMAN	Homo sapiens Human placenta poly(A) (H1498a) Homo sapiens cDNA clone GEN516H08 5'
69	10048	19857	5.8	0.0E+00	M60576.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
61	10047	19856	2.76	0.0E+00	M60576.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
69	10054	19859	1.77	0.0E+00	4759977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
69	10054	19870	1.77	0.0E+00	4759977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
71	10054	19886	1.49	0.0E+00	4759977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
71	10054	19870	1.49	0.0E+00	4759977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
74	10058	19876	42.13	0.0E+00	AA59370.1	EST_HUMAN	SW-TM042 Human P29268 TROMODULIN ;
76	10060	19877	1.06	0.0E+00	4901600	NT	Homo sapiens amelotin binding protein 1 (emlin oxidase (copper-containing))(ABP1), nuclear gene encoding mitochondrial protein, mRNA
77	10061	19880	14.77	0.0E+00	4304444	NT	Homo sapiens asfzn, beta (ACTB) mRNA
86	10070	19886	47.26	0.0E+00	5016088	NT	Homo sapiens asfzn, beta (ACTB) mRNA
89	10073	19889	13.39	0.0E+00	U93277.1	EST_HUMAN	Human poly(hemolysis 1) hemoglobin (HBB) mRNA, partial cds
94	10079	19895	1.46	0.0E+00	AI114743.1	EST_HUMAN	HA1347 Human fetal liver cDNA library Homo sapiens cDNA
95	10090	19896	1.03	0.0E+00	AB027784.1	NT	Homo sapiens mRNA for KIAA1353 protein, partial cds
102	10095	19901	6.13	0.0E+00	X91213.1	NT	H. sapiens next gene (exam. 2)
110	10091	19906	1.36	0.0E+00	AB23701.1	EST_HUMAN	389005.1 NCL CGAP_U48 Homo sapiens cDNA clone IMAGE:220833.3 similar to TR-Q96551 Q96551
111	10091	19906	1.88	0.0E+00	AB23701.1	EST_HUMAN	389005.1 NCL CGAP_U48 Homo sapiens cDNA clone IMAGE:220833.3 similar to TR-Q96551 Q96551

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
112	12393	18907	1.83	0.0E+00	N96040.1	EST_HUMAN	y01093.1 Soares melanocytes 2NH-H1 Homo sapiens cDNA clone IMAGE:270017 5'
112	12393	18908	1.83	0.0E+00	N96040.1	EST_HUMAN	y01093.1 Soares melanocytes 2NH-H1 Homo sapiens cDNA clone IMAGE:270017 5'
115	10094	19913	0.86	0.0E+00	4906458	NT	Homo sapiens neuropilin 2 (NRP2) mRNA
126	10100	19921	3.17	0.0E+00	4906538	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A (220B) (POLR2A) mRNA
126	10100	19922	3.17	0.0E+00	4906538	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A (220B) (POLR2A) mRNA
126	10100	19922	3.17	0.0E+00	4906538	NT	y03504.2 21Strategie fetal spleen (#637205) Homo sapiens cDNA clone IMAGE:98310 5'
135	10108	19929	1.49	0.0E+00	T69546.1	EST_HUMAN	y03504.2 21Strategie fetal spleen (#637205) Homo sapiens cDNA clone IMAGE:98310 5'
135	10108	19930	1.49	0.0E+00	T69546.1	EST_HUMAN	Homo sapiens heterogenous nuclear ribonucleoprotein A1 (HNRA1) mRNA
147	10121		9.05	0.0E+00	4804444	EST_HUMAN	601460375F1 NIH_MGC_ 60 Homo sap ens cDNA clone IMAGE:3963803 5'
161	10125	19943	2.42	0.0E+00	BF039891.1	EST_HUMAN	Homo sapiens heterogenous nuclear ribonucleoprotein A1 (HNRA1) mRNA
165	10127		15.84	0.0E+00	4904444	NT	Homo sapiens serine thiolyl transferase, subunit II gene, complete cds, and unknown genes
166	10130	19946	1.36	0.0E+00	AF111198.2	EST_HUMAN	601114270F1 NIH_MGC_ 17 Homo sap ens cDNA clone IMAGE:352984 5'
166	10130	19947	1.11	0.0E+00	BE238973.1	EST_HUMAN	601114270F1 NIH_MGC_ 17 Homo sap ens cDNA clone IMAGE:352984 5'
169	10132	19947	1.18	0.0E+00	BE238973.1	EST_HUMAN	601114270F1 NIH_MGC_ 17 Homo sap ens cDNA clone IMAGE:352984 5'
180	10133						y02504.1 Soares fetal thymus (NH47187) Homo sapiens cDNA clone IMAGE:345201 5' similar to
180	10133	19948	2.99	0.0E+00	W73973.1	EST_HUMAN	g0140262.2 ZINC FINGER PROTEIN CLONE 047 (HUMAN);
184	10134	19949	1.91	0.0E+00	AF244088.1	NT	Homo sapiens zinc finger protein mRNA, complete cds
184	10137	19952	18.37	0.0E+00	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
184	10137	19953	18.37	0.0E+00	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
174	10145	19980	4.26	0.0E+00	BE018970.1	EST_HUMAN	b040412.1 NIH_MGC_ 14 Homo sapiens cDNA clone IMAGE:2663854 5' similar to WP-67A10A.Z
174	10145	19981	4.26	0.0E+00	BE018970.1	EST_HUMAN	b040412.1 NIH_MGC_ 14 Homo sapiens cDNA clone IMAGE:2663854 5' similar to WP-67A10A.Z
179	10150	19954	1.98	0.0E+00	AB018327.1	NT	Homo sapiens mRNA for KIA0784 protein, partial cds
179	10150	19955	1.98	0.0E+00	AB018327.1	NT	Homo sapiens mRNA for KIA0784 protein, partial cds
187	10159	19976	130.42	0.0E+00	D30659.1	NT	Human gamma-cytoplasmic actin (ACTG5) pseudogene
187	10159	19976	130.42	0.0E+00	D30659.1	NT	Homo sapiens CTCL tumor antigen set4.3 mRNA, complete cds
192	10164	19981	2.83	0.0E+00	AF273045.1	NT	Homo sapiens CTCL tumor antigen set4.3 mRNA, complete cds
192	10164	19982	2.83	0.0E+00	AF273045.1	NT	Homo sapiens chromosome X MSJ.3.2 protein mRNA, complete cds
194	10165	19984	2.92	0.0E+00	AF167174.1	NT	Homo sapiens chromosome X MSJ.3.2 protein mRNA, complete cds
194	10165	19985	2.92	0.0E+00	AF167174.1	NT	Homo sapiens chromosome X MSJ.3.2 protein mRNA, complete cds
203	12681	19991	9.33	0.0E+00	AF607308.1	EST_HUMAN	y04093.1 NCI_G04P_U8 Homo sapiens cDNA clone IMAGE:2207847 3' similar to gp-33191 PROFILIN 1 (HUMAN);
203	12681	19992	9.33	0.0E+00	AF607308.1	EST_HUMAN	y04093.1 NCI_G04P_U8 Homo sapiens cDNA clone IMAGE:2207847 3' similar to gp-33191 PROFILIN 1 (HUMAN);
205	10176	19994	1.94	0.0E+00	AF199593.1	NT	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar EST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
208	10179		16.60	0.0E+00	4506632	NT	Homo sapiens fibronectin protein L31 (RPL31) mRNA
209	10190		3.46	0.0E+00	AF132000.1	NT	Homo sapiens TADA1 protein mRNA, complete cds
215	10165	19959	2.45	0.0E+00	AB016264.1	NT	Homo sapiens mRNA for KIAA0721 protein, partial cds
216	10166	19959	1.65	0.0E+00	AB016264.1	NT	Homo sapiens mRNA for KIAA0721 protein, partial cds
217	10167	20000	1.61	0.0E+00	6078444	NT	Mus musculus testis-specific protein, Y-encoded like (Tey), mRNA
224	10195	20004	3.43	0.0E+00	BE246780.1	EST_HUMAN	TCBAP-TE468 Pediatric pre-B cell acute lymphoblastic leukemia BAYor-HGSC project-TCSA Homo sapiens cDNA clone TCBAP-468
224	10195	23005	3.43	0.0E+00	BE246780.1	EST_HUMAN	TCBAP-TE468 Pediatric pre-B cell acute lymphoblastic leukemia BAYor-HGSC project-TCSA Homo sapiens cDNA clone TCBAP-468
224	10195	20006	3.43	0.0E+00	BE246780.1	EST_HUMAN	TCBAP-TE468 Pediatric pre-B cell acute lymphoblastic leukemia BAYor-HGSC project-TCSA Homo sapiens cDNA clone TCBAP-468
225	10195	20004	3.99	0.0E+00	BE246780.1	EST_HUMAN	TCBAP-TE468 Pediatric pre-B cell acute lymphoblastic leukemia BAYor-HGSC project-TCSA Homo sapiens cDNA clone TCBAP-468
225	10195	20005	3.99	0.0E+00	BE246780.1	EST_HUMAN	TCBAP-TE468 Pediatric pre-B cell acute lymphoblastic leukemia BAYor-HGSC project-TCSA Homo sapiens cDNA clone TCBAP-468
225	10195	20006	3.99	0.0E+00	BE246780.1	EST_HUMAN	TCBAP-TE468 Pediatric pre-B cell acute lymphoblastic leukemia BAYor-HGSC project-TCSA Homo sapiens cDNA clone TCBAP-468
226	10195	20004	12.62	0.0E+00	BE246780.1	EST_HUMAN	TCBAP-TE468 Pediatric pre-B cell acute lymphoblastic leukemia BAYor-HGSC project-TCSA Homo sapiens cDNA clone TCBAP-468
226	10195	23005	12.62	0.0E+00	BE246780.1	EST_HUMAN	TCBAP-TE468 Pediatric pre-B cell acute lymphoblastic leukemia BAYor-HGSC project-TCSA Homo sapiens cDNA clone TCBAP-468
226	10195	20006	12.62	0.0E+00	BE246780.1	EST_HUMAN	TCBAP-TE468 Pediatric pre-B cell acute lymphoblastic leukemia BAYor-HGSC project-TCSA Homo sapiens cDNA clone TCBAP-468
238	10206	20023	4.66	0.0E+00	6453903	NT	Homo sapiens NS1-associated protein 1 (NSAP1) mRNA
240	10208		6.64	0.0E+00	AF16301.2	NT	Homo sapiens chromosome 21 segment H021001
247	10213	20029	3.75	0.0E+00	AF231918.1	NT	Homo sapiens chromosome 21 unknown mRNA
248	10216	20032	1.46	0.0E+00	X89772.1	NT	H1 sapiens mRNA for Interferon alpha/beta receptor (long form)
287	10223		6.81	0.0E+00	AF231918.1	NT	Homo sapiens chromosome 21 unknown mRNA
289	10234	20030	1.14	0.0E+00	4607900	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
289	10234	20051	1.14	0.0E+00	4607900	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
270	10236	20033	2.57	0.0E+00	7700268	NT	Homo sapiens hypochlorite protein (LOC51280), mRNA
281	10240	20066	1.11	0.0E+00	D83327.1	NT	Homo sapiens DORR1 mRNA, partial cds
281	10240	20067	1.11	0.0E+00	D83327.1	NT	Homo sapiens DORR1 mRNA, partial cds
282	10247		0.95	0.0E+00	AI645303.1	EST_HUMAN	IL2-C10051-1E189-020-B03 C10051 Homo sapiens cDNA

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon NO:	ORF SEQ ID NO:	Expression Signal	Mean Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
290	10254	20074	5.26	0.0E+00	4557029	NT	Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 15 (KCNJ15) mRNA
291	10254	20076	5.26	0.0E+00	4557029	NT	Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 15 (KCNJ15) mRNA
300	10265	20086	-4.03	0.0E+00	A902842.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
302	10266	20086	3.11	0.0E+00	A902842.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
303	12064		5.3	0.0E+00	4506728	NT	Homo sapiens fibronectin protein SE (FSP5) mRNA
304	10267	20087	1.99	0.0E+00	4503914	NT	Homo sapiens phosphatidylcholine formyltransferase, phosphatidylcholine synthetase, phospholipid:hemolyside synthetase (GABT) mRNA
305	10268		2.03	0.0E+00	AA480002.1	EST_HUMAN	218008.r1 Sense: NHAHPU. S1 Homo sapiens cDNA clone IMAGE:753934.5
306	10269	20088	13.28	0.0E+00	4507162	NT	Homo sapiens SON DNA binding protein (SON) mRNA
307	10269	20088	9.68	0.0E+00	4507162	NT	Homo sapiens SON DNA binding protein (SON) mRNA
311	10273	20092	2.23	0.0E+00	AF114488.1	NT	Homo sapiens ataxin-1 protein (ATN1) mRNA, complete cds
324	10285	20101	0.9	0.0E+00	O14487	SWISSPROT	TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC-HOMOLOG 1) (H42603)
324	10286	20102	0.9	0.0E+00	O14487	SWISSPROT	TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC-HOMOLOG 1) (H42603)
325	10288	20103	4.18	0.0E+00	7657213	NT	Homo sapiens homophilic/uniplexin net tumor-associated kinase (HUNK) mRNA
326	10288	20103	2.31	0.0E+00	7657213	NT	Homo sapiens homophilic/uniplexin net tumor-associated kinase (HUNK) mRNA
341	10300	20116	3.41	0.0E+00	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (t(11q24) (Crispallia) homodig, translocated to, 4 (MLL1) mRNA
343	10301	20116	0.80	0.0E+00	4506259	NT	Homo sapiens nucleolin (NCL) mRNA
345	10304	20120	3.78	0.0E+00	4527057	NT	Homo sapiens X-box binding protein 1 (XBP1) mRNA
346	10307	20120	0.8	0.0E+00	U71600.1	NT	Human zinc finger protein zfp371 (ZFP371) mRNA, partial cds
353	10311	20129	2.15	0.0E+00	AF231910.1	NT	Homo sapiens chromosome 21 unknown mRNA
353	10311	20130	2.15	0.0E+00	AF231910.1	NT	Homo sapiens chromosome 21 unknown mRNA
354	12055	20131	3.4	0.0E+00	AF231910.1	NT	Homo sapiens chromosome 21 unknown mRNA
356	10313	20133	0.89	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TAM1) mRNA
358	10315	20136	1.4	0.0E+00	4503854	NT	Homo sapiens CA-binding protein transcription factor, alpha subunit (CBAT) (GABPA) mRNA
359	10316	20137	1.37	0.0E+00	D80006.1	NT	Human mRNA for KIAA0184 gene, partial cds
360	10316	20137	1.52	0.0E+00	D80006.1	NT	Human mRNA for KIAA0184 gene, partial cds
372	10328	20149	1.13	0.0E+00	AF114488.1	EST_HUMAN	AUI134569 PLACE1 Homo sapiens cDNA clone PLACE1000839.5
381	10365	20188	5.35	0.0E+00	A902842.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
382	10366	20189	1.01	0.0E+00	A9363014.1	EST_HUMAN	hg19HG.11 NCL CGAP B2626 Homo sapiens cDNA clone IMAGE:2018467.5 similar to gb-X64169
387	10384	20196	3.43	0.0E+00	A11754180.1	EST_HUMAN	PHOSPHORIBOSYLAMINE-GLYCINE LYASE (HUMAN)
390	10386	20199	1.38	0.0E+00	4503950	NT	RC3-OT3020-300700-019-a09 OT3020 Homo sapiens cDNA
391	10337	20100	2.04	0.0E+00	4503980	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA

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Table 4
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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
361	10337	20161	2.04	0.0E+00	4503980	NT	Homo sapiens IgG Fc binding protein (FQ/GAMMA/BP) mRNA
362	10338	20162	1.17	0.0E+00	4503980	NT	Homo sapiens IgG Fc binding protein (FQ/GAMMA/BP) mRNA
363	10339	20163	1.94	0.0E+00	4503980	NT	Homo sapiens IgG Fc binding protein (FQ/GAMMA/BP) mRNA
364	10340	20164	1.94	0.0E+00	4503980	NT	Homo sapiens IgG Fc binding protein (FQ/GAMMA/BP) mRNA
365	10341	20165	2.43	0.0E+00	4503980	NT	Homo sapiens IgG Fc binding protein (FQ/GAMMA/BP) mRNA
366	10342	20166	0.9	0.0E+00	4503980	NT	Homo sapiens IgG Fc binding protein (FQ/GAMMA/BP) mRNA
367	10343	20167	0.84	0.0E+00	X74870.1	NT	H. sapiens gene for RNA pol II largest subunit, exons 23-29
368	10344	20168	0.84	0.0E+00	X74870.1	NT	H. sapiens gene for RNA pol II largest subunit, exons 23-29
400	10346	20169	43.06	0.0E+00	4503980	NT	Homo sapiens ribosomal protein L19 (RPL19) mRNA
401	9681	19772	1.31	0.0E+00	4503980	EST_HUMAN	y69502.r1 Scores infant brain N18 Homo sapiens cDNA clone IMAGE:31652.5'
422	10367	20171	2.61	0.0E+00	4506728	NT	Homo sapiens ribosomal protein S5 (RPS5) mRNA
423	10368	20190	2.42	0.0E+00	4506728	NT	Homo sapiens ribosomal protein S5 (RPS5) mRNA
424	10369	20191	4.7	0.0E+00	4507152	NT	Homo sapiens SON DNA binding protein (SON) mRNA
425	10370	20192	4.7	0.0E+00	4507152	NT	Homo sapiens SON DNA binding protein (SON) mRNA
426	10371	20193	3.91	0.0E+00	AF109697.1	NT	Mus musculus truncated SON protein (Son) mRNA, complete cds
428	10382	20208	2.01	0.0E+00	4557875	NT	Homo sapiens interferon gamma receptor 1 (IFNGR1) mRNA
443	10387	20209	0.98	0.0E+00	AF109697.1	EST_HUMAN	Homo sapiens interferon gamma receptor 1 (IFNGR1) mRNA
444	10388	20210	0.91	0.0E+00	BE254447.1	EST_HUMAN	6011150F1 NIH_MGC_16 Homo sapiens cDNA 5' end
445	10389	20220	3.15	0.0E+00	4504532	NT	90111250F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:352348.5'
446	10390	20221	3.15	0.0E+00	4504532	NT	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1B (HTR1B) mRNA
447	10391	20222	1.27	0.0E+00	4504532	NT	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1B (HTR1B) mRNA
448	10392	20228	1.27	0.0E+00	4507897	NT	Homo sapiens keratin 18 (KRT18) mRNA
449	10393	20229	1.27	0.0E+00	4507897	NT	Homo sapiens keratin 18 (KRT18) mRNA
450	10394	20235	2.26	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C048
476	10416	20236	7.05	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C048
477	10417	20237	7.05	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C048
485	10428	20242	2.86	0.0E+00	AF030305.1	EST_HUMAN	Homo sapiens mRNA for KIAA1200 protein, partial cds
487	10430	20244	1.64	0.0E+00	AU132888.1	EST_HUMAN	AU132888.NT28P4 Homo sapiens cDNA clone N728P400037.5'
488	10431	20250	2.17	0.0E+00	BE3851.44	EST_HUMAN	00127466F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:391576.5'
489	12968	20261	1.05	0.0E+00	AF059825.1	EST_HUMAN	PMO-DT0065-130-00-002-c06 DT0065 Homo sapiens cDNA
490	12968	20261	1.05	0.0E+00	AF059825.1	EST_HUMAN	Novel human gene mapping to chromosome 1
498	10441	20253	1.94	0.0E+00	AL117233.1	NT	Homo sapiens PCS20 protein (PC320), mRNA
499	10441	20253	1.94	0.0E+00	AL117233.1	NT	Homo sapiens PCS20 protein (PC320), mRNA
508	10450	20263	3.91	0.0E+00	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C070
511	12969	20267	1.97	0.0E+00	BE081527.1	EST_HUMAN	QV2-B-10635-160-00-142-H05 B10635 Homo sapiens cDNA
520	10462	20273	1.13	0.0E+00	BE029005.1	EST_HUMAN	00176458F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:396958.5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
526	10468	20280	1.16	0.0E+00	AB010909.1	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds
529	10471	20283	11.27	0.0E+00	6000030	NT	Homo sapiens transcription elongation factor B (SII), polypeptide 1-like (TCEB1L) mRNA
530	10472	20284	3.96	0.0E+00	4504039	NT	Homo sapiens guanine nucleotide binding protein (G protein), alpha 11 (Gq class) (GNA11) mRNA
530	10472	20285	3.96	0.0E+00	4504039	NT	Homo sapiens guanine nucleotide binding protein (G protein), alpha 11 (Gq class) (GNA11) mRNA
536	10477		5.78	0.0E+00	AF003528.1	NT	Homo sapiens X-linked arylsulfatase ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
544	10485	20295	1.79	0.0E+00	AW13524.1	EST_HUMAN	U1-HB1-acb-h-q-0.01.1 NGL CGAP Sub3 Homo sapiens cDNA clone IMAGE:2713951 3'
554	10495		3.15	0.0E+00	DT0383.1	NT	Homo sapiens RGH1 gene, retrovirus-like element
571	10510	20318	2.85	0.0E+00	5174742	NT	Homo sapiens uncoupled cytochrome c reductase, Rieske iron-sulfur polypeptide 1 (UQCRFS1), nuclear gene encoding mitochondrial protein, mRNA
584	10522		5.28	0.0E+00	J04096.1	NT	Human apolipoprotein A-I (ApoA-I) gene, exon 1
587	10529	20322	1.73	0.0E+00	BF014988.1	EST_HUMAN	801822827F1 NIH_MGC_76 Homo sapiens cDNA clone IMAGE:4045447 5'
589	10529	20336	1.45	0.0E+00	4501854	NT	Homo sapiens alpha-2-macroglobulin precursor (human)
598	10534	20342	1.05	0.0E+00	AF221712.1	NT	Homo sapiens Smad1 and Olf1-anchoring zinc finger protein mRNA, partial cds
598	10534	20343	1.05	0.0E+00	AF221712.1	NT	Homo sapiens Smad1 and Olf1-anchoring zinc finger protein mRNA, partial cds
607	10543	20351	1.38	0.0E+00	AF149775.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
610	10546	20354	0.95	0.0E+00	6803918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
611	10547	20355	2.22	0.0E+00	6803918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
611	10547	20356	2.22	0.0E+00	6803918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
612	10548	20357	0.93	0.0E+00	6803918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
612	10548	20358	0.93	0.0E+00	6803918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
619	10565	20368	1.34	0.0E+00	AA354966.1	EST_HUMAN	260607.1 Scores, 100% NHT Homo sapiens cDNA clone IMAGE:7267632 5'
623	10569	20372	6.37	0.0E+00	DT1078.1	NT	Homo sapiens RGH2 gene, retrovirus-like element
627	10584	20375	3.17	0.0E+00	W78811.1	EST_HUMAN	2519104.1 Scores, 100% Jive_spiken, 100% NHT Homo sapiens cDNA clone IMAGE:4155667 5' similar to gpA21187 ALPHA-2-MACROGLOBULIN PRECURSOR (HUMAN);
627	10584	20376	3.17	0.0E+00	W78811.1	EST_HUMAN	2519104.1 Scores, 100% Jive_spiken, 100% NHT Homo sapiens cDNA clone IMAGE:4155667 5' similar to gpA21187 ALPHA-2-MACROGLOBULIN PRECURSOR (HUMAN);
630	10587		3.28	0.0E+00	4855529	NT	Homo sapiens guanine nucleotide binding protein 3 (NSP3) mRNA
637	10574	20388	2.80	0.0E+00	6000003	NT	Homo sapiens guanine nucleotide binding protein 3 (NSP3) mRNA
638	10576	20391	1.09	0.0E+00	5031624	NT	Homo sapiens guanine nucleotide binding protein 3 (NSP3) mRNA
642	10579	20395	1.41	0.0E+00	U06236.1	NT	Homo sapiens neutral amino acid transporter (ASCT1) gene, exon 8
646	10583	20398	2.18	0.0E+00	AF108389.1	NT	Homo sapiens sodium/calcium exchanger isoform NaCa2 (NCX1) mRNA, complete cds
649	10583	20399	2.18	0.0E+00	AF108389.1	NT	Homo sapiens sodium/calcium exchanger isoform NaCa2 (NCX1) mRNA, complete cds
652	10588	20404	3.98	0.0E+00	4520847	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
652	10388	20405	3.98	0.0E+00	4828947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
658	12672		0.95	0.0E+00	X59747.1	NT	Human endogenous nervous p1E.1 (ERV9)
667	10801	20419	4.56	0.0E+00	490424	NT	Human sapiens high-mobility group (nonhistone chromosomal) protein 1 (HMG) mRNA
672	10606	20423	4.35	0.0E+00	AB02012.1	NT	Homo sapiens mRNA for KIAA1059 protein, partial cds
682	10615	20438	2.03	0.0E+00	7857468	NT	Homo sapiens similar to rat integral membrane glycoprotein POMT21 (F0M121L1), mRNA
682	10625	20450	19.46	0.0E+00	AA014537.1	EST_HUMAN	np49401.s1 NCL CGAP Br1.1 Homo sapiens cDNA clone IMAGE:1129633 3' similar to gp.X57352
696	10620	20454	7.66	0.0E+00	M60675.1	NT	INTERFERON-INDUCIBLE PROTEIN 1-8U (HUMAN)
696	10620	20455	7.66	0.0E+00	M60675.1	NT	Human von Willebrand factor gene, exons 23 through 34
705	10639	20464	1.45	0.0E+00	5032102	NT	Homo sapiens TNF receptor-associated factor 1 (TRAF1) mRNA
712	10644	20470	3.89	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
712	10644	20471	3.89	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
714	10646	20474	9.78	0.0E+00	11545800	NT	Homo sapiens hypophyseal protein FLJ21834 (FLJ21834), mRNA
716	10651	20481	1.7	0.0E+00	BE241877.1	EST_HUMAN	TCAP-D01778 Pediatric acute myelogenous leukemia cell (FAB M1) Bayle-HGSG project= CAA Homo sapiens cDNA clone TCAP0179
736	10670	20505	1.12	0.0E+00	AF236950.2	NT	Homo sapiens MHC class I antigen (HLA-G) mRNA, HLA-G1 allele, complete cds
736	10670	20506	1.12	0.0E+00	AF236950.2	NT	Homo sapiens MHC class I antigen (HLA-G) mRNA, HLA-G1 allele, complete cds
740	10671	20507	2.4	0.0E+00	AF170492.1	NT	Homo sapiens chloride channel GUCY (CC) mRNA, complete cds
743	10674	20510	1.95	0.0E+00	J33784.1	NT	Homo sapiens chloride channel GUCY (CC) mRNA, complete cds
743	10674	20511	1.95	0.0E+00	J33784.1	NT	Human, plasmidogen activator inhibitor-1 gene, exons 2 & 9
743	10676	20512	0.78	0.0E+00	AB033760.1	NT	Homo sapiens mRNA for KIAA1339 protein, partial cds
746	10677	20513	1.12	0.0E+00	AB033760.1	NT	Homo sapiens zinc finger protein 212 (ZNF212), mRNA
747	10678	20514	0.81	0.0E+00	6912748	NT	Homo sapiens mRNA for repressor protein, partial cds
748	10678	20515	2.17	0.0E+00	D30681.1	NT	Homo sapiens mRNA for repressor protein, partial cds
748	10682	20519	3.38	0.0E+00	BE869736.1	EST_HUMAN	g54608.11 Scores breast 2Nb18st Homo sapiens cDNA clone IMAGE:154046 5'
753	10683	20520	2.4	0.0E+00	D30681.1	EST_HUMAN	Homo sapiens splicing factor 3a, subunit 1, 120KD (SF3A1), mRNA
753	10682	20520	2.4	0.0E+00	AB011399.1	NT	Homo sapiens gene for AL-5, complete cds
765	10686	20533	1.98	0.0E+00	AB011399.1	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
765	10686	20533	2.97	0.0E+00	7661969	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
775	10705	20544	1.17	0.0E+00	D80006.1	NT	Human mRNA for KIAA0184 gene, partial cds
775	10705	20545	1.17	0.0E+00	D80006.1	NT	Human mRNA for KIAA0184 gene, partial cds
780	10710	20549	2.84	0.0E+00	X6877.1	NT	H sapiens mRNA for interferon alpha/beta receptor (long form)
784	10714	20553	2.37	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
784	10714	20554	2.37	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
789	10718	20560	6.84	0.0E+00	51147478	NT	Homo sapiens pectinectin (PCNT) mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
790	10719	20491	7.06	0.0E+00	4807500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
807	10726	20492	1.51	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK) mRNA
808	10737	20492	4.43	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK) mRNA
810	10739	20494	3.91	0.0E+00	4857680	NT	Homo sapiens potassium voltage-gated channel, Isk-related family, member 1 (KONE1) mRNA
816	10744	20490	1.24	0.0E+00	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNKH) mRNA, complete cds
818	10744	20491	1.24	0.0E+00	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNKH) mRNA, complete cds
821	10749	20496	1.14	0.0E+00	AF108830.1	NT	Homo sapiens G-kinase protein transcription factor, alpha subunit (GKTF) (GABPA) mRNA
825	10752	20501	1.55	0.0E+00	4507900	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
825	10752	20502	1.55	0.0E+00	4507900	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
832	10759	20513	1.57	0.0E+00	AF027183.1	NT	Homo sapiens sodium-dependent cotransporter (SLC5A3) gene, complete cds
838	10763	20513	3.37	0.0E+00	AF026942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
838	10763	20514	3.37	0.0E+00	AF026942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
837	10764	20515	7.38	0.0E+00	4907152	NT	Homo sapiens SON DNA binding protein (SON) mRNA
838	10765	20516	3.03	0.0E+00	AF026942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
839	10766	20517	2.02	0.0E+00	4906728	NT	Homo sapiens ribosomal protein S2 (RP-S2) mRNA
843	10770	20520	1.25	0.0E+00	AF020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
843	10770	20521	1.25	0.0E+00	AF020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
844	10771	20522	1.97	0.0E+00	AA533272.1	EST	HUMAN
844	10771	20523	1.97	0.0E+00	AA533272.1	EST	HUMAN
845	10772	20524	7.39	0.0E+00	BF577664.1	EST	HUMAN
849	10776	20524	1.3	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK) mRNA
849	10776	20525	1.3	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK) mRNA
850	10777	20526	2.16	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK) mRNA
850	10777	20527	2.16	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK) mRNA
873	10799	20650	0.87	0.0E+00	AF163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
880	10806	20655	1.85	0.0E+00	BE080592.1	EST	HUMAN
880	10806	20656	1.85	0.0E+00	BE080592.1	EST	HUMAN
890	10816	20665	3.93	0.0E+00	AF163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
900	10825	20673	7.45	0.0E+00	4904956	NT	Homo sapiens laminin receptor 1 (LR1), ribosomal protein SA (LAMR1), mRNA
900	10825	20674	7.45	0.0E+00	4904956	NT	Homo sapiens laminin receptor 1 (LR1), ribosomal protein SA (LAMR1), mRNA
904	10826	20673	1.5	0.0E+00	AF098747.1	NT	Homo sapiens alpha 1-antitrypsin precursor, mRNA, partial cds
905	10826	20674	0.99	0.0E+00	S09364.1	NT	protein C inhibitor [human, leukocytes, Genomic, 1216 nt, segment 2 of 5]
905	10826	20675	0.99	0.0E+00	S09364.1	NT	protein C inhibitor [human, leukocytes, Genomic, 1216 nt, segment 2 of 5]
905	10826	20676	0.99	0.0E+00	S09364.1	NT	protein C inhibitor [human, leukocytes, Genomic, 1216 nt, segment 2 of 5]

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
606	10630	20677	2.14	0.0E+00	Z8101.1	NT	Homo sapiens kallistatin (P14) gene, exons 1-4, complete cds
609	10633	20680	105.13	0.0E+00	Z20695.1	NT	Homo sapiens of cardiac alpha-myosin heavy chain gene
609	10633	20681	105.13	0.0E+00	Z20695.1	NT	Homo sapiens of cardiac alpha-myosin heavy chain gene
610	10634	20682	167.64	0.0E+00	Z20695.1	NT	Homo sapiens of cardiac alpha-myosin heavy chain gene
610	10634	20683	167.64	0.0E+00	Z20695.1	NT	Homo sapiens of cardiac alpha-myosin heavy chain gene
635	10650	20706	30.3	0.0E+00	M37160.1	NT	Human rra inhibitor mRNA, 3' end
636	10651	20707	13.25	0.0E+00	M37160.1	NT	Human rra inhibitor mRNA, 3' end
637	10652	20708	53.71	0.0E+00	M37160.1	NT	Human rra inhibitor mRNA, 3' end
638	10653	20709	1.9	0.0E+00	4507430	NT	Homo sapiens tyrosinophilic embryonic factor (TEF) mRNA
638	10653	20710	1.9	0.0E+00	4507430	NT	Homo sapiens tyrosinophilic embryonic factor (TEF) mRNA
646	12681	20717	2.46	0.0E+00	A001948.1	EST_HUMAN	cd88a3.11 NGL CGAP GC5 Homo sapiens cDNA clone IMAGE1613404.3'
646	12681	20718	2.46	0.0E+00	A001948.1	EST_HUMAN	cd88a3.11 NGL CGAP GC5 Homo sapiens cDNA clone IMAGE1613404.3'
648	10672	20720	7.21	0.0E+00	7657205	NT	Homo sapiens KIAA0029 protein Mac2 interacting nuclear target (MINT) homolog (KIAA0029), mRNA
659	10632	20730	2.52	0.0E+00	A503569.1	NT	Homo sapiens mRNA for PS23, complete cds
659	10632	20730	2.52	0.0E+00	A503569.1	NT	Homo sapiens mRNA for PS23, complete cds
657	10630	20736	4.64	0.0E+00	BF306974.1	EST_HUMAN	PH2.GN0014-05000-001-402 GN0014 Homo sapiens cDNA
657	10630	20737	4.64	0.0E+00	BF306974.1	EST_HUMAN	PH2.GN0014-05000-001-402 GN0014 Homo sapiens cDNA
657	10630	20738	4.64	0.0E+00	BF306974.1	EST_HUMAN	PH2.GN0014-05000-001-402 GN0014 Homo sapiens cDNA
658	10631	20739	1.27	0.0E+00	X32207.1	NT	Homo sapiens partial c-fgr gene, exons 2 and 3
658	10631	20740	1.27	0.0E+00	X32207.1	NT	Homo sapiens partial c-fgr gene, exons 2 and 3
677	10000	20747	1.25	0.0E+00	4757959	NT	Homo sapiens partial c-fgr gene, exons 2 and 3
688	10010	20755	1.05	0.0E+00	U63698.1	NT	Homo sapiens chromodomain protein, Y chromosome-like (CDYL) mRNA
689	10011	20756	7.48	0.0E+00	U63698.1	NT	Homo sapiens chromodomain protein, Y chromosome-like (CDYL) mRNA
690	10011	20756	6.89	0.0E+00	U63698.1	NT	Homo sapiens chromodomain protein, Y chromosome-like (CDYL) mRNA
693	10014	20761	1.99	0.0E+00	AF169460.1	NT	Human beta-tubulin (TUB4a) gene, complete cds
694	10014	20761	1.99	0.0E+00	AF169460.1	NT	Human beta-tubulin (TUB4a) gene, complete cds
697	10017	20761	0.84	0.0E+00	AF111770.3	NT	Homo sapiens 8q22.1 region and MTG8 (CBFA2T1) gene, partial cds
698	10017	20761	1.43	0.0E+00	AF111770.3	NT	Homo sapiens 8q22.1 region and MTG8 (CBFA2T1) gene, partial cds
699	10017	20761	1.43	0.0E+00	AF111770.3	NT	Homo sapiens 8q22.1 region and MTG8 (CBFA2T1) gene, partial cds
1000	10018	20762	2.23	0.0E+00	AF111770.3	NT	Homo sapiens 8q22.1 region and MTG8 (CBFA2T1) gene, partial cds
1003	10021	20765	2.28	0.0E+00	AF111770.3	NT	Homo sapiens 8q22.1 region and MTG8 (CBFA2T1) gene, partial cds
1007	10925	20769	2.66	0.0E+00	5803114	NT	Homo sapiens DKFZP568M127 protein (DKFZP568M122), mRNA
1007	10925	20769	2.66	0.0E+00	5803114	NT	Homo sapiens DKFZP568M127 protein (DKFZP568M122), mRNA
1007	10925	20769	2.66	0.0E+00	5803114	NT	Homo sapiens DKFZP568M127 protein (DKFZP568M122), mRNA
1000	10927		1.94	0.0E+00	AA466890.1	EST_HUMAN	sw5907.v1 Stragene fetal retina 937202 Homo sapiens cDNA clone IMAGE395236.3' similar to SW-PRSS_HUMAN PA7120 26S PROTEASE REGULATORY SUBUNIT 9 ;

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1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
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Probe SEQ ID NO.	Euon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
1012	10320	20774	1.04	0.0E+00	N43182.1	EST_HUMAN	BST51024 WATM1 Homo sapiens cDNA clone 5124 similar to DNA-DIRECTED RNA POLYMERASE II (segment 5' and Pro with BLASTX c.p)
1012	10320	20775	1.04	0.0E+00	N43182.1	EST_HUMAN	BS10124 KIA1101 Homo sapiens cDNA clone 5124 similar to DNA-DIRECTED RNA POLYMERASE II (segment 5' and Pro with BLASTX c.p)
1013	10331	20776	0.97	0.0E+00	U795249	NT	Homo sapiens TGF- β family member-associated NFR- β activator (TANK) mRNA
1013	10331	20777	0.97	0.0E+00	U795249	NT	Homo sapiens TGF- β family member-associated NFR- β activator (TANK) mRNA
1017	10335	20781	2.19	0.0E+00	6822553	NT	Homo sapiens hypothetical protein FLJ11156 (FLJ11156)
1031	10349	20782	4.49	0.0E+00	U795959	NT	Homo sapiens heat shock 70MD protein 98 (heat-shock 70) mRNA
1049	10356	20806	1.88	0.0E+00	4826072	NT	Homo sapiens cadherin 6, K-cadherin (retal kidney) (CDH6) mRNA
1049	10356	20807	1.88	0.0E+00	4826072	NT	Homo sapiens cadherin 6, K-cadherin (retal kidney) (CDH6) mRNA
1093	10370	20812	2.92	0.0E+00	6823524	NT	Homo sapiens hypothetical protein FLJ20693 (FLJ20693)
1093	10370	20813	2.92	0.0E+00	6823524	NT	Homo sapiens hypothetical protein FLJ20693 (FLJ20693)
1094	10371	20814	38.24	0.0E+00	AJ245622.1	NT	Homo sapiens mRNA for alpha-tubulin 8 (TUBA8 gene)
1095	10373	20816	0.93	0.0E+00	6823087	NT	Homo sapiens hypothetical protein FLJ20800 (TUBA8 gene)
1098	10378	20821	3.28	0.0E+00	U714594	NT	Homo sapiens death repair, a1c3 homolog (ABT1) mRNA
1098	10378	20822	3.98	0.0E+00	U793117	NT	Homo sapiens death associated protein 3 (DAP3) mRNA
1080	10366	20837	3.78	0.0E+00	BC006208.1	EST_HUMAN	MRO-BN0115-200300-005-H03 BN0115 Homo sapiens cDNA
1103	11016	20861	3.79	0.0E+00	U770134	NT	Homo sapiens potassium channel, subfamily K, member 6 (KCNR6), mRNA
1103	11016	20862	3.79	0.0E+00	U770134	NT	Homo sapiens potassium channel, subfamily K, member 6 (KCNR6), mRNA
1116	11081	20872	1.12	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
1116	11081	20873	1.12	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
1117	11082	20874	5.7	0.0E+00	4826912	NT	Homo sapiens ribosomal protein S27a (RPS27A) mRNA
1116	11084	20876	0.86	0.0E+00	8823290	NT	Homo sapiens hypothetical protein FLJ20305 (FLJ20305)
1121	11098	20878	10.18	0.0E+00	A3002096.1	NT	Homo sapiens DNA for Human P20X, complete cds
1121	11098	20879	12.02	0.0E+00	A3002096.1	NT	Homo sapiens similar to rat integral membrane glycoprotein POM21 (POM21), mRNA
1123	11098	20880	2.03	0.0E+00	A3002096.1	NT	Homo sapiens similar to rat integral membrane glycoprotein POM21 (POM21), mRNA
1124	11098	20881	2.03	0.0E+00	U767468	NT	Homo sapiens similar to rat integral membrane glycoprotein NpwBP (LOC51729), mRNA
1124	11098	20884	0.95	0.0E+00	U706900	NT	gb2210.4.1 Source, program, uterus, Nbf1P1 Homo sapiens cDNA clone IMAGE:1697011.3
1128	11043	20885	1.44	0.0E+00	A147050.1	EST_HUMAN	Homo sapiens mRNA for KIAA0935 protein, partial cds
1131	11043	20887	1.44	0.0E+00	A300270.1	EST_HUMAN	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
1140	11054	20890	1.13	0.0E+00	5906844	NT	Homo sapiens glutamate decarboxylase 1 (brain, 67kD), transcript variant GAD25, mRNA
1152	11055	20900	2.31	0.0E+00	U750576	NT	Homo sapiens glutamate decarboxylase 1 (brain, 67kD) (GAD1), transcript variant GAD25, mRNA
1152	11055	20901	2.31	0.0E+00	U750576	NT	Homo sapiens glutamate decarboxylase 1 (brain, 67kD) (GAD1), transcript variant GAD25, mRNA
1154	11067	20911	1.59	0.0E+00	A3037835.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1161	11074	20520	1.02	0.0E+00	4657887	NT	Homo sapiens keratin 18 (KRT18) mRNA
1191	11101		1.13	0.0E+00	7957339	NT	Homo sapiens mull. (E. coli) homolog 3 (MLH3) mRNA
1206	11116	20562	1.14	0.0E+00	AF294750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1205	11115	20563	1.14	0.0E+00	AF294750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1207	11117	20564	1.31	0.0E+00	AF294750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1209	12897	20565	0.95	0.0E+00	AF294750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1226	11134	20566	3.92	0.0E+00	AF109718.1	NT	Homo sapiens chromosome 3 subtelomeric region
1227	11135	20569	1.3	0.0E+00	4650396	NT	Homo sapiens chondroin sulfate proteoglycan 4 (melanoma-associated) (CSPG4) mRNA
1245	11152		1.48	0.0E+00	Y18000.1	NT	Homo sapiens NF2 gene
1263	11160	21009	45.99	0.0E+00	4500719	NT	Homo sapiens fibronectin protein S2 (FBS2) mRNA
1260	11107	21016	3.95	0.0E+00	AF044479.1	NT	Homo sapiens Williams-Buren syndrome deletion transcript 6 (WBSOR6) mRNA, complete cds
1265	11173	21023	1.71	0.0E+00	AB040940.1	NT	Homo sapiens mRNA for KIAA1507 protein, partial cds
1266	11173	21023	1.71	0.0E+00	AB040940.1	NT	Homo sapiens mRNA for KIAA1507 protein, partial cds
1276	11169	21036	8.42	0.0E+00	5174748	NT	Homo sapiens Wolfman syndrome (WFS) mRNA
1278	11168	21037	8.42	0.0E+00	5174748	NT	Homo sapiens Wolfman syndrome (WFS) mRNA
1279	11168	21038	8.42	0.0E+00	5174748	NT	Homo sapiens Wolfman syndrome (WFS) mRNA
1279	11187		2.0	0.0E+00	AF056155.1	NT	Homo sapiens protein phosphatase 2A B1 gamma subunit gene, exon 5
1289	12889	21050	1.1	0.0E+00	7857539	NT	Homo sapiens halsud tumor deletion region protein 1 (RTDR1) mRNA
1289	12889	21051	1.1	0.0E+00	7857539	NT	Homo sapiens halsud tumor deletion region protein 1 (RTDR1) mRNA
1291	11202	21057	1.71	0.0E+00	5603748	NT	Homo sapiens halsud tumor deletion region protein 1 (RTDR1) mRNA
1291	11203	21058	0.82	0.0E+00	4635004	NT	Homo sapiens halsud tumor deletion region protein 1 (RTDR1) mRNA
1298	11205	21059	1.07	0.0E+00	5603748	NT	Homo sapiens halsud tumor deletion region protein 1 (RTDR1) mRNA
1300	11207	21061	4.1	0.0E+00	AB011148.1	NT	Homo sapiens halsud tumor deletion region protein 1 (RTDR1) mRNA
1301	11208	21062	1.06	0.0E+00	7857539	NT	Homo sapiens halsud tumor deletion region protein 1 (RTDR1) mRNA
1302	11210	21063	4.94	0.0E+00	7857539	NT	Homo sapiens halsud tumor deletion region protein 1 (RTDR1) mRNA
1303	11210	21064	4.1	0.0E+00	7857539	NT	Homo sapiens halsud tumor deletion region protein 1 (RTDR1) mRNA
1303	11210	21065	4.1	0.0E+00	7857539	NT	Homo sapiens halsud tumor deletion region protein 1 (RTDR1) mRNA
1315	11221	21078	1.35	0.0E+00	M14123.1	NT	Human endogenous retrovirus HERV-K10
1395	11291	21147	0.89	0.0E+00	AJ250014.1	NT	Homo sapiens mRNA for Familial Cyclo-oxygenase cyd gene
1393	11290	21150	9.13	0.0E+00	AJ277892.1	NT	Homo sapiens partial TTN gene for titin
1395	11301	21190	0.95	0.0E+00	AJ209755.1	EST_HUMAN	gq3503.x1 Soares_1616_NHT Homo sapiens cDNA IMAGE:4837427 5' similar to WP-T27A.1.6 CE14213 ;
1397	11302	21191	8.18	0.0E+00	6042206	NT	RAN, member RAS oncogene family/Homo sapiens RAN, member RAS oncogene family (RAN), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Meat Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1407	11312	21173	1.4	0.0E+00	4505949	NT	Homo sapiens propeptin convertase subtilisin/kexin type 2 (PCSK2) mRNA
1407	11312	21174	1.4	0.0E+00	4505949	NT	Homo sapiens propeptin convertase subtilisin/kexin type 2 (PCSK2) mRNA
1409	11314	21177	2.54	0.0E+00	7705565	NT	Homo sapiens KIAA1114 protein (KIAA1114), mRNA
1409	11314	21178	2.54	0.0E+00	7705565	NT	Homo sapiens KIAA1114 protein (KIAA1114), mRNA
1421	11317	21190	5.25	0.0E+00	AJ239033.1	NT	Homo sapiens partial AF-4 gene, exons 2 to 7 and Alu repeat elements
1421	11327	21192	3.51	0.0E+00	AF038260.1	NT	Homo sapiens aliphatic glucosyltransferase (alipat1-8)uc.1 gene, exon 7
1432	11337	21203	6.7	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
1432	11337	21203	6.7	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
1437	11342	21208	1.02	0.0E+00	4507720	NT	Human nebulin mRNA, partial cds
1445	11350	21214	3.05	0.0E+00	AJ35637.1	NT	Human nebulin mRNA, partial cds
1445	11350	21214	3.05	0.0E+00	AL129869.1	NT	Novel human gene mapping to chromosome 20
1447	11352	21215	1.03	0.0E+00	AL137864.1	NT	Novel human gene mapping to chromosome 1
1451	11356	21220	1.22	0.0E+00	D87077.1	NT	Human mRNA for KIAA0240 gene, partial cds
1454	11359	21223	4.97	0.0E+00	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
1454	11359	21223	4.97	0.0E+00	7691995	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1456	11361	21226	1.51	0.0E+00	7691995	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1457	11362	21228	1.51	0.0E+00	7691995	NT	Homo sapiens FBX30 gene for RING finger protein
1461	11367	21231	0.97	0.0E+00	Y07620.2	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
1462	11367	21232	3.95	0.0E+00	N55075.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
1465	11366	21259	1.32	0.0E+00	N55075.1	NT	Homo sapiens HD-C for homolog of Drosophila headcase (LOC1026), mRNA
1465	11366	21259	1.32	0.0E+00	N55075.1	NT	aa0403-CT1 NC1_CQBP-QCBT Homo sapiens cDNA clone IMAGE315118.5
1508	11414	21273	0.95	0.0E+00	AA481172.1	EST	Carcinophilous epithelial cytoplasmic A mRNA, complete cds
1515	11420	21276	11.95	0.0E+00	AF023960.1	NT	Carcinophilous epithelial cytoplasmic A mRNA, complete cds
1515	11420	21277	11.95	0.0E+00	AF023960.1	NT	Carcinophilous epithelial cytoplasmic A mRNA, complete cds
1517	11422	21280	0.97	0.0E+00	D10864.1	NT	Bovine mRNA for neurocalcin
1519	11424		2.03	0.0E+00	U79027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44), and F1P3 (F1P3) genes, complete cds
1520	11425	21283	3.9	0.0E+00	4505404	NT	Homo sapiens transthyretin glycoprotein (GPNMB) mRNA
1520	11425	21284	3.9	0.0E+00	4505404	NT	Homo sapiens transthyretin glycoprotein (GPNMB) mRNA
1521	11426	21285	3.12	0.0E+00	7692405	NT	Homo sapiens transthyretin glycoprotein (GPNMB) mRNA
1522	11427		8.41	0.0E+00	7695072	NT	Homo sapiens TNF-inducible protein CG12-1 (CG12-1), mRNA
1527	11432	21296	5.02	0.0E+00	M89478.1	NT	Human transglutaminase mRNA, complete cds
1530	11435	21281	5.75	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
1530	11435	21282	5.75	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
1531	12697		10.12	0.0E+00	4505954	NT	Homo sapiens ribosomal protein L5 (RPL5) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF-SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1532	11436	21293	11.11	0.0E+00	M14190.1	NT	Human laminin receptor (2H5 epitope) mRNA, 5' end
1541	11446	21306	5.81	0.0E+00	4507720	NT	Homo sapiens Bin (TTN) mRNA
1541	11446	21307	5.81	0.0E+00	4507720	NT	Homo sapiens Bin (TTN) mRNA
1543	11448	21308	12.91	0.0E+00	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
1552	11467	21325	1.66	0.0E+00	283738.1	NT	H.sapiens H2Bale gene
1553	11468	21326	1.35	0.0E+00	5921460	NT	H.sapiens leukophilin, subfamily 2, member A1 (BTU2A1), mRNA
1553	11468	21327	1.35	0.0E+00	5921460	NT	H.sapiens leukophilin, subfamily 2, member A1 (BTU2A1), mRNA
1554	11469	21328	5.5	0.0E+00	AV90853.1	EST_HUMAN	AV90853.1 GKHC Homo sapiens cDNA clone GKCB0F02.5
1554	11469	21329	5.5	0.0E+00	AV90853.1	EST_HUMAN	AV90853.1 GKHC Homo sapiens cDNA clone GKCB0F02.5
1555	12593	21330	1.5	0.0E+00	AB040965.1	NT	Human sapiens mRNA for KIAA1472 protein, partial cds
1570	11474	21331	0.88	0.0E+00	AF167476.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
1572	11476	21334	2.49	0.0E+00	7692183	NT	Homo sapiens KIA0659 gene product (KIA0659) mRNA
1572	11476	21335	2.49	0.0E+00	7692183	NT	Homo sapiens KIA0659 gene product (KIA0659) mRNA
1574	11478	21336	14.05	0.0E+00	5728876	NT	Homo sapiens heat shock 70MD protein 10 (HSC71) (HSPA10), mRNA
1574	11478	21337	14.05	0.0E+00	5728876	NT	Homo sapiens heat shock 70MD protein 10 (HSC71) (HSPA10), mRNA
1574	11480	21339	0.94	0.0E+00	M61103.1	NT	Human sodium channel mRNA
1576	11480	21339	0.94	0.0E+00	M61103.1	NT	Human sodium channel mRNA
1591	11485	21355	4.67	0.0E+00	H29073.1	EST_HUMAN	yo76263.5 Soares adult brain N2544-B557 Homo sapiens cDNA clone IMAGE:183346.3
1591	11485	21355	4.67	0.0E+00	H29073.1	EST_HUMAN	yo76263.5 Soares adult brain N2544-B557 Homo sapiens cDNA clone IMAGE:183346.3
1602	11607	21358	-	1.4	0.0E+00	AB040829.1	Homo sapiens mRNA for KIAA1609 protein, partial cds
1602	11607	21359	1.4	0.0E+00	AB040829.1	NT	Homo sapiens mRNA for KIAA1609 protein, partial cds
1645	11549	21410	1.27	0.0E+00	AT08104.1	EST_HUMAN	wg51107.x1 Soares_NSF_F8_3W_OT_PA_31 Homo sapiens cDNA clone IMAGE:2371477.3 similar to
1646	11550	21411	3.33	0.0E+00	AF057177.1	NT	TR-Q62768 Q62768 CY52H52 ZINC FINGER PROTEIN. ;
1650	11553	21415	1.49	0.0E+00	M23590.1	NT	Homo sapiens 1-cell receptor gamma V1 gene region
1650	11553	21415	1.49	0.0E+00	M23590.1	NT	Homo sapiens 1-cell receptor gamma V1 gene region
1650	11553	21416	1.56	0.0E+00	M26150.1	NT	Human zinc-finger protein 7 (ZFP7) mRNA, complete cds
1652	11555	21418	1.22	0.0E+00	4557897	NT	Human sapiens keratin 18 (KRT18) mRNA
1653	11556	21419	0.92	0.0E+00	7957095	NT	Homo sapiens vello aden erythroblast virus E26 oncogene related (ERO), mRNA
1657	11559	21423	1.11	0.0E+00	4557610	NT	Homo sapiens vello aden erythroblast virus E26 oncogene related (ERO), mRNA
1659	11561	21428	2.99	0.0E+00	H30132.1	EST_HUMAN	y95908.11 Soares breast 3NH1Bst Homo sapiens cDNA clone IMAGE:182245.5 similar to gb:M64099
1659	11561	21427	2.99	0.0E+00	H30132.1	EST_HUMAN	y95908.11 Soares breast 3NH1Bst Homo sapiens cDNA clone IMAGE:182245.5 similar to gb:M64099
1661	11563	21429	1.21	0.0E+00	Z30780.1	NT	GAMMA-GLUTAMYL TRANSPEPTIDASE 5 PRECURSOR (HUMAN)
1661	11563	21430	1.21	0.0E+00	Z30780.1	NT	GAMMA-GLUTAMYL TRANSPEPTIDASE 5 PRECURSOR (HUMAN)
1664	11565		7.65	0.0E+00	5031748	NT	H.sapiens H2Bh1 gene
1664	11565		7.65	0.0E+00	5031748	NT	H.sapiens H2Bh1 gene
1664	11565		7.65	0.0E+00	5031748	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 17 (HMG17), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1672	11574	21442	4.55	0.0E+00	802884	NT	Homo sapiens FOXJ1 forkhead factor (LOC55810) mRNA
1677	11579	21448	1.02	0.0E+00	M75903.1	NT	Human hepatocyte growth factor gene, exon 15
1677	11579	21448	1.02	0.0E+00	M75903.1	NT	Human hepatocyte growth factor gene, exon 15
1680	11582	21453	1.43	0.0E+00	4928973	NT	Homo sapiens RNA binding motif protein, Y chromosome, family 1, member A1 (RBMY1A1) mRNA
1685	11587	21460	2.59	0.0E+00	AB025842.1	NT	Homo sapiens WAVE2 mRNA for WASP-family protein, complete cds
1687	11589	21461	2.6	0.0E+00	S8400.1	NT	TCR zeta human, GenomicRNA, 365 nt, segment 1 of 8
1689	11592	21472	0.97	0.0E+00	1114591.1	NT	Homo sapiens NOD2 protein (NOD2) mRNA
1710	12181	21481	1.75	0.0E+00	A72784.1	NT	Homo sapiens SMC7 (SMC7) gene, complete cds
1745	12703	21518	13.81	0.0E+00	4509718	NT	Homo sapiens fibronectin protein S2 (RP52) mRNA
1749	12749	21517	0.9	0.0E+00	4597569	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA
1749	12749	21518	0.9	0.0E+00	4597569	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA
1751	11581	21521	1.23	0.0E+00	U05933.1	NT	Human CSF-1 receptor (TNF8) gene, complete cds, and (SMF) gene, partial cds
1754	11654	21525	1.13	0.0E+00	W76571.1	EST_HUMAN	z550599.1 Scores, fetal, heart NHBT1997 Homo sapiens cDNA clone IMAGE:345694.5'
1755	12704	21525	3.89	0.0E+00	4508323	NT	Homo sapiens nuclear autoantigenic sperm protein (histone-binding) (NA-SP) mRNA
1755	11654	21538	7.25	0.0E+00	A14067.1	NT	Human fibronectin protein L21 mRNA, complete cds
1757	11656	21541	4.6	0.0E+00	AB000239.1	NT	Human mRNA for KIAA0333 gene, partial cds
1758	11657	21542	4.34	0.0E+00	4502264	NT	Homo sapiens activating transcription factor 4 (tax-responsive enhancer element 967) (ATFA) mRNA
1758	11657	21543	4.34	0.0E+00	4502264	NT	Homo sapiens activating transcription factor 4 (tax-responsive enhancer element 967) (ATFA) mRNA
1759	11657	21544	4.34	0.0E+00	4502264	NT	Homo sapiens activating transcription factor 4 (tax-responsive enhancer element 967) (ATFA) mRNA
1761	11660	21559	1.04	0.0E+00	4504626	NT	Homo sapiens immunoglobulin superfamily, member 3 (IGSF3) mRNA, and translated products
1761	11660	21559	1.04	0.0E+00	4504626	NT	Homo sapiens immunoglobulin superfamily, member 3 (IGSF3) mRNA, and translated products
1763	11661	21565	10.22	0.0E+00	6005855	NT	Homo sapiens Refina-derived POU-domain factor 1 (RP1F-1) mRNA
1763	11661	21567	10.22	0.0E+00	6005855	NT	Homo sapiens Refina-derived POU-domain factor 1 (RP1F-1) mRNA
1804	11701	21576	3.19	0.0E+00	4526763	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
1804	11701	21577	3.19	0.0E+00	4526763	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
1805	11702	21578	4.52	0.0E+00	U07147.1	NT	Human retinal degeneration slow (RDS) gene, exon 1
1805	11702	21579	4.52	0.0E+00	U07147.1	NT	Human retinal degeneration slow (RDS) gene, exon 1
1809	11706	21584	1.47	0.0E+00	AW207380.1	EST_HUMAN	U1-HBH-afin-407-5UL1 at NC1 CGAP Sub3 Homo sapiens cDNA clone IMAGE:2722933.3'
1809	11706	21585	1.47	0.0E+00	AW207380.1	EST_HUMAN	U1-HBH-afin-407-5UL1 at NC1 CGAP Sub3 Homo sapiens cDNA clone IMAGE:2722933.3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Mean (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1832	11729	21003	2.08	0.0E+00	BE277465.1	EST_HUMAN	501175164.F1 NH1_MGC_20 Homo sapiens cDNA clone IMAGE3547239.5'
1832	11729	21004	2.08	0.0E+00	BE277465.1	EST_HUMAN	501175164.F1 NH1_MGC_20 Homo sapiens cDNA clone IMAGE3547239.5'
1832	11748	21023	2.02	0.0E+00	BE069232.1	EST_HUMAN	RC2.BN01238-200300-072.504.BN0128 Homo sapiens cDNA
1831	11777	21051	3.52	0.0E+00	4506384	NT	Homo sapiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products
1831	11777	21052	3.52	0.0E+00	4506384	NT	Homo sapiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products
1830	11765	21051	1.95	0.0E+00	AF167476.1	NT	Homo sapiens DNA polymerase beta catalytic subunit (REV3) mRNA, complete cds
1890	12707	21061	4.05	0.0E+00	M98476.1	NT	Human transglutaminase mRNA, complete cds
1890	12707	21062	4.05	0.0E+00	M98476.1	NT	Human transglutaminase mRNA, complete cds
1895	11790	21059	2.28	0.0E+00	4507464	NT	Homo sapiens transforming growth factor, beta 3 (TGFB3) mRNA
1895	11790	21070	2.28	0.0E+00	4507464	NT	Homo sapiens transforming growth factor, beta 3 (TGFB3) mRNA
1898	11764	21070	5.26	0.0E+00	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
1903	11769	21070	1.9	0.0E+00	M55932.1	NT	Human lactoferrin pseudogene 1
1905	12708	21078	0.94	0.0E+00	5901605	NT	Homo sapiens butyrophilin, subfamily 3, member A2 (BTN3A2) mRNA
1913	11803	21085	1.97	0.0E+00	4906233	NT	Homo sapiens histidine ammonia-lyase (HAL) mRNA
1913	11803	21086	1.97	0.0E+00	4906233	NT	Homo sapiens histidine ammonia-lyase (HAL) mRNA
1924	11819	21086	1.12	0.0E+00	AL163262.2	NT	Homo sapiens chromosome 21 segment HS21C062
1924	11821	21700	1.15	0.0E+00	8400719	NT	Homo sapiens nebulin (NEB) mRNA
1926	11821	21701	1.15	0.0E+00	8400719	NT	Homo sapiens nebulin (NEB) mRNA
1927	11822	21702	8.13	0.0E+00	4526538	NT	Homo sapiens actinin, alpha 4 (ACTN4) mRNA
1927	11822	21703	8.13	0.0E+00	4526538	NT	Homo sapiens actinin, alpha 4 (ACTN4) mRNA
1937	11832	21715	1.21	0.0E+00	AB010333.1	NT	Homo sapiens mRNA for KIAA0750 protein, partial cds
1937	11832	21716	1.21	0.0E+00	AB010333.1	NT	Homo sapiens mRNA for KIAA0750 protein, partial cds
1943	11838	21720	2.01	0.0E+00	M33782.1	NT	Human TEB protein mRNA, partial cds
1943	11838	21721	2.01	0.0E+00	M33782.1	NT	Human TEB protein mRNA, partial cds
1945	11840	21722	1.33	0.0E+00	AW169024.1	EST_HUMAN	AB9601.X1 NC1 CGAP_Peri1 Homo sapiens cDNA clone IMAGE2679913.3'
1945	11840	21723	1.33	0.0E+00	AW169024.1	EST_HUMAN	AB9601.X1 NC1 CGAP_Peri1 Homo sapiens cDNA clone IMAGE2679913.3'
1946	11841	21724	8.4	0.0E+00	6912467	NT	Homo sapiens calcitriol binding protein 1 (KIAA0339), mRNA
1946	11841	21725	8.4	0.0E+00	6912467	NT	Homo sapiens calcitriol binding protein 1 (KIAA0339), mRNA
1948	11843	21727	0.92	0.0E+00	Z47666.1	NT	H sapiens genes for semaphorin I and semaphorin II
1948	11843	21728	0.92	0.0E+00	Z47666.1	NT	H sapiens genes for semaphorin I and semaphorin II
1855	11850	21737	2.31	0.0E+00	AB040046.1	NT	Homo sapiens mRNA for KIAA1513 protein, partial cds
1975	11866	21759	0.85	0.0E+00	AF223841.1	NT	Homo sapiens SMCY (SMCY) gene, complete cds
1975	11866	21760	0.85	0.0E+00	AF223841.1	NT	Homo sapiens SMCY (SMCY) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar Top Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
20111	11803	21763	1.09	0.0E+00	BE743216.1	EST_HUMAN	G01573895F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3935186 5'
20111	11803	21764	1.09	0.0E+00	BE743216.1	EST_HUMAN	G01573895F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3935186 5'
20111	11803	21764	1.09	0.0E+00	BE743216.1	EST_HUMAN	Homo sapiens coagulation factor IX (plasma thromboplastic component, Christmas disease, hemophilia B) (F9) mRNA
20114	11809	21765	0.96	0.0E+00	4503648	NT	AJ1140831 PLACE4 Homo sapiens cDNA clone PLACE4000321 5'
2014	11900	21766	5.48	0.0E+00	ALU140831.1	EST_HUMAN	Homo sapiens KIAA1114 protein (KIAA1114), mRNA
2015	11314	21777	1.01	0.0E+00	7765565	NT	Homo sapiens KIAA1114 protein (KIAA1114), mRNA
2015	11314	21778	1.01	0.0E+00	7765565	NT	7B22E10 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B22E10
2017	11809	21768	1.95	0.0E+00	AA077589.1	EST_HUMAN	7B22E10 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B22E10
2017	11809	21768	1.95	0.0E+00	AA077589.1	EST_HUMAN	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
2019	11910	21769	2.34	0.0E+00	7697468	NT	Homo sapiens phosphodiesterase 6A, cAMP-specific, rod, alpha (PDE6A), mRNA
2021	11912	21801	1.6	0.0E+00	4868963	NT	HSC03021 normalized infant brain cDNA Homo sapiens cDNA clone c-002
2022	11913	21802	0.92	0.0E+00	Z43369.1	EST_HUMAN	g00085.x1 NC1_CGAP_UG Homo sapiens cDNA clone IMAGE:168871 3' similar to contains Alu repetitive element
2024	11915		1.94	0.0E+00	AL24247.1	EST_HUMAN	g00085.x1 NC1_CGAP_UG Homo sapiens cDNA clone IMAGE:168871 3' similar to contains Alu repetitive element
2026	11920	21811	2.90	0.0E+00	BE677235.1	EST_HUMAN	G01093146F1 NIH_MGC_89 Homo sapiens cDNA clone IMAGE:3987747 5'
2031	11922	21813	1.5	0.0E+00	BE6713328.1	EST_HUMAN	G01093090F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4136320 5'
2031	11922	21814	1.5	0.0E+00	BE6713328.1	EST_HUMAN	G01093090F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4136320 5'
2039	11926	21816	2.42	0.0E+00	BE597125.1	EST_HUMAN	RC3-C10413-20700-022470 C10413 Homo sapiens cDNA
2039	11926	21820	2.42	0.0E+00	BE597125.1	EST_HUMAN	RC3-C10413-20700-022470 C10413 Homo sapiens cDNA
2040	11931	21826	2.93	0.0E+00	L00620.1	NT	Human plasma membrane calcium ATPase isoform 2 (ATP2B2) mRNA, complete cds
2040	11931	21827	2.93	0.0E+00	L00620.1	NT	Human plasma membrane calcium ATPase isoform 2 (ATP2B2) mRNA, complete cds
2045	11956	21837	1.32	0.0E+00	4790488	NT	Homo sapiens GTP binding protein 1 (GTPBP1) mRNA
2045	11956	21837	1.32	0.0E+00	4790488	NT	Homo sapiens GTP binding protein 1 (GTPBP1) mRNA
2067	11957		2.93	0.0E+00	BE767664.1	EST_HUMAN	QY1-GN0005-149000-318-510 GN0005 Homo sapiens cDNA
2068	11968		1.13	0.0E+00	AF078963.1	NT	Homo sapiens X-linked invetral retinoid protein (XLRP) gene, exon 6 and complete cds
2070	11960	21854	3.09	0.0E+00	BF027562.1	EST_HUMAN	G01672006F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:394785 5'
2071	11961	21855	2	0.0E+00	4503750	NT	Homo sapiens flexin containing monooxygenase 2 (FMO2) mRNA
2073	11963	21856	0.89	0.0E+00	AF240788.1	NT	Homo sapiens glutathione S-transferase theta 1 (GSTT1) genes, complete cds
2074	11964	21857	1.16	0.0E+00	AW752708.1	EST_HUMAN	L3-C7021819-271068-022-G10 C10219 Homo sapiens cDNA
2076	11966	21860	1.96	0.0E+00	AB04640.1	EST_HUMAN	QY-87065-020395-052 B7065 Homo sapiens cDNA
2076	11966	21860	1.96	0.0E+00	AB04640.1	EST_HUMAN	QY-87065-020395-052 B7065 Homo sapiens cDNA
2112	12001		1.16	0.0E+00	7657232	NT	Homo sapiens potassium large conductance calcium-activated channel, subfamily M, beta member 3-like (KCNMB3), mRNA
2132	12020		1.6	0.0E+00	LA1787.1	NT	Human DNA-binding protein mRNA, 3' end

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2360	12276	22172	2.28	0.0E+00	AF106275.1	NT	Homo sapiens immunoglobulin-like transcript 1c, variant 4 (L1c) gene, exon 6
2402	12287	22176	0.98	0.0E+00	BF345274.1	EST_HUMAN	6020718058F1 NCL_GGAP_Eln67 Homo sapiens cDNA clone IMAGE:306655 3'
2410	12287	22185	3.95	0.0E+00	5729177	NT	Homo sapiens collagen, type XI, alpha 1 (COL12A1), mRNA
2414	12291	22188	0.97	0.0E+00	BE631003.1	EST_HUMAN	CAC-MT 0003-15000-428-H11 MT0033 Homo sapiens cDNA
2414	12291	22189	0.97	0.0E+00	BE631003.1	EST_HUMAN	CAC-MT 0003-15000-428-H11 MT0033 Homo sapiens cDNA
2410	12290	22193	2.27	0.0E+00	AF599144.1	EST_HUMAN	h6d404.x1 NCL_GGAP_K412 Homo sapiens cDNA clone IMAGE:307759 3'
2428	12305	22201	2.66	0.0E+00	AW46922.1	EST_HUMAN	h6d404.x1 NCL_GGAP_K412 Homo sapiens cDNA clone IMAGE:307759 3'
2430	12307	22202	3.45	0.0E+00	AW46922.1	EST_HUMAN	h6d404.x1 NCL_GGAP_K412 Homo sapiens cDNA clone IMAGE:307759 3'
2444	12321	22216	2.08	0.0E+00	AW10101.1	EST_HUMAN	UHF-EPop-ale<-07-U1 NH_MGC_51 Homo sapiens cDNA clone IMAGE:3072760 5'
2444	12321	22220	2.08	0.0E+00	5453963	NT	Homo sapiens protein kinase, AMP-activated, alpha 2 catalytic subunit (PRKAA2), mRNA
2467	12334	22233	2.35	0.0E+00	AW133853.1	EST_HUMAN	Homo sapiens protein kinase, AMP-activated, alpha 2 catalytic subunit (PRKAA2), mRNA
2463	12339	22233	16.13	0.0E+00	BE705642.1	EST_HUMAN	RG3-3710197-50300-016-04-ST0167 Homo sapiens cDNA
2463	11762	21671	1.18	0.0E+00	7667038	NT	601592350F1 NH_MGC_7 Homo sapiens cDNA clone IMAGE:3946518 5'
2464	12340	22234	1.8	0.0E+00	BF509482.1	EST_HUMAN	Homo sapiens death receptor 8 (DR8), mRNA
2467	12343	22236	2.25	0.0E+00	Z02884.2	NT	U1-H3L1-acc3-282-U1.x1 NCL_GGAP_S145 Homo sapiens cDNA clone IMAGE:306655 3'
2469	12345	22236	3.37	0.0E+00	5453971	NT	Homo sapiens mRNA for mena and transport protein (X) gene
2471	12347	22236	1.89	0.0E+00	5453971	NT	Homo sapiens mRNA for mena and transport protein (X) gene
2472	12348	22241	1.89	0.0E+00	7857438	EST_HUMAN	Homo sapiens mRNA for mena and transport protein (X) gene
2473	12349	22241	55.78	0.0E+00	BE705511.1	EST_HUMAN	Homo sapiens mRNA for mena and transport protein (X) gene
2474	12350	22242	1.14	0.0E+00	BE705511.1	EST_HUMAN	Homo sapiens mRNA for mena and transport protein (X) gene
2475	12351	22243	3.21	0.0E+00	8623340	NT	RC4-H10276-10020-013-045 H1 0276 Homo sapiens cDNA
2481	12357	22249	1.64	0.0E+00	U63269.1	NT	Human Sec22 (Sec22) mRNA, complete cds
2486	12361	22255	4.39	0.0E+00	BE705511.1	EST_HUMAN	Homo sapiens Sec22 (Sec22) mRNA, complete cds
2486	12361	22256	4.39	0.0E+00	BE705511.1	EST_HUMAN	Homo sapiens Sec22 (Sec22) mRNA, complete cds
2488	12363	22256	0.97	0.0E+00	AF245505.1	NT	Homo sapiens Sec22 (Sec22) mRNA, complete cds
2504	12378	22267	1.27	0.0E+00	BE508052.1	EST_HUMAN	Homo sapiens Sec22 (Sec22) mRNA, complete cds
2509	12383	22274	3.8	0.0E+00	AF143277.1	EST_HUMAN	601064738F1 NH_MGC_10 Homo sapiens cDNA clone IMAGE:3481161 5'
2510	12384	22276	3.8	0.0E+00	AF143277.1	EST_HUMAN	601064738F1 NH_MGC_10 Homo sapiens cDNA clone IMAGE:3481161 5'
2510	12384	22276	1.19	0.0E+00	AF143277.1	EST_HUMAN	601064738F1 NH_MGC_10 Homo sapiens cDNA clone IMAGE:3481161 5'
2510	12384	22277	1.19	0.0E+00	AF143277.1	EST_HUMAN	601064738F1 NH_MGC_10 Homo sapiens cDNA clone IMAGE:3481161 5'
2511	12385	22278	0.99	0.0E+00	BF723041.1	EST_HUMAN	76271212x1 NCL_GGAP_G028 Homo sapiens cDNA clone IMAGE:3481161 5'
2514	12388	22280	7.05	0.0E+00	AF245505.1	NT	HYPOPHYSICAL 9.3 KD PROTEIN
2540	12414	22304	1.05	0.0E+00	BE286613.1	EST_HUMAN	Homo sapiens Sec22 (Sec22) mRNA, complete cds

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Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Meat Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2553	12654	22318	2.37	0.0E+00	AB007836.1	NT	Homo sapiens mRNA for KIAA1415 protein, partial cds
2554	12654	22319	2.37	0.0E+00	AB007836.1	NT	Homo sapiens mRNA for KIAA1415 protein, partial cds
2554	12654	22319	2.37	0.0E+00	AB007836.1	NT	UHHBW1-amp-412-UL1 NCI CGAP_Sub07 Homo sapiens cDNA clone IMAGE:3070631 3'
2560	12432	22325	3.85	0.0E+00	BF073835.1	EST_HUMAN	602152635F1 NH1.MGC.81 Homo sapiens cDNA clone IMAGE:4283612 5'
2562	12434		1.6	0.0E+00	BF072918.1	EST_HUMAN	601278673F1 NH1.MGC.39 Homo sapiens cDNA clone IMAGE:3821766 5'
2569	12440	22332	1.34	0.0E+00	BE616695.1	EST_HUMAN	Homo sapiens mRNA for KIAA1321 protein, partial cds
2570	12441	22333	0.97	0.0E+00	AB037742.1	NT	h19809.3 NCI CGAP_Bio25 Homo sapiens cDNA clone IMAGE:2166055 3' similar to gb123677
2571	12442	22334	2.27	0.0E+00	AI571757.1	EST_HUMAN	CALCIUM-TRANSPORTING ATPASE PLASMA MEMBRANE BRAIN ISOFORM 2 (HJMAN);
2573	12444	22336	5.78	0.0E+00	5032150	NT	Homo sapiens TATA box binding protein (TBP)-associated factor, RNA polymerase II, 28kD (TAF2)
2574	12445	22337	1.03	0.0E+00	AB007850.1	NT	Homo sapiens mRNA for KIAA1438 protein, partial cds
2574	12445	22338	1.03	0.0E+00	BE795445.1	EST_HUMAN	601500108F1 NH1.MGC.7 Homo sapiens cDNA clone IMAGE:3944304 5'
2574	12448	22339	1.1	0.0E+00	BE795445.1	EST_HUMAN	601500108F1 NH1.MGC.7 Homo sapiens cDNA clone IMAGE:3944304 5'
2574	12448	22339	1.1	0.0E+00	BE795445.1	EST_HUMAN	601500108F1 NH1.MGC.7 Homo sapiens cDNA clone IMAGE:3944304 5'
2585	12460		10.42	0.0E+00	BE792472.1	EST_HUMAN	601594906F1 NH1.MGC.7 Homo sapiens cDNA clone IMAGE:393222 5'
2585	12465	22356	2.46	0.0E+00	4504596	NT	Homo sapiens IMP (invariant monophosphate) dehydrogenase 1 (IMPDH1) mRNA
2601	12727	22365	7.02	0.0E+00	4507726	NT	Homo sapiens Bcl-2 protein, complete cds
2608	12476		1.09	0.0E+00	U78927.1	NT	Homo sapiens Bcl-2 protein, complete cds
2609	12477	22369	5.19	0.0E+00	AF173227.1	NT	Homo sapiens Bcl-2 protein, complete cds
2613	12481	22370	1.17	0.0E+00	AB011108.1	NT	Homo sapiens Bcl-2 protein, complete cds
2616	12485	22373	0.96	0.0E+00	AI153385.1	EST_HUMAN	Homo sapiens Bcl-2 protein, complete cds
2617	12485	22374	1.41	0.0E+00	U66233.1	NT	Homo sapiens Bcl-2 protein, complete cds
2619	12487	22376	1.21	0.0E+00	AI153403.1	EST_HUMAN	Human Induced Pluripotent Antigen (BPAIS) mRNA, complete cds
2619	12487	22377	1.21	0.0E+00	AI153403.1	EST_HUMAN	AI153403.1 NT293 Homo sapiens cDNA clone NT293-300779 5'
2622	12490	22380	1.29	0.0E+00	AI153403.1	EST_HUMAN	AI153403.1 NT293 Homo sapiens cDNA clone NT293-300779 5'
2626	12494	22385	1.29	0.0E+00	AI153403.1	EST_HUMAN	AI153403.1 NT293 Homo sapiens cDNA clone NT293-300779 5'
2627	12494	22386	3.25	0.0E+00	BE790018.1	EST_HUMAN	h191905.1 NCI CGAP_Cord1 Homo sapiens cDNA clone IMAGE:3316689 3'
2628	12496	22386	1.74	0.0E+00	BE790018.1	EST_HUMAN	h191905.1 NCI CGAP_Cord1 Homo sapiens cDNA clone IMAGE:3316689 3'
2628	12496	22386	1.74	0.0E+00	BE790018.1	EST_HUMAN	h191905.1 NCI CGAP_Cord1 Homo sapiens cDNA clone IMAGE:3316689 3'
2650	12523	22413	1.74	0.0E+00	BE531363.1	EST_HUMAN	601278373F1 NH1.MGC.39 Homo sapiens cDNA clone IMAGE:3610267 5'
2650	12523	22413	1.74	0.0E+00	8622843	NT	Homo sapiens Hypothetical protein FLJ11052 (FLJ11052), mRNA
2650	12555		8.72	0.0E+00	AA316723.1	EST_HUMAN	EST:189414 HCC cell line (malaisialis, lo liver in mouse) II Homo sapiens cDNA 5' end similar to ribosomal protein L20
2691	12556	22443	0.98	0.0E+00	BE794984.1	EST_HUMAN	601500629F1 NH1.MGC.7 Homo sapiens cDNA clone IMAGE:3943597 5'
2698	12562	22452	3.99	0.0E+00	U68293.1	NT	Human beta-prime-agglutinin (BAM22) gene, exon 5

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2700	12684	22454	1.08	0.0E+00	7069517	NT	Homo sapiens neuregulin 1 (NRG1) transcript variant SMDP, mRNA
2701	12685	22455	10.23	0.0E+00	AF110783.1	NT	Homo sapiens skeletal muscle LIM protein 1 (PHL1) gene, complete cds
2708	12671	22462	10.37	0.0E+00	BE776876.1	EST_HUMAN	H015018921 F1H1.MGC_7 Homo sapiens cDNA clone IMAGE:3946853 5'
2709	12672	22463	3.2	0.0E+00	BF090632.1	EST_HUMAN	002105923 F1H1.MGC_83 Homo sapiens cDNA clone IMAGE:4287132 5'
2712	12731	22467	13.51	0.0E+00	BE569433.1	EST_HUMAN	001335485 F1H1.MGC_39 Homo sapiens cDNA clone IMAGE:3089564 5'
2713	12675		1.28	0.0E+00	AV721647.1	EST_HUMAN	AV721647 HTB Homo sapiens cDNA clone HTB57E09 5'
2716	12677	22470	2.17	0.0E+00	5174469	NT	Homo sapiens spermatogenesis associated PD1 (KIA03757) mRNA
2716	12677	22471	2.17	0.0E+00	5174469	NT	Homo sapiens spermatogenesis associated PD1 (KIA03757) mRNA
2716	12678	22473	0.9	0.0E+00	8623441	NT	Homo sapiens hypodermal protein FLJ20477 (FLJ20477), mRNA
2717	12679	22474	2.2	0.0E+00	8623441	NT	Homo sapiens hypodermal protein FLJ20477 (FLJ20477), mRNA
2718	12680		15.87	0.0E+00	AF200195.1	EST_HUMAN	AV051006 GLC Homo sapiens cDNA clone GLCGLD07 3'
2719	12681	22475	1.72	0.0E+00	AF651066.1	EST_HUMAN	GM1-TN0141-350900-439-b08 TN0141 Homo sapiens cDNA
2719	12681	22476	1.72	0.0E+00	BF377897.1	EST_HUMAN	GM1-TN0141-350900-439-b08 TN0141 Homo sapiens cDNA
2723	12685	22479	3.21	0.0E+00	4757983	NT	Homo sapiens cerebellar degeneration-related protein (34C) (GDR1) mRNA
2723	12685	22480	3.21	0.0E+00	4757983	NT	Homo sapiens cerebellar degeneration-related protein (34C) (GDR1) mRNA
2727	12686	22485	2.2	0.0E+00	BE747163.1	EST_HUMAN	601589032 F1H1.MGC_9 Homo sapiens cDNA clone IMAGE:3829472 5'
2730	12692	22488	0.97	0.0E+00	BE176936.1	EST_HUMAN	RC4-H10592-70300-012-411 HT0587 Homo sapiens cDNA
2741	12693		1.3	0.0E+00	AL153931.2	NT	Homo sapiens chromosome 21, segment HS21C091
2742	12694	22488	3.47	0.0E+00	BF551410.1	EST_HUMAN	U1-HBN7 Homo e-07 QUILTY1 NCL CGAP_5367 Homo sapiens cDNA clone IMAGE:3071940 3'
2743	12610		1.07	0.0E+00	4630068	NT	Homo sapiens chromosome 21, segment HS21C091
2744	12610	22507	4.95	0.0E+00	BF577684.1	EST_HUMAN	Homo sapiens chondrin sulfate proteoglycan 4 (mednoma-associated) (CSPG4), mRNA
2758	12620	22513	1.73	0.0E+00	7427622	NT	00205793 F1H1.MGC_83 Homo sapiens cDNA clone IMAGE:426916 5'
2761	12623	22515	9.86	0.0E+00	AV755834.1	EST_HUMAN	Homo sapiens protein tyrosine phosphatase, receptor type, 1 (PTPR1), mRNA
2761	12623	22516	9.86	0.0E+00	AV755834.1	EST_HUMAN	AV755834 H1C Homo sapiens cDNA clone HTCC0303 5'
2763	12625		11.16	0.0E+00	AF879163.1	EST_HUMAN	af85504.1y1 Schmidt fetal brain 00004 Homo sapiens cDNA clone IMAGE:2018003 5' similar to SW-RT3A, HUMAN P4029 605 REBOSOMAL PROTEIN L31a ;
2768	12628	22621	1.87	0.0E+00	BF550061.1	EST_HUMAN	00207195 F1H1.MGC_3967 Homo sapiens cDNA clone IMAGE:4214678 5'
2767	12629	22622	2.81	0.0E+00	BE372783.1	EST_HUMAN	00145992 F1H1.MGC_85 Homo sapiens cDNA clone IMAGE:3884642 5'
2769	12631	22623	1.11	0.0E+00	AF131641.1	EST_HUMAN	AU131484 HT29P3 Homo sapiens cDNA clone N72RP03002672 5'
2769	12631	22624	1.11	0.0E+00	AF131641.1	EST_HUMAN	AU131484 HT29P3 Homo sapiens cDNA clone N72RP03002672 5'
2770	12632	22626	10.1	0.0E+00	BE300344.1	EST_HUMAN	00084704 F1H1.MGC_17 Homo sapiens cDNA clone IMAGE:2950906 5'
2770	12632	22626	10.1	0.0E+00	BE300344.1	EST_HUMAN	00084704 F1H1.MGC_17 Homo sapiens cDNA clone IMAGE:2950906 5'
2775	10151	18966	4.6	0.0E+00	S76830.1	NT	glycocalyx D-Duffy group antigen [human, blood, Genomic DNA, 3088 nt]

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Probe SEQ ID NO.	Exon ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) BLAST E Value	Top HR Accession No.	Top Hit Database Source	Top Hit Descriptor
2778	12638		1.94	0.0E+00	AB033281.1	NT	Homo sapiens BTG2P 2 mRNA for F-box and WD-repeats protein isoform C, complete cds
2784	10649	20479	1.37	0.0E+00	AF294750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
2784	10649	20480	1.37	0.0E+00	AF294750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
2789	10841	20784	3.89	0.0E+00	4503202	NT	Homo sapiens cytochrome P450, subfamily (dioxin-inducible), polypeptide 1 (glaucoma 3, primary infantile) (CYP1B1) mRNA
2789	10841	20785	3.89	0.0E+00	4503202	NT	Homo sapiens cytochrome P450, subfamily (dioxin-inducible), polypeptide 1 (glaucoma 3, primary infantile) (CYP1B1) mRNA
2805	12735	22584	2.39	0.0E+00	X65690.1	NT	H sapiens serine hydroxymethyltransferase pseudogene
2805	12736		1.27	0.0E+00	AF066524.1	NT	Homo sapiens 5-aminolevulinic synthase 2 (ALA2) gene, complete cds
2808	12738		1.1	0.0E+00	AB010900.1	NT	Homo sapiens mRNA for KIAA1827 protein, partial cds
2814	12743		1.07	0.0E+00	AJ236852.1	NT	Homo sapiens partial p8 gene for ribosomal protein L3, U62 snRNA, U8a snRNA and U83b snRNA genes
2815	12744	22588	2.24	0.0E+00	AL183301.2	NT	Homo sapiens chromosome 21 segment HS21C001
2819	12748	22581	5.54	0.0E+00	X65920.1	NT	Human HNRNAK nucleoprotein mRNA, 5' end
2822	12751	22543	1.86	0.0E+00	BE154504.1	EST_HUMAN	P40-170343-281298-038-402 HT0343 Homo sapiens cDNA
2822	12751	22544	1.86	0.0E+00	BE154504.1	EST_HUMAN	P40-170343-281298-038-402 HT0343 Homo sapiens cDNA
2824	12753		1.39	0.0E+00	X74236.1	NT	H sapiens l38 gene for HJ1 type transcription factor
2830	12759		2.84	0.0E+00	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C088
2833	12757	22547	2.88	0.0E+00	X68475.1	NT	Human transglutaminase mRNA, complete cds
2833	12757	22551	43.46	0.0E+00	X50057.1	NT	Homo sapiens gamma-globulin chain (AC) (G-3) pseudogene
2833	12761	22552	43.46	0.0E+00	X50057.1	NT	Homo sapiens gamma-globulin chain (AC) (G-3) pseudogene
2837	12768	22556	1.34	0.0E+00	AL066957.1	NT	Novel human mRNA from chromosome 1, which has similarities to SK12 genes
2838	12768		4.82	0.0E+00	Y10066.1	NT	H sapiens mRNA for nuclear DNA helicase II
2839	12767		0.86	0.0E+00	AF12303.1	NT	Homo sapiens proteasome alpha C1 (PC4H-alpha-C1) mRNA, complete cds
2840	12768	22556	25.08	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
2840	12768	22557	25.08	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
2851	12779	22568	2.42	0.0E+00	4507280	NT	Homo sapiens serine/threonine kinase 9 (STK9) mRNA
2851	12782	22572	1.35	0.0E+00	AL047599.1	EST_HUMAN	DKF7J696C0021.11 992 (cyonym: huter) Homo sapiens cDNA clone DKF7J696C0021
2855	12783	22573	1.25	0.0E+00	7891883	NT	Homo sapiens KIAA0054 gene product: Helicase (KIAA0054), mRNA
2855	12783	22574	1.25	0.0E+00	7891883	NT	Homo sapiens KIAA0054 gene product: Helicase (KIAA0054), mRNA
2859	12784		3.42	0.0E+00	BE091890.1	EST_HUMAN	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
2859	12786	22576	4.95	0.0E+00	BE091890.1	EST_HUMAN	QV22570595-130400-138-103 BT0538 Homo sapiens cDNA
2859	12786	22577	4.95	0.0E+00	BE091890.1	EST_HUMAN	QV22570595-130400-138-103 BT0538 Homo sapiens cDNA
2866	12794	22586	1.54	0.0E+00	AL183203.2	NT	Homo sapiens chromosome 21 segment HS21C096

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2866	12704	22580	1.94	0.0E+00	AL1183206.2	NT	Homo sapiens chromosome 21 segment: HS21C006 zr08111.x1 NOL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:383517 3' similar to contains A1u repetitive element;
2867	12705	22580	1.08	0.0E+00	AA215579.1	EST_HUMAN	
2871	12801	22560	3.00	0.0E+00	U192410.1	NT	Homo sapiens HH5 gene for hair keratin, exons 1 to 9
2877	12804	22560	1.16	0.0E+00	4756279	NT	Homo sapiens ERNA4 (EPHA4) mRNA
2878	12805	22200	18.06	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
2879	12805	22501	1.25	0.0E+00	AE561002.1	EST_HUMAN	U18407.x1 NOL_CGAP_Bn25 Homo sapiens cDNA clone IMAGE:2167261 3' similar to TRC16247 O16247 F4E7.2 PROTEIN ;
2879	12805	22502	1.25	0.0E+00	AE561002.1	EST_HUMAN	U18407.x1 NOL_CGAP_Bn25 Homo sapiens cDNA clone IMAGE:2167261 3' similar to TRC16247 O16247 F4E7.2 PROTEIN ;
2881	12808	22604	1.87	0.0E+00	P52740	SWISSPROT	ZINC FINGER PROTEIN 132
2882	12809	22595	1.5	0.0E+00	AF163238.1	NT	Homo sapiens proteoglycan gamma C4 (PGC4-gamma-C4) mRNA, complete cds
2887	12824	22577	1.34	0.0E+00	AF163238.1	NT	Homo sapiens mRNA for KIAA1267 protein, partial cds
2888	12825	22579	1.34	0.0E+00	AF163238.1	NT	Homo sapiens mRNA for KIAA1267 protein, partial cds
2888	12825	22579	4.98	0.0E+00	AB040941.1	NT	Homo sapiens mRNA for KIAA1598 protein, partial cds
2888	12825	22579	4.98	0.0E+00	AB040941.1	NT	Homo sapiens mRNA for KIAA1598 protein, partial cds
2901	12828	22623	2.66	0.0E+00	7661903	NT	Homo sapiens KIAA100 gene product (KIAA100), mRNA
2901	12828	22624	2.66	0.0E+00	7661903	NT	Homo sapiens KIAA100 gene product (KIAA100), mRNA
2902	12829	22625	3.23	0.0E+00	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (t(11hox); (Drosophila) homolog); translocated to 4 (MLL1) mRNA
2902	12829	22626	3.23	0.0E+00	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (t(11hox); (Drosophila) homolog); translocated to 4 (MLL1) mRNA
2907	12833	22630	1.27	0.0E+00	BF110702.1	EST_HUMAN	7n4003.x1 NOL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3867028 3' similar to TRQ9V/LN1 Q9V/LN1 CG17258 PROTEIN ;
2907	12833	22631	1.27	0.0E+00	BF110702.1	EST_HUMAN	7n4003.x1 NOL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3867028 3' similar to TRQ9V/LN1 Q9V/LN1 CG17258 PROTEIN ;
2907	12833	22631	1.27	0.0E+00	BF110702.1	EST_HUMAN	7n4003.x1 NOL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3867028 3' similar to TRQ9V/LN1 Q9V/LN1 CG17258 PROTEIN ;
2915	12842	22642	2.03	0.0E+00	4500084	NT	Homo sapiens melanoma antigen, family B, 4 (MAGEB4), mRNA
2915	12842	22643	2.03	0.0E+00	4500084	NT	Homo sapiens melanoma antigen, family B, 4 (MAGEB4), mRNA
2917	12844	22646	0.84	0.0E+00	4893214	NT	Homo sapiens verb-a avian erythroblastic leukemia viral oncogene homolog-like 4 (ERBB4) mRNA
2917	12844	22646	0.84	0.0E+00	4893214	NT	Homo sapiens verb-a avian erythroblastic leukemia viral oncogene homolog-like 4 (ERBB4) mRNA
2924	12851	22651	1.6	0.0E+00	4759827	NT	Homo sapiens neurotin III (NRXN3) mRNA
2924	12851	22651	1.6	0.0E+00	X15306.1	NT	H sapiens NF-H gene, exon 4
2927	12854	22655	1.3	0.0E+00	X15306.1	NT	H sapiens NF-H gene, exon 4
2927	12854	22655	1.3	0.0E+00	X15306.1	NT	H sapiens NF-H gene, exon 4
2929	12856	22657	7.93	0.0E+00	AI-105275.1	NT	Homo sapiens immunoglobulin-like transcript 1c variant 1c (LT1c) gene, exon 6

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Mean Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2943	12670		1.13	0.0E+00	AF148860.1	EST_HUMAN	gfr3r39.AT Soares, testis_NHT Homo sapiens cDNA clone IMAGE1752909 3'
2952	12678	22677	0.84	0.0E+00	AF1261074.1	NT	Homo sapiens neurtropin 2 (NR2P2) gene, complete cds, alternatively spliced
2952	12678	22678	0.84	0.0E+00	AF1261074.1	NT	Homo sapiens neurtropin 2 (NR2P2) gene, complete cds, alternatively spliced
2953	12680	22679	0.97	0.0E+00	4506118	NT	Homo sapiens prosopo-related homeobox 1 (PROX1) mRNA
2954	12681	22680	2.15	0.0E+00	A3004694.1	NT	Homo sapiens mRNA for PKU-alpha, partial cds
2954	12691	22680	1.33	0.0E+00	7662273	NT	Homo sapiens KIA00797 gene product (KIA00797), mRNA
2955	12692	22690	1.39	0.0E+00	5729755	NT	Homo sapiens calcium channel, voltage-dependent, gamma subunit 3 (CACNG3), mRNA
2955	12692	22691	1.59	0.0E+00	5729755	NT	Homo sapiens calcium channel, voltage-dependent, gamma subunit 3 (CACNG3), mRNA
2956	12616		0.99	0.0E+00	AF1463468.2	NT	Homo sapiens chromosome 21 segment HS21C0946
2957	12620	22714	1.04	0.0E+00	AF4998.1	NT	Human displacement protein (GCAAT) mRNA
3001	12626	22721	0.82	0.0E+00	4506983	NT	Homo sapiens anion channel (SEMG1) mRNA
3008	12634		4.85	0.0E+00	AF185963.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
3009	12637	22730	7.88	0.0E+00	AF199395.1	NT	Homo sapiens beta shock 7000 protein 1 (HSPX1A), mRNA
3009	12637	22731	7.88	0.0E+00	4579469	NT	Homo sapiens beta shock 7000 protein 1 (HSPX1A), mRNA
3011	12639		5.08	0.0E+00	AF135943.1	NT	Upform 2 of a novel human mRNA from chromosomes 22
3014	12642	22735	2.02	0.0E+00	AF017453.1	NT	Homo sapiens putative transcription factor CR3 (CR3) mRNA, partial cds
3017	12645		1.74	0.0E+00	AF190779.1	NT	Homo sapiens transcription factor GCM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, complete cds, and L-type calcium channel α_2
3019	12647	22739	0.99	0.0E+00	AF190779.1	NT	Homo sapiens transcription factor GCM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, complete cds, and L-type calcium channel α_2
3038	12666	22760	2.79	0.0E+00	X05526.1	NT	Homo sapiens interleukin 2 receptor, beta (IL2RB) mRNA
3043	12670		1.85	0.0E+00	AF199395.1	NT	Homo sapiens gene 16.1 for Ig lambda L-chain C region (Ig-L16.1)
3047	12674	22767	1.89	0.0E+00	AF064599.1	NT	Homo sapiens F-box protein FBL3 (FBL3) mRNA, complete cds
3088	12695	22768	2.85	0.0E+00	AF265298.1	NT	Homo sapiens melanoma-associated antigen (MAGE-G1) gene, complete cds
3099	12696	22767	3.97	0.0E+00	AF146973.1	NT	Homo sapiens SWI SNF complex protein p270 mRNA, partial cds
3074	13001	22781	4.21	0.0E+00	7662138	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
3075	13002	22782	1.64	0.0E+00	AF02075.1	NT	Homo sapiens KIA00469 gene product (KIA00469), mRNA
3102	13026	22824	3.45	0.0E+00	4620769	NT	Homo sapiens olfactory receptor-like protein (OLFR_422) gene, OLFR_42B-9110 allele, partial cds
3111	13036	22832	10.64	0.0E+00	L20941.1	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCMB1) mRNA
3115	13040	22836	1.79	0.0E+00	AB011121.1	NT	Homo sapiens mRNA for KIA03549 protein, partial cds
3115	13040	22837	1.79	0.0E+00	AB011121.1	NT	Homo sapiens mRNA for KIA03549 protein, partial cds
3123	13048	22845	8.41	0.0E+00	T84870.1	EST_HUMAN	yes2026.31 Stragene lung (8637210) Homo sapiens cDNA clone IMAGE:19453 3' similar to SP S29539 S29539 BASIC PROTEIN, 28k -

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Table 4

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Probe SEQ ID NO:	Exon NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3138	13063	22862	1.1	0.0E+00	BF243336.1	EST_HUMAN	0018750071 NH1_MGC_55 Homo sapiens cDNA clone IMAGE:4107433 6
3140	13065	22863	1.03	0.0E+00	AI898048.1	EST_HUMAN	wtd12h10.x1 NC1_COAP_G06 Homo sapiens cDNA clone IMAGE:2416803 3'
3145	13070	22870	3.99	0.0E+00	X98622.1	EST	H sapiens mRNA for gamma-glutamyltransferrase
3145	13070	22871	3.99	0.0E+00	X98622.1	NT	H sapiens mRNA for gamma-glutamyltransferrase
3150	13081	22883	1.5	0.0E+00	4785827	NT	Homo sapiens neurexin II (NRXN2) mRNA
3150	13081	22884	1.5	0.0E+00	4785827	NT	Homo sapiens neurexin II (NRXN2) mRNA
3163	13088	22892	7.73	0.0E+00	4504658	NT	Homo sapiens interleukin 1 receptor, type I (IL1R1) mRNA
3164	13089	22893	3.26	0.0E+00	4507726	NT	Homo sapiens titin (TTN) mRNA
3164	13089	22894	3.26	0.0E+00	4507726	NT	Homo sapiens titin (TTN) mRNA
3180	13105	22910	2.44	0.0E+00	M28956.1	NT	Homo sapiens nuclear phosphogluconate 625 (NPG1) mRNA, complete cds
3183	13108	22912	2.23	0.0E+00	4520268	NT	Homo sapiens sdc1a family 25 (mitochondrial carrier, adenosine nucleoside translocator), member 6 (SLC26A5), nuclear gene encoding mitochondrial protein, mRNA
3188	13113	22918	0.82	0.0E+00	4758065	NT	Homo sapiens CREB binding protein (Rb1/CREB1) mRNA
3188	13113	22919	0.82	0.0E+00	4758065	NT	Homo sapiens CREB binding protein (Rb1/CREB1) mRNA
3190	13116	22920	28.3	0.0E+00	AA747483.1	EST_HUMAN	00187511 x1 Shikayama schizo brain S11 Homo sapiens cDNA clone IMAGE:971103 3'
3198	13123	22928	4.93	0.0E+00	AF266583.1	NT	Homo sapiens angiotensin binding protein 1 mRNA, complete cds
3198	13123	22929	4.93	0.0E+00	AF266583.1	NT	Homo sapiens angiotensin binding protein 1 mRNA, complete cds
3210	13154	22948	1.56	0.0E+00	4557632	NT	Homo sapiens titin (TTN) mRNA
3215	13158	22942	3.35	0.0E+00	4507726	NT	Homo sapiens titin (TTN) mRNA
3224	13148		4.39	0.0E+00	M65183.1	NT	Human common 45 increased pseudogene
3225	13149	22949	1.19	0.0E+00	AF010413.1	NT	Homo sapiens HLA class II region containing translocase X (translocase-X) gene, partial cds; cyclochrome P450 21C hydroxylase (CYP21B), complement component C4 (C4B) G11, hallease (SM2X), ND, complement factor B (B), and complement component C2 (C2) genes, >
3227	13151	22951	4.15	0.0E+00	AF050694.1	NT	Homo sapiens very large G-protein coupled receptor-1 (VLCGR1) mRNA, complete cds
3237	13066	22959	3.48	0.0E+00	4520141	NT	Homo sapiens A kinase (PKA) anchor protein 1 (AKAP1), mRNA
3237	13066	22960	3.48	0.0E+00	4520141	NT	Homo sapiens A kinase (PKA) anchor protein 1 (AKAP1), mRNA
3252	13175	22973	2	0.0E+00	AF265503.1	NT	Homo sapiens SW1SNF complex protein p70 mRNA, partial cds
3253	13176	22974	0.89	0.0E+00	8923629	NT	Homo sapiens histone H4 protein FLJ20096 (FLJ20096), mRNA
3282	13203	23003	4.86	0.0E+00	AI850394.1	EST_HUMAN	H5808.32 NC1_COAP_Phen1 Homo sapiens cDNA clone IMAGE:2222836 3' similar to SW-RL11, RAT
3289	13211	23011	2.98	0.0E+00	AF128893.1	NT	P25121 G05 RIBOSOMAL PROTEIN L11, contains A19 repetitive element
3289	13211	23012	2.98	0.0E+00	AF128893.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-6
3290	13212	23013	1	0.0E+00		NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-6
3290	13212	23014	1	0.0E+00	7657213	NT	Homo sapiens homonally upregulated neu tumor-associated kinase (HUNK), mRNA
3290	13212	23014	1	0.0E+00	7657213	NT	Homo sapiens homonally upregulated neu tumor-associated kinase (HUNK), mRNA

Table 4

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Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3440	13357	23103	2.06	0.0E+00	AF045492.1	NT	Homo sapiens cell-line KG1 transcriptional regulatory protein p54 mRNA, complete cds
3440	13357	23164	2.06	0.0E+00	AF045492.1	NT	Homo sapiens cell-line KG1 transcriptional regulatory protein p54 mRNA, complete cds
3448	13365	23172	1.23	0.0E+00	AF291022.1	NT	Homo sapiens chromosome 21 unknown mRNA
3450	13371	23175	0.94	0.0E+00	AA626677.1	EST_HUMAN	ab31112.1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE 844367 5'
3455	13371	23175	0.94	0.0E+00	AA626677.1	EST_HUMAN	ab31112.1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE 844367 5'
3455	13371	23177	0.94	0.0E+00	AA626677.1	EST_HUMAN	ab31112.1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE 844367 5'
3458	13374	23180	1.11	0.0E+00	4508028	NT	Homo sapiens zinc finger protein 45 (a Kruppel-associated box (KRAB) domain polypeptide) (ZNF45) mRNA
3461	13377	23182	2.23	0.0E+00	BE304791.1	EST_HUMAN	001143333F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE 3051373 5'
3461	13377	23183	2.23	0.0E+00	BE304791.1	EST_HUMAN	001143333F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE 3051373 5'
3465	13378	23186	1.45	0.0E+00	4820769	NT	Homo sapiens potassium voltage-gated channel, likely related family, member 2 (KCNE2) mRNA
3470	13386	23191	0.92	0.0E+00	AB364007.1	EST_HUMAN	ic9512.1 Soares NIHMPU_S1 Homo sapiens cDNA clone IMAGE 2088742 3' similar to TR-000468
3473	13388	23194	0.95	0.0E+00	MT0276.1	NT	004468 MYASTHENIA GRAVIS AUTOANTIGEN GRAVIN
3485	13412	23217	0.92	0.0E+00	4820884	NT	Homo sapiens retroviral DNA (L1), complete retroviral segment
3487	13414	23217	1.15	0.0E+00	AF070886.1	NT	Homo sapiens homologous yeast-41.3 protein mRNA, complete cds
3503	13422	23226	1.38	0.0E+00	AL 03204.1	NT	Novel human gene encoding chromosome X
3507	13423	23226	0.95	0.0E+00	AB043068.1	NT	Homo sapiens mRNA for RALX4170 protein, partial cds
3527	13443		0.98	0.0E+00	AB01807.1	EST_HUMAN	007611.1 Soares NIHMPU_S1 Homo sapiens cDNA clone IMAGE 1923566 3' similar to WP11684.4
3528	13443	23242	1.26	0.0E+00	6329463	NT	Homo sapiens butyrophilin, subfamily 3, member A3 (BTN3A3) mRNA
3533	13449		4.93	0.0E+00	AW852717.1	EST_HUMAN	Q1047-02255-200003-166-001 C10225 Homo sapiens cDNA
3540	13456		0.95	0.0E+00	AF110846.1	NT	Homo sapiens gamma-glutamylcysteine synthetase (GLC1) gene, partial cds
3541	13457	23250	7.43	0.0E+00	BF676393.1	EST_HUMAN	002084839F1 NIH_MGC_381 Homo sapiens cDNA clone IMAGE-3246866 5'
3554	13478		1.11	0.0E+00	4820697	NT	Homo sapiens retinol-binding protein 2 (RBP2) mRNA
3566	13480	23266	0.98	0.0E+00	AW004063.1	EST_HUMAN	H84601.1 Soares NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE 2979024 3'
3566	13480	23270	0.98	0.0E+00	AW004063.1	EST_HUMAN	H84601.1 Soares NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE 2979024 3'
3568	13483	23274	1.13	0.0E+00	4820763	NT	Homo sapiens heparan sulfate (glycosaminoglycan) 3-O-sulfotransferase 1 (HS3ST1) mRNA
3571	13485	23277	0.98	0.0E+00	76022319	NT	Homo sapiens KIA0060 gene product (KIA0060), mRNA
3578	13492	23282	0.78	0.0E+00	4557752	NT	Homo sapiens midline 1 (ChazBBB syndrome) (MID1) mRNA
3578	13492	23283	0.78	0.0E+00	4557752	NT	Homo sapiens midline 1 (ChazBBB syndrome) (MID1) mRNA
3596	13510	23297	1.91	0.0E+00	D87327.1	NT	Homo sapiens mRNA for G protein-coupled inward rectifier potassium channel, complete cds
3600	13514		28.67	0.0E+00	7693467	NT	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GAPD) mRNA
3616	13530	23316	4.26	0.0E+00	AB026542.1	NT	Homo sapiens WAVE2 mRNA for WASP-family protein, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3619	13533	23318	3.26	0.0E+00	AF124280.1	NT	Homo sapiens SH2-containing protein Nap2 mRNA, complete cds
3619	13533	23318	3.26	0.0E+00	AF124280.1	NT	Homo sapiens SH2-containing protein Nap2 mRNA, complete cds
3623	13537	23323	1.5	0.0E+00	AA952743.1	EST_HUMAN	NHTBCae15g091 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBCae15g09
3623	13537	23324	1.5	0.0E+00	AA952743.1	EST_HUMAN	NHTBCae15g091 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBCae15g09
3626	13540	23326	2.2	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
3626	13540	23327	2.2	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
3630	13544	23331	1.70	0.0E+00	5728628	NT	Homo sapiens matrix metalloproteinase 24 (membrane-anchored) (MMP24), mRNA
3632	13546	23333	1.25	0.0E+00	AB918339.1	NT	Homo sapiens mRNA for KIAA0766 protein, partial cds
3645	13559	23344	3.53	0.0E+00	AF129134.1	EST_HUMAN	UH-HBW0-96-5-12.0.U1.s1 NCL CGAP_S105 Homo sapiens cDNA clone IMAGE:2733022.3
3645	13559	23345	3.53	0.0E+00	AF129134.1	EST_HUMAN	UH-HBW0-96-5-12.0.U1.s1 NCL CGAP_S105 Homo sapiens cDNA clone IMAGE:2733022.3
3668	13582	23359	0.99	0.0E+00	AF014630.1	NT	Human gene for Type XIX collagen of chitin, exon 8
3669	13583	23370	1.03	0.0E+00	AA463655.1	EST_HUMAN	SV-KRBL1_SHEEP_P2045 KEBAITIN, HIGH-SULFUR MATRIX PROTEIN [JBA 11]
3677	13591	23377	3.35	0.0E+00	7637468	NT	Homo sapiens similar to rat integral membrane glycoprotein POMT21 (POM121L1), mRNA
3687	13601	23387	0.91	0.0E+00	AF037895.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
3689	13603	23397	3.88	0.0E+00	7602183	NT	Homo sapiens ribosomal protein S2 (RP-S2) mRNA
3701	13615	23399	7.88	0.0E+00	4956718	NT	Homo sapiens x-ata avian erythroblast virus E28 oncogene related (ERO), mRNA
3705	13618	23401	1.02	0.0E+00	7657065	NT	Homo sapiens soluble neuropilin-1 mRNA, complete cds
3705	13618	23402	1.02	0.0E+00	7657065	NT	Homo sapiens soluble neuropilin-1 mRNA, complete cds
3745	13658	23441	1.13	0.0E+00	AF145712.1	NT	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds
3747	13660	23442	1.01	0.0E+00	AF165055.1	NT	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds
3748	13661	23442	2.3	0.0E+00	AF179733.1	NT	Human gene for Type XIX collagen of chitin, exon 8
3751	13664	23446	1.66	0.0E+00	7657468	NT	Human gene for Type XIX collagen of chitin, exon 8
3751	13664	23447	1.66	0.0E+00	7657468	NT	Human gene for Type XIX collagen of chitin, exon 8
3752	13665	23448	1.45	0.0E+00	AF020091.1	NT	Homo sapiens similar to rat integral membrane glycoprotein POMT21 (POM121L1), mRNA
3759	13659	23453	1.1	0.0E+00	1018138	NT	Homo sapiens smooth muscle myosin heavy chain SM1 mRNA, alternatively spliced, partial cds
3758	13671	23455	1.7	0.0E+00	AF162460.1	EST_HUMAN	Mus musculus junctophilin 1 (jpl-pending), mRNA
3759	13672	23456	1.7	0.0E+00	AF162460.1	EST_HUMAN	hcs570.X1 Scores: NFI_1_GBC, S1 Homo sapiens cDNA clone IMAGE:2061307.3
3760	13673	23456	4.45	0.0E+00	4759196	NT	Homo sapiens protofibrin beta 3 (PCOH-beta3) mRNA, complete cds
3760	13673	23456	4.45	0.0E+00	4759196	NT	Homo sapiens desmoplamin (DPL, DPL1) (DSP) mRNA
3763	13675	23459	11.57	0.0E+00	S76595.1	NT	Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ6/BIR1) gene, complete cds
3764	13677	23459	2	0.0E+00	7710148	NT	Homo sapiens methyl CpG binding protein 2 (MECP2), mRNA

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Probe SEQ ID NO:	Exon NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) HITE BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3893	13803	23587	4.6	0.0E+00	AF116195.1	NT	Homo sapiens cancer-testis antigen CT10 (CT10) gene, complete cds
3893	13803	23586	4.6	0.0E+00	AF116195.1	NT	Homo sapiens cancer-testis antigen CT10 (CT10) gene, complete cds
3893	13813	23586	3.03	0.0E+00	M23910.1	NT	Human MHC class II lymphocyte antigen DP- α -beta-2 pseudogene, exon 2
3905	13815	23603	5.44	0.0E+00	AL163303.2	NT	Human chromosome 21 segment HS21C103
3912	13822	23603	1.33	0.0E+00	AL118494.1	NT	Novel human gene mapping to chromosome 20
3916	13825	23605	2.85	0.0E+00	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C084
3924	13833	23613	1.46	0.0E+00	AL163308.2	NT	Homo sapiens chromosome 21 segment HS21C084
3935	13844	23623	25.75	0.0E+00	4593470	NT	Homo sapiens chromosome 21 segment HS21C084
3939	13847	23623	1.18	0.0E+00	7092163	NT	Homo sapiens chromosome 21 segment HS21C084
3940	13848	23624	2.05	0.0E+00	U99368.1	NT	Homo sapiens chromosome 21 segment HS21C084
3940	13848	23624	6.34	0.0E+00	AB015610.1	NT	Homo sapiens chromosome 21 segment HS21C084
3968	13875	23645	3.70	0.0E+00	A1236517.1	NT	Human zinc finger protein ZNF153
3976	13883	23648	3.28	0.0E+00	A2727276.1	NT	Human zinc finger protein ZNF153
3976	13883	23648	3.28	0.0E+00	A2727276.1	NT	Human zinc finger protein ZNF153
3981	13888	23653	5.93	0.0E+00	5632228	NT	Human zinc finger protein ZNF153
3981	13888	23654	5.93	0.0E+00	5632228	NT	Human zinc finger protein ZNF153
3983	13900	23677	0.81	0.0E+00	4593514	NT	Human zinc finger protein ZNF153
4000	13906	23682	4.86	0.0E+00	4865598	NT	Human zinc finger protein ZNF153
4001	13907	23683	1.94	0.0E+00	A5008625.1	NT	Human zinc finger protein ZNF153
4003	13908	23684	1.28	0.0E+00	4759607	NT	Human zinc finger protein ZNF153
4004	13910	23685	6.1	0.0E+00	11419207	NT	Human zinc finger protein ZNF153
4005	13911	23686	1.58	0.0E+00	AL006557.1	NT	Human zinc finger protein ZNF153
4013	13916	23685	2.7	0.0E+00	AF165527.1	NT	Human zinc finger protein ZNF153
4017	15071	23687	0.85	0.0E+00	AF167476.1	NT	Human zinc finger protein ZNF153
4022	11031	23672	0.8	0.0E+00	4826917	NT	Human zinc finger protein ZNF153
4022	11031	23673	0.8	0.0E+00	4826917	NT	Human zinc finger protein ZNF153
4028	13931	23707	0.99	0.0E+00	5001005	NT	Human zinc finger protein ZNF153
4029	13932	23708	1.16	0.0E+00	4590354	NT	Human zinc finger protein ZNF153
4029	13932	23708	1.16	0.0E+00	4590354	NT	Human zinc finger protein ZNF153
4032	13935	23711	1.05	0.0E+00	8022391	NT	Human zinc finger protein ZNF153
4032	13935	23712	1.05	0.0E+00	8022391	NT	Human zinc finger protein ZNF153
4041	13944	23722	4.59	0.0E+00	A1982597.1	EST	Human zinc finger protein ZNF153
4041	13944	23723	4.59	0.0E+00	A1982597.1	EST	Human zinc finger protein ZNF153

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4044	13646	23725	0.98	0.0E+00	BE164850.1	EST_HUMAN	MR1-HT0707-000500-001-402 HT0707 Homo sapiens cDNA
4044	13646	23726	0.98	0.0E+00	BE164850.1	EST_HUMAN	MR1-HT0707-000500-001-402 HT0707 Homo sapiens cDNA
4048	13650		1.99	0.0E+00	BE274217.1	EST_HUMAN	8011207781 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2957690 5'
4055	13657	23733	0.97	0.0E+00	4507476.NT		Homo sapiens transglutaminase 3 (E polypeptide, protein-glutamine-gamma-glutamyltransferase) (TGMS3) mRNA
4056	13659	23734	1.98	0.0E+00	5729725.NT		Homo sapiens sodium receptor coinductor 3 (NCOA3), mRNA
4064	13660		8.19	0.0E+00	AW675599.1	EST_HUMAN	ba51104.x1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2800095 3' similar to SW-TH2_BOVIN
4069	13671	23748	1.52	0.0E+00	AW408768.1	EST_HUMAN	Q96108 BTK-CHONDRIAL THOREDOXIN PRECURSOR
4071	13673	23761	1.33	0.0E+00	9522469.NT		ULF6-BTK-actc-02-03.U11 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3033147 5'
4071	13673	23761	1.33	0.0E+00	9522469.NT		Homo sapiens hypochelated protein FLJ10485 (FLJ10485) mRNA
4071	13673	23762	1.33	0.0E+00	9522469.NT		Homo sapiens hypochelated protein FLJ10485 (FLJ10485) mRNA
4081	13683		1.96	0.0E+00	5174632.NT		Homo sapiens polykaryotic kidney disease (polykaryotic) and REL (eparm receptor for egg jelly), see urchin homologue (PKOREL) mRNA
4086	13686	23775	7.92	0.0E+00	AA401438.1	EST_HUMAN	zfa9807.x1 Soares, Jutta, NIH Homo sapiens cDNA clone IMAGE:743197 3' similar to contains AU repetitive element; contains element MIER35 negative element
4086	13686	23776	7.92	0.0E+00	AA401438.1	EST_HUMAN	zfa9807.x1 Soares, Jutta, NIH Homo sapiens cDNA clone IMAGE:743197 3' similar to contains AU repetitive element; contains element MIER35 negative element
4113	14013	23781	3.79	0.0E+00	4507728.NT		Homo sapiens bin (TTN) mRNA
4113	14013	23782	3.79	0.0E+00	4507728.NT		Homo sapiens bin (TTN) mRNA
4128	14026	23801	0.97	0.0E+00	4505662.NT		Homo sapiens annexin I (SEUG1) mRNA
4130	14030	23803	8.21	0.0E+00	4739168.NT		Homo sapiens desmoplamin (DPI, DPPI) (DSP) mRNA
4130	14030	23804	8.21	0.0E+00	4739168.NT		Homo sapiens desmoplamin (DPI, DPPI) (DSP) mRNA
4137	14037		0.98	0.0E+00	AL163933.2	NT	Homo sapiens chromosome 21 segment HS21C103
4137	14037	23837	1.13	0.0E+00	AA063145.1	NT	Homo sapiens mRNA for olfactory receptor protein, pseudogene
4137	14037	23837	1.13	0.0E+00	AA063145.1	NT	Homo sapiens mRNA for olfactory receptor protein, pseudogene
4176	14076	23851	7.84	0.0E+00	U02670.1	EST_HUMAN	Human apolipoprotein B-100 mRNA, complete cds
4176	14076	23851	7.84	0.0E+00	U02670.1	EST_HUMAN	Human apolipoprotein B-100 mRNA, complete cds
4180	14090	23868	0.95	0.0E+00	AW193689.1	EST_HUMAN	PM2-DT1025-080500-004-408 DT1023 Homo sapiens cDNA
4186	14096	23876	0.98	0.0E+00	4928627.NT		Homo sapiens myotubular myopathy syndrome 1 (MOTST) mRNA
4186	14096	23876	0.98	0.0E+00	4928627.NT		Homo sapiens myotubular myopathy syndrome 1 (MOTST) mRNA
4186	14096	23877	0.98	0.0E+00	4928627.NT		Homo sapiens myotubular myopathy syndrome 1 (MOTST) mRNA
4186	14096	23879	5.73	0.0E+00	AF174590.1	NT	Homo sapiens F-box protein F34 (FBL4) mRNA, partial cds
4206	14105		1.92	0.0E+00	AF189844.1	EST_HUMAN	gd23003.x1 Soares, Jutta, NIH Homo sapiens cDNA clone IMAGE:1724679 3' similar to contains MER20 l2 MER20 repetitive element
4206	14105		1.92	0.0E+00	AF189844.1	EST_HUMAN	gd23003.x1 Soares, Jutta, NIH Homo sapiens cDNA clone IMAGE:1724679 3' similar to contains MER20 l2 MER20 repetitive element
4224	14122	23897	0.98	0.0E+00	U14520.1	NT	Human ORF43 (Cf6a3) gene, partial cds
4224	14122	23897	0.98	0.0E+00	4509640.NT		Homo sapiens proprotein convertase subtilisin/kexin type 2 (PCSK2) mRNA
4230	14128	23904	0.97	0.0E+00	6593384.NT		Homo sapiens protein kinase C, nu (PRKCN), mRNA

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Probe SEQ ID NO.	Exon ID NO.	ORF SEQ ID NO.	Expression Signal	Mean (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4230	14128	23905	0.87	0.0E+00	6553384	NT	Homo sapiens protein kinase C, α (PRCKC), mRNA
4237	14135	23911	1.77	0.0E+00	UT0091.1	NT	Human G2 protein mRNA, partial cds
4237	14135	23912	1.77	0.0E+00	UT0091.1	NT	Human G2 protein mRNA, partial cds
4245	14144	23917	10.2	0.0E+00	6912281	NT	Homo sapiens COMPLEMENT COMPONENT C1q RECEPTOR (CTQR), mRNA
4243	14162	23923	1.15	0.0E+00	AF13047.2	NT	Homo sapiens gip junction protein comsln-30 (CX30) gene, complete cds
4258	14167	23943	1.59	0.0E+00	J03801.1	NT	Human Ig light chain V L1 region germline (humV125) gene, partial cds
4274	14173	23950	5.77	0.0E+00	L14561.1	NT	Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds
4278	14177	23955	2.78	0.0E+00	Z0780.1	NT	H sapiens H2B3h gene
4278	14177	23956	2.78	0.0E+00	Z0780.1	NT	H sapiens H2B3h gene
4284	14183	23962	1.98	0.0E+00	X00463.1	NT	H sapiens H4d gene for H4 histone
4284	14183	23963	1.98	0.0E+00	X00463.1	NT	H sapiens H4d gene for H4 histone
4289	14187	23969	8.95	0.0E+00	7092091	NT	Homo sapiens KIAA0350 gene product (KIAA0350), mRNA
4290	14187	23970	8.95	0.0E+00	7092091	NT	Homo sapiens KIAA0350 gene product (KIAA0350), mRNA
4290	14187	23970	8.95	0.0E+00	7092091	NT	Homo sapiens KIAA0350 gene product (KIAA0350), mRNA
4292	14200	23984	10.31	0.0E+00	AB037781.1	NT	Homo sapiens caudal type homeo box transcription factor 4 (CDX4), mRNA
4292	14200	23984	10.31	0.0E+00	AB037781.1	NT	Homo sapiens caudal type homeo box transcription factor 4 (CDX4), mRNA
4330	14230	24012	1.11	0.0E+00	AF106683.1	NT	Homo sapiens myosin regulatory light chain flasecing protein (MIR), mRNA
4341	14238	24026	8.85	0.0E+00	AF106683.1	NT	Homo sapiens myosin regulatory light chain flasecing protein (MIR), mRNA
4346	14243	24026	8.11	0.0E+00	AF106683.1	NT	Homo sapiens myosin regulatory light chain flasecing protein (MIR), mRNA
4346	14243	24026	8.11	0.0E+00	AF106683.1	NT	Homo sapiens myosin regulatory light chain flasecing protein (MIR), mRNA
4398	14264	24051	1.52	0.0E+00	AF20025.1	NT	Homo sapiens ACTN2 gene for alpha-actinin 2, exon 10
4401	14290	24090	40.23	0.0E+00	AW064964.1	EST HUMAN	xb060601.1 NC_033497.2 Homo sapiens cDNA clone IMAGE2585446 3' similar to SW-6203 HUMAN Q60906 NEUROBLAST DIFFERENTIATION ASSOCIATED PROTEIN AHNAK ;
4403	15073		1.81	0.0E+00	8051619	NT	Homo sapiens LIM domain kinase 2 (LMK2), transcript variant 2a, mRNA
4405	14296	24093	1.38	0.0E+00	AF010690.1	NT	Homo sapiens vesicular endothelial cell growth factor 105 receptor/neuropilin (VEGFR165) mRNA, complete cds
4405	14296	24093	1.38	0.0E+00	AF010690.1	NT	Homo sapiens vesicular endothelial cell growth factor 105 receptor/neuropilin (VEGFR165) mRNA, complete cds
4408	14302		7.5	0.0E+00	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
4410	14304		1.29	0.0E+00	AW381970.1	EST HUMAN	PMH-HT0305-01169-002-403 HT0305 Homo sapiens cDNA
4411	14310	24067	1.29	0.0E+00	AW381970.1	NT	PMH-HT0305-01169-002-403 HT0305 Homo sapiens cDNA
4416	14310	24064	1.83	0.0E+00	AF1278120.1	NT	Homo sapiens mRNA for putative ankyrin-repeat containing protein (ORF1)
4416	14310	24066	1.83	0.0E+00	AF1278120.1	NT	Homo sapiens mRNA for putative ankyrin-repeat containing protein (ORF1)
4418	14312	24097	3.91	0.0E+00	4759487	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
4418	14312	24097	3.91	0.0E+00	4759487	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
4419	14313	24098	2.3	0.0E+00	AF106830.1	NT	Homo sapiens serine-threonine protein kinase (MNHR), complete cds
4424	14318	24104	1.47	0.0E+00	Z66202.1	NT	H sapiens pancreatic polypeptide receptor PP1 gene
4429	14324	24111	1.12	0.0E+00	S76884.1	NT	Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit 1 (KCNJ6BIR1) gene, exon

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4430	14325	24112	1.55	0.0E+00	AF111163.1	NT	Homo sapiens pyrin (MEFV) gene, complete cds
4430	14325	24113	1.55	0.0E+00	AF111163.1	NT	Homo sapiens pyrin (MEFV) gene, complete cds
4430	15074	24123	1.98	0.0E+00	6005973	NT	Homo sapiens zinc finger protein 165 (ZNF165), mRNA
4444	14338	24128	5.37	0.0E+00	AF208161.1	NT	Homo sapiens synovial precursor, mRNA, complete cds
4449	14343	24135	1.52	0.0E+00	AF152337.1	NT	Homo sapiens prothrombin gamma C3 (FODH-gamma-C3) mRNA, complete cds
4452	14346	24139	1.36	0.0E+00	5454175	NT	Homo sapiens zinc finger protein 211 (ZNF211), mRNA
4462	14356	24147	15.15	0.0E+00	493470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
4473	14367	24155	1.47	0.0E+00	4503096	NT	Homo sapiens chondroclatin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
4477	14371	24161	1.58	0.0E+00	4502568	NT	Homo sapiens calcium/calmodulin-dependent protein kinase IV (CAMK4) mRNA
4481	14375	24161	2.78	0.0E+00	L35485.1	NT	Homo sapiens dicarboxylate sulphotase (DS) gene, complete cds
4483	14377	24163	9.78	0.0E+00	7992061	NT	Homo sapiens KIA0390 gene product (KIA0390), mRNA
4483	14377	24164	9.78	0.0E+00	7992061	NT	Homo sapiens KIA0390 gene product (KIA0390), mRNA
4486	14382	24177	2.04	0.0E+00	AF143314.1	NT	Homo sapiens PTEN (PTEN) gene, exons 3 through 5
4500	14394	24179	8.97	0.0E+00	AF143314.1	NT	Homo sapiens mRNA for G7c protein (G7c gene located in the class III region of the major histocompatibility complex)
4500	14394	24180	8.97	0.0E+00	AJ245418.1	NT	Homo sapiens mRNA for G7c protein (G7c gene located in the class III region of the major histocompatibility complex)
4511	14404		0.34	0.0E+00	0387575.1	NT	Homo sapiens DNA for myoid precursor protein, complete cds
4523	14410		1.5	0.0E+00	AA1147472.1	EST_HUMAN	gp150h3.1 Shalogenus full (ref: 83722) Homo sapiens 3DUA clone IMAGE 30654.3
4528	14421		1.22	0.0E+00	7857449	NT	Homo sapiens cdc (cdi) O222m, Drosophila homolog 1 (ODZ1), mRNA
4528	14422	24205	1.71	0.0E+00	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4530	14423	24206	4.57	0.0E+00	AF164110.1	NT	Homo sapiens cytoplasmic-related protein (NKIR) gene, complete cds
4531	14424		1.89	0.0E+00	AB037521.1	NT	Homo sapiens chromosome 21 segment HS21C100
4541	14434	24216	1.91	0.0E+00	4557897	NT	Homo sapiens gene for matured protein, partial cds
4541	14434	24217	1.91	0.0E+00	4557897	NT	Homo sapiens keratin 18 (KRT18) mRNA
4542	14435	24218	1.3	0.0E+00	AF163919.1	NT	Homo sapiens inwardly-rectifying potassium channel Kir2.1 (KCNJ2) gene, exon 2 and complete cds
4542	14435	24219	1.3	0.0E+00	AF163919.1	NT	Homo sapiens inwardly-rectifying potassium channel Kir2.1 (KCNJ2) gene, exon 2 and complete cds
4543	14436	24220	1.18	0.0E+00	AF167441.1	NT	Mouse myosin E-cadherin binding protein E7 mRNA, complete cds
4554	14013	23751	7.43	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
4554	14013	23752	7.43	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
4560	14432	24238	21.96	0.0E+00	Y18850.1	NT	Human endogenous retrovirus type K (HERV-K), gag, pol and env genes

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4556	14458	24246	2.32	0.0E+00	BE081527.1	EST_HUMAN	QV2/ET06835-00490-142 hts BT06835 Homo sapiens cDNA
4574	14465		2.01	0.0E+00	AF096441.1	NT	Homo sapiens functional transmembrane (TM) (TM) genes, peritrichal and TMX gene recombination breakpoint region
4580	14470	24257	2.65	0.0E+00	AF0307620.1	NT	Homo sapiens mRNA for KIAA1369 protein, partial cds
4580	14470	24258	2.65	0.0E+00	AF0307620.1	NT	Homo sapiens mRNA for KIAA1369 protein, partial cds
4581	14471	24259	2.65	0.0E+00	M740369.1	NT	Human displacement protein (CDAN1) mRNA
4585	14474	24262	1.82	0.0E+00	6453812	NT	Homo sapiens tyroporin, subfamily 2, member A2 (BTN2A2), mRNA
4586	14474	24263	1.82	0.0E+00	6453812	NT	Homo sapiens tyroporin, subfamily 2, member A2 (BTN2A2), mRNA
4586	10108	19933	1.03	0.0E+00	U55945.1	EST_HUMAN	y5g04.122 <i>Staphylococcus aureus</i> (483/203) Homo sapiens cDNA clone IMAGE 68310 5'
4586	10108	19933	1.03	0.0E+00	U55945.1	EST_HUMAN	y5g04.122 <i>Staphylococcus aureus</i> (483/203) Homo sapiens cDNA clone IMAGE 68310 5'
4587	14475	24267	1.11	0.0E+00	AF18410.1	NT	60125693247 NH1 MGCC 44 Homo sapiens cDNA clone IMAGE3360321 8'
4590	14481	24281	3.78	0.0E+00	U606002.1	NT	Human ARHAK nucleoporin mRNA, 5' end
4591	14523	24290	3.14	0.0E+00	U609197.1	NT	Human haptoglobin and haptoglobin-related protein (HP and HPR) genes, complete cds
4591	14523	24290	3.14	0.0E+00	U609197.1	NT	Human haptoglobin and haptoglobin-related protein (HP and HPR) genes, complete cds
4591	14523	24294	3.14	0.0E+00	AF18410.1	NT	Homo sapiens cyclophilin-related protein (NCPR) genes, complete cds
4620	14505	24297	1.12	0.0E+00	AF18410.1	NT	Homo sapiens cyclophilin-related protein (NCPR) genes, complete cds
4621	14505	24298	1.12	0.0E+00	7062181	NT	Human CYP27A2 pseudogene for cyclochrome P450 27B
4639	14524	24301	1.54	0.0E+00	X98467.1	NT	Human CYP27A2 pseudogene for cyclochrome P450 27B
4644	14532	24310	0.95	0.0E+00	7304022	NT	Homo sapiens bromodomain adjacent to zinc finger domain, ZB (BAZ2B), mRNA
4644	14532	24310	0.95	0.0E+00	7304022	NT	Homo sapiens bromodomain adjacent to zinc finger domain, ZB (BAZ2B), mRNA
4652	14538	24327	1.09	0.0E+00	AF020606.1	NT	Homo sapiens alpha-3 type II collagen (COLA3) gene, promoter region, and exon 1, 2B
4655	14541	24330	0.92	0.0E+00	7019820	NT	Homo sapiens protein00008 (AD013), mRNA
4655	14541	24331	0.92	0.0E+00	7019820	NT	Homo sapiens protein00008 (AD013), mRNA
4678	14592	24351	1.78	0.0E+00	AF444837.1	EST_HUMAN	UJF-HB3-glyc-c-04-J1-21 NC1, COMP Sub5 Homo sapiens cDNA clone IMAGE2733204 3'
4681	14597	24363	1.11	0.0E+00	AF030154.1	NT	Homo sapiens aldehyde dehydrogenase 12 (ALDH12) mRNA, complete cds
4680	14572		1.18	0.0E+00	AF06342.1	NT	Homo sapiens HSPC024-like mRNA, complete cds
4697	14683		2.04	0.0E+00	M05106.1	NT	Human connectin 43 processed pseudogene
4735	14620		2.78	0.0E+00	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
4737	14622	24406	2.78	0.0E+00	AF12051.1	NT	Alfa-fetoprotein mRNA for metalloproteinase-like, chitinase-like protein, 1/1a
4739	14624	24410	1.3	0.0E+00	AF064478.1	NT	Homo sapiens Williams-Buren syndrome deletion transcript 9 (WBSCR9) mRNA, complete cds
4740	14624	24411	1.47	0.0E+00	AF064478.1	NT	Alfa-musculin zinc finger transcription factor Kasso mRNA, complete cds
4741	14626	24412	3.51	0.0E+00	AF097474.1	NT	Homo sapiens fragile X mental retardation 2 (FMR2) mRNA
4743	14628	24414	51.82	0.0E+00	48503706	NT	Homo sapiens actin, alpha, cardiac muscle (ACTG), mRNA

Table 4

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4744	14829	24415	1.4	0.0E+00	P52749	SWISSPROT	ZINC FINGER PROTEIN 192
4746	14831	24417	0.97	0.0E+00	8622180	NT	Homo sapiens hypothetical protein DKF76702E1312 (DKF76702E1312), mRNA
4748	14833	24419	0.8	0.0E+00	AL163203.2	NT	Homo sapiens chromosome 21 segment H82C0003
4750	14835	24421	7.78	0.0E+00	8623080	NT	Homo sapiens hypothetical protein FLJ20073 (FLJ20073), mRNA
4752	14837	24423	0.85	0.0E+00	7061979	NT	Homo sapiens LYAO187 gene product (LYAO187), mRNA
4754	14839	24425	1.86	0.0E+00	M84081.1	NT	Human Tor-C- α -cella gene, exons 1-2; Tor-V- α -cella gene, exons 1-2; Tor-V- α -cella gene, exons 1-4
4756	14841	24427	1.86	0.0E+00	M84081.1	NT	Human Tor-C- α -cella gene, exons 1-4; Tor-V- α -cella gene, exons 1-2; Tor-V- α -cella gene, exons 1-4
4758	14843	24429	1.86	0.0E+00	M84081.1	NT	Human Tor-C- α -cella gene, exons 1-4; Tor-V- α -cella gene, exons 1-2; Tor-V- α -cella gene, exons 1-4
4760	14845	24431	1.86	0.0E+00	M84081.1	NT	Human Tor-C- α -cella gene, exons 1-4; Tor-V- α -cella gene, exons 1-2; Tor-V- α -cella gene, exons 1-4
4762	14847	24433	1.86	0.0E+00	M84081.1	NT	Human Tor-C- α -cella gene, exons 1-4; Tor-V- α -cella gene, exons 1-2; Tor-V- α -cella gene, exons 1-4
4764	14849	24435	1.86	0.0E+00	M84081.1	NT	Human Tor-C- α -cella gene, exons 1-4; Tor-V- α -cella gene, exons 1-2; Tor-V- α -cella gene, exons 1-4
4766	14851	24437	3.22	0.0E+00	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
4768	14853	24439	0.99	0.0E+00	5032150	NT	Homo sapiens TATA box binding protein (TBP)-associated factor, RNA polymerase II, 1, 28kD (TAF-23)
4769	14854	24440	0.82	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein related protein 2 (LDLRP), mRNA
4770	14855	24441	1.44	0.0E+00	X02841.1	NT	H. sapiens, MHC class I
4771	14856	24463	1.97	0.0E+00	4688942	NT	Homo sapiens zinc finger protein (XZAP412), mRNA
4772	14857	24464	1.18	0.0E+00	AB014533.1	NT	Homo sapiens MYRNA for XZAP033 protein, partial cds
4774	14859	24465	2.28	0.0E+00	5077048	NT	Mus musculus zinc finger protein interacting with K protein 1 (ZK1), mRNA
4775	14860	24467	1.05	0.0E+00	5714560	NT	Homo sapiens meningococci expressed antigen 6 (called cod. for mcr-1) (MGEA6), mRNA
4777	14862	24469	8.64	0.0E+00	4788198	NT	Homo sapiens desmoplakin (DP1, DP11) (DSP), mRNA
4779	14864	24471	1.2	0.0E+00	Y16723.1	NT	Homo sapiens gene encoding filensin, exon 8
4800	14885	24472	1.61	0.0E+00	7705646	NT	Homo sapiens zinc-finger DNA-binding protein (HUMHOXY1), mRNA
4801	14886	24480	1.33	0.0E+00	AJ010442.1	NT	Homo sapiens zinc-finger protein for immunoglobulin kappa light chain, anti-RPD, theraed 7
4806	14890	24477	24.91	0.0E+00	AF050666.1	NT	Homo sapiens MHC class I region
4808	14892	24481	2.43	0.0E+00	4956508	NT	Homo sapiens opioid receptor, delta 1 (OPRD1), mRNA
4809	14893	24480	2.46	0.0E+00	AF091711.1	NT	Homo sapiens splice variant AKAP350 mRNA, partial cds
4812	14913	23791	5.48	0.0E+00	4507720	NT	Homo sapiens filin (TTN), mRNA
4812	14913	23792	5.48	0.0E+00	4507720	NT	Homo sapiens filin (TTN), mRNA
4814	14897	21484	0.95	0.0E+00	AJ277892.1	NT	Homo sapiens filin, TTN, gene for titin
4820	14908	24460	12.01	0.0E+00	4507720	NT	Homo sapiens filin (TTN), mRNA
4824	14709	24463	0.95	0.0E+00	D63389.1	NT	Homo sapiens COL4A6 gene for α 1(VI) collagen, exon 44 and partial cds

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Probe SEQ ID NO:	Exon NO:	CRF SEQ ID NO:	Expression Signal	Best Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4831	14713	24406	1.52	0.0E+00	4503894	NT	Homo sapiens fameryl diphosphate synthase (farnesyl pyrophosphate synthetase, dihydrallyltransferase, geranyltransferase) (FDPs) mRNA
4837	14519	24105	1.06	0.0E+00	4809652	NT	Homo sapiens sialyltransferase 8 (alpha-N-acetylneuraminic: alpha-2,8-sialyltransferase, GD3 synthase) (SIAT8) mRNA
4845	14726	24505	1.31	0.0E+00	DT5050.1	NT	Human mRNA for transcription factor AREB8, complete cds
4845	14726	24505	1.31	0.0E+00	DT5050.1	NT	Human mRNA for transcription factor AREB8, complete cds
4854	14734	24516	0.96	0.0E+00	AB028893.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
4871	14751	24530	1.34	0.0E+00	AL183294.2	NT	Homo sapiens chromosome 21 segment HS21C084
4879	14759	24536	1.45	0.0E+00	AW452726.1	EST_HUMAN	UH-B18-alk-A2-DJL1 NCI QGAP Sub8 Homo sapiens cDNA clone IMAGE:3069891 3'
4895	14766	24542	1.2	0.0E+00	8622928	NT	Homo sapiens hypothetical protein FLJ11190 (FLJ11190), mRNA
4896	14769	24550	7.99	0.0E+00	4807720	NT	Homo sapiens titin (TTN) mRNA
4898	14768	24544	2.81	0.0E+00	AF098332.1	NT	Homo sapiens titin (TTN) gene, alternative splice products, partial cds
4898	14768	24544	2.81	0.0E+00	AF098332.1	NT	Homo sapiens titin (TTN) gene, alternative splice products, partial cds
4894	14774	24562	2.95	0.0E+00	4807720	NT	Homo sapiens titin (TTN) mRNA
4897	14771		4.34	0.0E+00	U14597.1	EST	Human fibronectin protein L21 mRNA, complete cds
4910	14769		2.68	0.0E+00	5E408883.1	EST_HUMAN	6073337261 NH_MGC 21 Homo sapiens cDNA clone IMAGE:363818 5'
4915	14764	24590	5.37	0.0E+00	4758192	NT	Homo sapiens desmoplakin (DP1) (DP1) (DSP) mRNA
4925	14804	24574	0.39	0.0E+00	AB028893.1	NT	Homo sapiens mRNA for KIAA0C3 (KIAA0C3), partial cds
4938	14817	24554	1.36	0.0E+00	8623441	NT	Homo sapiens hypothetical protein FLJ20477 (FLJ20477), mRNA
4938	14817	24555	1.36	0.0E+00	8623441	NT	Homo sapiens hypothetical protein FLJ20477 (FLJ20477), mRNA
							Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2a), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2b), melanoma antigen family A3 (MAGEA3), collectrin (CAL1), NAD(P)H dehydrogenase-like protein (NSDHL), and L12
4983	14830	24593	1.06	0.0E+00	UG2871.2	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2a), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2b), melanoma antigen family A3 (MAGEA3), collectrin (CAL1), NAD(P)H dehydrogenase-like protein (NSDHL), and L12
4983	14830	24593	1.06	0.0E+00	UG2871.2	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2a), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2b), melanoma antigen family A3 (MAGEA3), collectrin (CAL1), NAD(P)H dehydrogenase-like protein (NSDHL), and L12
4957	14713	23761	5.81	0.0E+00	4807720	NT	Homo sapiens titin (TTN) mRNA
4957	14713	23762	5.81	0.0E+00	4807720	NT	Homo sapiens titin (TTN) mRNA
4959	14834	24602	3.51	0.0E+00	4807720	NT	Homo sapiens titin (TTN) mRNA
4960	14835	24603	7.78	0.0E+00	4807720	NT	Homo sapiens titin (TTN) mRNA
4968	14843		1.17	0.0E+00	4758225	NT	Homo sapiens E2F transcription factor 2 (E2F-2) mRNA
4978	14853	24619	1.35	0.0E+00	AF016705.1	NT	Homo sapiens E6-AP ubiquitin-protein ligase (UBE6A) gene, exon 3
4987	14862		1.33	0.0E+00	AL183298.2	NT	Homo sapiens chromosome 21 segment HS21C089

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4950	14865		37.78	0.0E+00	D06057.1	NT	Homo sapiens gamma-cytoplasmic actin (ACT/GP3) pseudogene
5000	14875	24539	2.26	0.0E+00	AJ27692.1	NT	Homo sapiens parval TTN gene for tlin
5001	14879	24540	3.02	0.0E+00	4507720	NT	Homo sapiens tlin (TTN) mRNA
5003	14876	24542	4.23	0.0E+00	4507720	NT	Homo sapiens tlin (TTN) mRNA
5005	14873	23791	2.59	0.0E+00	4507720	NT	Homo sapiens tlin (TTN) mRNA
5005	14873	23792	2.59	0.0E+00	4507720	NT	Homo sapiens tlin (TTN) mRNA
5018	14892	24590	2.43	0.0E+00	X62888.1	NT	Bacillus amyloliquefaciens sacB gene for levanisucrase (EC 2.4.1.10)
5037	14809	24681	1.84	0.0E+00	AF240635.1	NT	Homo sapiens vascular endothelial cadherin 2 mRNA, complete cds
5037	14809	24682	1.84	0.0E+00	AF240635.1	NT	Homo sapiens vascular endothelial cadherin 2 mRNA, complete cds
5040	14812	24680	1.01	0.0E+00	5454153	NT	Homo sapiens cyclophilin (USA-CYP) mRNA
5054	14826	24688	1.22	0.0E+00	6977700	NT	Homo sapiens G-protein coupled receptor (RIZ2), mRNA
5055	14813	23791	11.22	0.0E+00	4507720	NT	Homo sapiens tlin (TTN) mRNA
5055	14813	23792	11.22	0.0E+00	4507720	NT	Homo sapiens tlin (TTN) mRNA
5056	14813	23791	14.5	0.0E+00	4507720	NT	Homo sapiens tlin (TTN) mRNA
5056	14813	23792	14.5	0.0E+00	4507720	NT	Homo sapiens tlin (TTN) mRNA
5056	14835	24708	1.38	0.0E+00	4557362	NT	Homo sapiens PR domain containing 1, with ZNF domain (PRDM1) mRNA
5070	14840	24713	1.03	0.0E+00	V10305.1	NT	Human cellular fibronectin mRNA
5070	14840	24714	1.03	0.0E+00	V10305.1	NT	Human cellular fibronectin mRNA
5071	14841	24715	1.06	0.0E+00	U81928.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (H2A-H) gene, Fokai gene, and sodium phosphate transporter (NPT3) gene, complete cds
5080	14850	24726	3.04	0.0E+00	4507720	NT	Homo sapiens tlin (TTN) mRNA
5086	14813	23791	6.27	0.0E+00	4507720	NT	Homo sapiens tlin (TTN) mRNA
5086	14813	23792	6.27	0.0E+00	4507720	NT	Homo sapiens tlin (TTN) mRNA
5088	14867	24743	1.24	0.0E+00	U35475.1	NT	Homo sapiens olfactory receptor-like gene, complete cds
5088	14867	24744	1.24	0.0E+00	U35475.1	NT	Homo sapiens olfactory receptor-like gene, complete cds
5089	14813	23791	9.38	0.0E+00	4507720	NT	Homo sapiens tlin (TTN) mRNA
5089	14813	23792	9.38	0.0E+00	4507720	NT	Homo sapiens tlin (TTN) mRNA
5095	14813	23792	9.38	0.0E+00	4507720	NT	Homo sapiens tlin (TTN) mRNA
5124	14892	24765	0.84	0.0E+00	AF165098.1	NT	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds
5124	14893	24766	1.35	0.0E+00	5900213	NT	Homo sapiens MYCIN 3 (GPC3) mRNA
5130	14897	24768	0.8	0.0E+00	AE000327.1	NT	Escherichia coli K-12 MG1655 section 217 of 400 of the complete genome
5140	15007	24776	1.06	0.0E+00	4855474	NT	Homo sapiens melanoma antigen, family C, 1 (MAGEC1), mRNA
5159	15026	24793	0.86	0.0E+00	4855474	NT	Homo sapiens melanoma antigen, family C, 1 (MAGEC1), mRNA
5162	15028	24794	1.59	0.0E+00	4758907	NT	Homo sapiens melanoma antigen, family C, 2 (MAGEC2), mRNA

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Probe SEQ ID NO:	Exon NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit ELAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5165	15031	24767	1.12	0.0E+00	AF245703.1	NT	Homo sapiens toll-like receptor 8 (TLR8) mRNA, complete cds
5165	15031	24768	1.12	0.0E+00	AF245703.1	NT	Homo sapiens toll-like receptor 8 (TLR8) mRNA, complete cds
5165	15090	24814	1.72	0.0E+00	AF006061.1	NT	Homo sapiens placental growth hormone isoform IGH-V3 (IGH-V) mRNA, complete cds
5167	14013	23761	10.43	0.0E+00	4507720	NT	Homo sapiens ltn (TTN) mRNA
5167	14013	23762	10.43	0.0E+00	4507720	NT	Homo sapiens ltn (TTN) mRNA
5168	15092	24816	6.75	0.0E+00	4507720	NT	Homo sapiens ltn (TTN) mRNA
5168	15092	24816	6.75	0.0E+00	4507720	NT	Homo sapiens ltn (TTN) mRNA
5168	15095	24822	3.87	0.0E+00	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5168	15095	24822	3.87	0.0E+00	4507720	NT	Homo sapiens ltn (TTN) mRNA
5168	15095	24823	3.87	0.0E+00	4507720	NT	Homo sapiens ltn (TTN) mRNA
5168	15095	24824	0.96	0.0E+00	4502386	NT	Homo sapiens acylase (ACO2) gene, nuclear gene encoding mitochondrial protein, exon 15
5208	15088	24524	15.66	0.0E+00	AF030083.1	NT	Homo sapiens ltn (TTN) mRNA
5214	15137	24830	2.25	0.0E+00	AF197286.1	NT	Homo sapiens ltn (TTN) mRNA
5214	15137	24831	2.25	0.0E+00	AF197286.1	NT	Homo sapiens ltn (TTN) mRNA
5228	15160	24917	2.89	0.0E+00	8264570	NT	Homo sapiens procalcitonin, alpha 13 (PCGHA13) mRNA
5234	15169	24928	3.82	0.0E+00	BE021080.1	EST_HUMAN	EC3-250076.510800719.103 ON0076 Homo sapiens cDNA
5238	15162	24930	3.12	0.0E+00	AF102334.1	NT	Homo sapiens polycystic kidney disease-like 2 protein (PKD2) mRNA, complete cds
5238	15162	24931	3.12	0.0E+00	AF102334.1	NT	Homo sapiens polycystic kidney disease-like 2 protein (PKD2) mRNA, complete cds
5248	15168	24940	1.82	0.0E+00	X57653.1	NT	H1 sapiens immunoglobulin heavy chain gene, variable region
5248	15168	24941	1.82	0.0E+00	X57653.1	NT	H1 sapiens immunoglobulin heavy chain gene, variable region
5307	15228	25022	3.8	0.0E+00	BE574984.1	EST_HUMAN	710006.X1 NC CGAP CL11 Homo sapiens cDNA clone IMAGE3165194.3 similar to SW Y064_HUMAN
5308	15228	25023	1.77	0.0E+00	BE207193.1	EST_HUMAN	H06002.X1 NC CGAP Luc4 Homo sapiens cDNA clone IMAGE3165194.3 similar to SW Y064_HUMAN
5309	15230	25034	1.67	0.0E+00	BE794412.1	EST_HUMAN	P4384 HYPOTHETICAL PROTEIN KIAA0054.1
5309	15230	25035	1.67	0.0E+00	BE794412.1	EST_HUMAN	601189422.F1 NH MCC.7 Homo sapiens cDNA clone IMAGE31643004.5
5311	15232	25037	5.46	0.0E+00	M29008.1	NT	Homo sapiens ornithine decarboxylase (ODF) gene, exon 7
5313	15234	25038	1.81	0.0E+00	A7191383.1	EST_HUMAN	086049.y6 NC CGAP K15 Homo sapiens cDNA clone IMAGE1472162.5 similar to gbAI18512 IG
5319	15442	25044	5.42	0.0E+00	11421039	NT	HEAVY CHAIN PRECURSOR V.J REGION (HUMAN);
5321	15444	25045	2.81	0.0E+00	BF695662.1	EST_HUMAN	Homo sapiens Sp1 transcription factor (SP4), mRNA
5324	15447	25052	1.92	0.0E+00	BF695662.1	EST_HUMAN	602118928.F1 NH MCC.56 Homo sapiens cDNA clone IMAGE4270284.5
5333	15293	25075	1.31	0.0E+00	BE538857.1	EST_HUMAN	601081488.F1 NH MCC.10 Homo sapiens cDNA clone IMAGE3447839.5
5333	15293	25076	1.31	0.0E+00	BE538857.1	EST_HUMAN	601105959.F1 NH MCC.15 Homo sapiens cDNA clone IMAGE268310.5
5337	15257	25080	1.8	0.0E+00	BF520328.1	EST_HUMAN	60207137.F1 NC CGAP Bmi64 Homo sapiens cDNA clone IMAGE4214272.5
5337	15257	25081	1.8	0.0E+00	BF520328.1	EST_HUMAN	60207137.F1 NC CGAP Bmi64 Homo sapiens cDNA clone IMAGE4214272.5
5348	15687	26122	1.71	0.0E+00	4557354	NT	Homo sapiens Bloom syndrome (GLM) mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9392	15272	25101	5.24	0.0E+00	AF257737.1	NT	Homo sapiens ciliary dyenin heavy chain 9 (ONAH9) mRNA, complete cds
9392	15272	25102	5.24	0.0E+00	AF257737.1	NT	Homo sapiens ciliary dyenin heavy chain 9 (ONAH9) mRNA, complete cds
9392	15282	25114	1.46	0.0E+00	D26395.1	NT	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)
9392	15292	25115	1.46	0.0E+00	D26395.1	NT	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)
9374	15294	25141	1.97	0.0E+00	11420919	NT	Homo sapiens adenylyl receptor, family 2, subfamily F, member 1 (OR25F1), mRNA
9399	15305	25165	3.29	0.0E+00	BF626031.1	EST_HUMAN	602042322.F1 NCI CGAP Brn97 Homo sapiens cDNA clone IMAGE:4179988 5'
9399	15305	25169	3.29	0.0E+00	BF626031.1	EST_HUMAN	602042322.F1 NCI CGAP Brn97 Homo sapiens cDNA clone IMAGE:4179988 5'
9399	15306	25161	2.35	0.0E+00	BF731359.1	EST_HUMAN	601897658.F1 NIH MGCC 19 Homo sapiens cDNA clone IMAGE:4128515 5'
9398	15315	25362	4.21	0.0E+00	11434392	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1G subunit (CACNA1G), mRNA
5420	15341		2.43	0.0E+00	AW587316.1	EST_HUMAN	MFO-SN0037.590.000-401-F07 SN0037 Homo sapiens cDNA
5431	15361	25405	3.05	0.0E+00	BE292989.1	EST_HUMAN	601105291.F1 NIH MGCC 15 Homo sapiens cDNA clone IMAGE:2987903 5'
5431	15361	25405	3.05	0.0E+00	BE292989.1	EST_HUMAN	601105291.F1 NIH MGCC 15 Homo sapiens cDNA clone IMAGE:2987903 5'
5444	15385	25420	1.31	0.0E+00	11420919	NT	Homo sapiens adenylyl receptor, family 2, subfamily F, member 1 (OR25F1), mRNA
5444	15385	25421	1.31	0.0E+00	11420919	NT	Homo sapiens adenylyl receptor, family 2, subfamily F, member 1 (OR25F1), mRNA
5491	15372	25439	6.35	0.0E+00	A7504254.1	NT	Homo sapiens wip long-chain acyl-CoA synthetase homolog 1 mRNA, complete cds
5491	15372	25439	6.35	0.0E+00	A7504254.1	NT	Homo sapiens wip long-chain acyl-CoA synthetase homolog 1 mRNA, complete cds
5495	15376	25435	2.9	0.0E+00	A1224529.1	NT	Homo sapiens SURF5 and SURF3 gene
5495	15376	25435	2.9	0.0E+00	A1224529.1	NT	Homo sapiens SURF5 and SURF3 gene
5470	15380	25453	6.99	0.0E+00	ME5716.1	EST_HUMAN	EST102236 T441 brain, S. sapiens (G8623209) Homo sapiens cDNA clone HF50M48
5474	15384	25459	3.97	0.0E+00	AW425472.1	EST_HUMAN	UHF-ELJ-5474-022-F1 NIH MGCC 37 Homo sapiens cDNA clone IMAGE:3051665 5'
5498	15406	25471	5.74	0.0E+00	AW391677.1	EST_HUMAN	PIB8-C10285-061258-007-105 C10283 Homo sapiens cDNA
5498	15406	25472	5.74	0.0E+00	AW391677.1	EST_HUMAN	PIB8-C10285-061258-007-105 C10283 Homo sapiens cDNA
5498	15408	25473	5.74	0.0E+00	AW391677.1	EST_HUMAN	PIB8-C10285-061258-007-105 C10283 Homo sapiens cDNA
5491	15410	25475	1.89	0.0E+00	U93981.1	NT	Homo beta-prime-actin (BAM22) gene, exon 13
5531	15448	25515	3.29	0.0E+00	A1186905.1	EST_HUMAN	7192811.1 Stragnum muscle 1837200 Homo sapiens cDNA clone IMAGE:327033 5' similar to gb-X03740
5532	15446	25516	1.5	0.0E+00	AJ006345.1	NT	MYOSIN HEAVY CHAIN, SKELETAL, M-SCLE (HUMAN);
5532	15446	25517	1.5	0.0E+00	AJ006345.1	NT	MYOSIN HEAVY CHAIN, SKELETAL, M-SCLE (HUMAN);
5537	15454	25524	2	0.0E+00	AJ207616.1	EST_HUMAN	Homo sapiens KVLQ171 gene
5548	15454	25534	3.98	0.0E+00	11418901	NT	HA2581 Human fetal liver cDNA library Homo sapiens cDNA
5555	15471	25542	1.78	0.0E+00	BE500082.1	EST_HUMAN	Homo sapiens proboscoidin beta 2 (PCDH22), mRNA
5555	15471	25542	1.78	0.0E+00	BE500082.1	EST_HUMAN	801345141.F1 NIH MGCC 8 Homo sapiens cDNA clone IMAGE:3077943 5'
5557	15473	25544	3.03	0.0E+00	U93981.1	NT	Mus musculus ezrinin (acz), mRNA
5557	15473	25544	3.03	0.0E+00	U93981.1	NT	Human L-type calcium channel beta-1 subunit (CACNLB1) gene, exon 13B and isoform beta-1B, complete cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression	Most Similar (Top) Hit BLAST E- Signal Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
5657	16473	29546	3.03	0.0E+00	U89031.1	NT	Human L-type calcium channel beta-1 subunit (CACNLB1) gene, clone 13B and isoform beta-1B; complete cds.
5658	15944	29553	2.11	0.0E+00	BF030925.1	EST_HUMAN	KCQ2G03Z725T NCL CGAP Brn45 Homo sapiens cDNA clone IMAGE:5143021 5'
5659	15969	29555	2.98	0.0E+00	BZ723983.1	EST_HUMAN	BM101405F NH_KJC_74 Homo sapiens cDNA clone IMAGE:5371483 5'
5671	15462	29560	1.74	0.0E+00	B-F06805.1	EST_HUMAN	BM2196S5D1 NH_KJC_48 Homo sapiens cDNA clone IMAGE:4510710 5'
5680	16370	29568	2.47	0.0E+00	AJ217288.1	NT	Homo sapiens cadherin 28 (CDH28) mRNA, complete cds
5687	15915	29568	1.89	0.0E+00	B-E53943.1	EST_HUMAN	RCDL0102Z7210X02-G10 E10227 Homo sapiens cDNA
5690	15676	29583	1.88	0.0E+00	B-E53943.1	EST_HUMAN	NK1-KJC_58 Homo sapiens cDNA clone IMAGE:5304345 5'
5691	15676	29583	1.41	0.0E+00	B-E53943.1	EST_HUMAN	NK1-KJC_58 Homo sapiens cDNA clone IMAGE:5327776 5'
5695	15530	29573	1.98	0.0E+00	B-G37423.1	EST_HUMAN	BT1580R05F NH_KJC_38 Homo sapiens cDNA clone IMAGE:3271776 5'
5696	15530	29574	1.98	0.0E+00	B-G37423.1	EST_HUMAN	BT1580R05F NH_KJC_38 Homo sapiens cDNA clone IMAGE:3271776 5'
6031	15265	29634	1.94	0.0E+00	B-W33069.1	EST_HUMAN	Z80806.11 Soares, parathyroid tumor, NGHPA Homo sapiens cDNA clone IMAGE:327185 5'
6031	15265	29634	1.94	0.0E+00	W13309.1	EST_HUMAN	Z80806.11 Soares, parathyroid tumor, NGHPA Homo sapiens cDNA clone IMAGE:327185 5'
6032	15246	29641	1.84	0.0E+00	W13309.1	EST_HUMAN	Homo sapiens lamellar irradial protein 2 (PML2) gene, exon 14
6032	15246	29641	2.15	0.0E+00	AJ012618.1	NT	Homo sapiens lamellar irradial protein 2 (PML2) gene, exon 14
6034	15546	29568	3.97	0.0E+00	B-C29197.1	EST_HUMAN	BM15815GF NH_KJC_24 Homo sapiens cDNA clone IMAGE:3305323 5'
6038	16591	29582	2.74	0.0E+00	B-E98960.1	EST_HUMAN	BM15815GF NH_KJC_24 Homo sapiens cDNA clone IMAGE:3305323 5'
6049	16591	29584	1.83	0.0E+00	I143307.1	EST_HUMAN	Homo sapiens KIAA0735 gene product, synaptic vesicle protein 2B homolog (KIAA0735), mRNA
6049	16591	29584	1.83	0.0E+00	I143307.1	EST_HUMAN	Homo sapiens KIAA0735 gene product, synaptic vesicle protein 2B homolog (KIAA0735), mRNA
6049	16591	29585	1.63	0.0E+00	I143307.1	NT	Homo sapiens KIAA0735 gene product, synaptic vesicle protein 2B homolog (KIAA0735), mRNA
5690	19450	29598	10.06	0.0E+00	G789896	NT	Homo sapiens pendulin vitelline-gated channel, Shal-related subfamily, member 2 (KCNC2), mRNA
5693	15574	29571	1.29	0.0E+00	AA189506.1	EST_HUMAN	Z40KH1.T Soares, NIH/NHLI_S1 Homo sapiens cDNA clone IMAGE:565905 5' similar to SWY005.HUMAN P42984 HYPOTHETICAL MYELOID CSLL LINE PROTEIN S.5
5693	15574	29572	1.26	0.0E+00	AA189506.1	EST_HUMAN	Z40KH1.T Soares, NIH/NHLI_S1 Homo sapiens cDNA clone IMAGE:565905 5' similar to SWY005.HUMAN P42984 HYPOTHETICAL MYELOID CSLL LINE PROTEIN S.5
5690	16599	29590	13.03	0.0E+00	UA4925.1	NT	Human T cell surface glycoprotein CD5-6 mRNA, complete cds
5690	16599	29591	13.03	0.0E+00	UA4925.1	NT	Human T cell surface glycoprotein CD5-6 mRNA, complete cds
5730	16538	29742	1.41	0.0E+00	AU13772.1	EST_HUMAN	HUMAN T cell surface glycoprotein CD5-6 mRNA, complete cds
5741	16549	29755	3.4	0.0E+00	UA4982.1	NT	HUMAN G-protein-coupled receptor GPR-4-6 gene, complete cds
5756	16993	29770	4.14	0.0E+00	AA204740.1	EST_HUMAN	xgflid03.1 Silageene INT neuron (#837233) Homo sapiens cDNA clone IMAGE:948005 5' similar to TR-G894-195 G894-195 LEUKOCYTE SURFACE PROTEIN. ;
5763	16994	29771	3.97	0.0E+00	I1646913	NT	Homo sapiens xlycoyltransferase II (XT2), mRNA
5769	16984	29782	3.97	0.0E+00	I1646913	NT	Homo sapiens xlycoyltransferase II (XT2), mRNA
5769	16984	29782	2.8	0.0E+00	B-E257173.1	EST_HUMAN	BM110652ZF NH_KJC_16 Homo sapiens cDNA clone IMAGE:330622 5'
5784	16590	29611	1.47	0.0E+00	L39630.1	NT	Human anion exchanger (AE1) gene, exons 1-20
5784	16590	29611	1.47	0.0E+00	L39630.1	NT	Homo sapiens peptide transporter 3 (LOC61539) mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8826	15732		8.1	0.0E+00	AF169020.1	EST_HUMAN	AV650020 GLC Homo sapiens cDNA clone GLC0409.3
8830	15736	28148	2.81	0.0E+00	AF159598.1	EST_HUMAN	UHF-BL0-dec-12-U1.1 NIH_MGC 37 Homo sapiens cDNA clone IMAGE:3058751.3
8832	15738	28180	4.21	0.0E+00	H01255.1	EST_HUMAN	Y7D03.1 Soares placenta IN24P Homo sapiens cDNA clone IMAGE:148933.5
8838	15744	28187	1.99	0.0E+00	X15377.1	NT	Human gene for the light and heavy chains of myeloperoxidase
8843	15749	28182	4.25	0.0E+00	BE735980.1	EST_HUMAN	801303088F1 NIH_MGC 39 Homo sapiens cDNA clone IMAGE:3639618.5
8843	15749	28183	4.25	0.0E+00	BE735980.1	EST_HUMAN	801303088F1 NIH_MGC 39 Homo sapiens cDNA clone IMAGE:3639618.5
8847	15753	28180	11.57	0.0E+00	AU119246.1	EST_HUMAN	AU119246 HEMBA1 Homo sapiens cDNA clone HEMBA100560.5
8854	15760	28178	1.96	0.0E+00	A098483.1	EST_HUMAN	we2507.x1 NCL_OGAP GC5 Homo sapiens cDNA clone IMAGE:248220.3
8859	15765	28182	4.81	0.0E+00	BE230153.1	EST_HUMAN	80110334F1 NIH_MGC 18 Homo sapiens cDNA clone IMAGE:2887663.5
8859	15765	28183	4.81	0.0E+00	BE230153.1	EST_HUMAN	80110334F1 NIH_MGC 18 Homo sapiens cDNA clone IMAGE:2887663.5
8901	15807	28021	1.36	0.0E+00	AF140548.1	EST_HUMAN	UHF-BL0-dec-12-U1.1 NIH_MGC 37 Homo sapiens cDNA clone IMAGE:3055931.5
8901	15807	28022	1.36	0.0E+00	AF140548.1	EST_HUMAN	UHF-BL0-dec-12-U1.1 NIH_MGC 37 Homo sapiens cDNA clone IMAGE:3055931.5
8921	15826	28031	1.89	0.0E+00	AF16444.1	EST_HUMAN	AV716444 GLC Homo sapiens cDNA clone GLCEH006.5
8930	15835	28038	2.24	0.0E+00	AF160840.1	NT	Homo sapiens low voltage-activated T-type calcium channel alpha 1G splice variant Cav1.1a (CAVNA10) mRNA, complete cds
8936	15841	28044	3.45	0.0E+00	AF163940.1	EST_HUMAN	af6808.v1 Schwabach fetal brain 00004 Homo sapiens cDNA clone IMAGE:2784169.5 similar to TR016330.016390.0724. [8] TR016340 TR049306.5
8936	15841	28045	3.45	0.0E+00	AF163940.1	EST_HUMAN	af6808.v1 Schwabach fetal brain 00004 Homo sapiens cDNA clone IMAGE:2784169.5 similar to TR016330.016390.0724. [8] TR016340 TR049306.5
8931	15850	28078	4.79	0.0E+00	BE736873.1	EST_HUMAN	80187569F1 NIH_MGC 71 Homo sapiens cDNA clone IMAGE:3041847.5
8935	15850	28081	7.23	0.0E+00	BE736873.1	EST_HUMAN	80187569F1 NIH_MGC 71 Homo sapiens cDNA clone IMAGE:3041847.5
8935	15850	28082	7.23	0.0E+00	BE736873.1	EST_HUMAN	80187569F1 NIH_MGC 71 Homo sapiens cDNA clone IMAGE:3041847.5
8931	15856	28088	3.71	0.0E+00	L24493.1	NT	Human antigen CD27 gene, exons 1-2
8964	15861	28091	2.15	0.0E+00	AF116204.2	NT	Homo sapiens chromosome 21 segment HS21C004
8964	15861	28092	2.15	0.0E+00	AF116204.2	NT	Homo sapiens chromosome 21 segment HS21C004
8970	15875	28099	3.84	0.0E+00	6005963	NT	Homo sapiens zona pellucida glycoprotein 3A (spERM receptor) (ZP3A), mRNA
8973	15877	28001	4.13	0.0E+00	AF638412.1	EST_HUMAN	IB111.1x1 NCL_OGAP GC6 Homo sapiens cDNA clone IMAGE:2242413.3 similar to SW:WNT3_MOUSE
8974	15878	28002	1.79	0.0E+00	L32832.1	NT	P17553 WNT-3 PHOTO-ONCOGENE PROTEIN PRECURSOR ;
8980	15885	28007	3.98	0.0E+00	AA344594.1	EST_HUMAN	Homo sapiens zinc finger homeodomain protein (ATBF1A) mRNA, complete cds
8991	15896	28017	1.48	0.0E+00	BE528875.1	EST_HUMAN	QV3-3N004.3 SOX800-278-cds BND047 Homo sapiens cDNA
8991	15896	28018	1.48	0.0E+00	BE528875.1	EST_HUMAN	QV3-3N004.3 SOX800-278-cds BND047 Homo sapiens cDNA
8011	15916	28044	7.44	0.0E+00	AU126028.1	EST_HUMAN	AU126028 NTRPM4 Homo sapiens cDNA clone NTRM4002430.5
8041	15944	28076	7.44	0.0E+00	BE11681.1	EST_HUMAN	PM8-HTD020-290200-002-cds HTD020 Homo sapiens cDNA

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Subs Expenditures

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
6042	18495	26077	1.81	0.0E+00	BF056667.1	EST	HUMAN
6043	18496	26077	1.81	0.0E+00	BF056667.1	EST	HUMAN
6063	18500	26191	3.15	0.0E+00	AF100768.1	EST	HUMAN
6071	18504	26201	6.98	0.0E+00	AF040523.1	EST	HUMAN
6071	18504	26202	6.98	0.0E+00	AF040523.1	EST	HUMAN
6075	18509	26268	3.07	0.0E+00	U1143928	NT	Homo sapiens CD4 antigen (CD4), mRNA
6084	18514	26367	1.98	0.0E+00	SE566338.1	EST	HUMAN
6095	18519	26481	13.16	0.0E+00	SE567889.1	EST	HUMAN
6099	18519	24873	13.16	0.0E+00	SE567889.1	EST	HUMAN
6101	18585	26130	2.07	0.0E+00	BE580162.1	EST	HUMAN
6101	18585	26131	2.07	0.0E+00	BE580162.1	EST	HUMAN
6118	18672	26150	1.40	0.0E+00	BF058376.1	EST	HUMAN
6121	18675	26153	3.84	0.0E+00	U4189106.1	EST	HUMAN
6126	18673		10.28	0.0E+00	11034810	NT	Homo sapiens calcitriol (calcitriol-associated protein), delta 2 (rears plectrophilin-related arm-repeat protein) (CTNND2), mRNA
6135	18682	26118	2.57	0.0E+00	BF566905.1	EST	HUMAN
6142	18680		2.82	0.0E+00	J030069.1	NT	HUMAN MYO2.L gene, complete cds
6146	18679	26157	2.8	0.0E+00	AF217289.1	NT	Homo sapiens cadherin 20 (CDH20) mRNA, complete cds
6146	18679	26158	2.8	0.0E+00	AF217289.1	NT	Homo sapiens cadherin 20 (CDH20) mRNA, complete cds
6154	18712	24876	2.76	0.0E+00	AF217289.1	NT	Homo sapiens cadherin 20 (CDH20) mRNA, complete cds
6158	18728	24842	5.03	0.0E+00	BE262941.1	EST	HUMAN
6169	18726	24843	2.32	0.0E+00	BE237976.1	NT	H sapiens mRNA for latent transforming growth factor-beta binding protein (LTBP-2)
6169	18726	24844	2.32	0.0E+00	BE237976.1	NT	H sapiens mRNA for latent transforming growth factor-beta binding protein (LTBP-2)
6170	18727	24845	2.83	0.0E+00	AF268773.1	NT	Homo sapiens salivary duct heavy chain 9 (CNAH9) mRNA, complete cds
6170	18727	24846	2.83	0.0E+00	AF268773.1	NT	Homo sapiens salivary duct heavy chain 9 (CNAH9) mRNA, complete cds
6176	18751	24851	1.35	0.0E+00	AF310105.1	EST	HUMAN
6176	18751	24851	1.35	0.0E+00	AF310105.1	EST	HUMAN
6178	18684	26261	2.18	0.0E+00	BF566403.1	EST	HUMAN
6181	18697	26224	3.58	0.0E+00	U016178.1	NT	Human type IV sodium channel alpha polypeptide (SCN4A) gene, exon 19
6190	18675	26224	5.01	0.0E+00	BF506666.1	EST	HUMAN
6165	18678	26227	1.76	0.0E+00	U41932.1	NT	Human chromosome 16 creatine transporter (SLC6A8) and (ODM) paralogous genes, complete cds
6226	18691	26241	1.34	0.0E+00	AF549406.1	EST	HUMAN
6226	18691	26241	1.34	0.0E+00	BE244103.1	EST	HUMAN
6226	18692	26242	1.41	0.0E+00	BE244103.1	EST	HUMAN

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6237	16103	26253	5.9	0.0E+00	AU13213.1	EST_HUMAN	AU13213.1 NT2P4 Homo sapiens cDNA clone NT2P401566 5'
6253	16119	26279	2.44	0.0E+00	AU143706.1	EST_HUMAN	AU143706.1 Y76AA1 Homo sapiens cDNA clone Y76AA1002385 5'
6260	16128	26279	1.31	0.0E+00	BE681263.1	EST_HUMAN	601431616F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3871164 5'
6260	16129	26280	1.31	0.0E+00	BE681263.1	EST_HUMAN	601431616F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3871164 5'
6273	15137	24830	1.97	0.0E+00	AF197390.1	NT	Homo sapiens keratin 12 (KRT12) gene, complete cds
6273	15137	24831	1.97	0.0E+00	AF197390.1	NT	Homo sapiens keratin 12 (KRT12) gene, complete cds
6286	16150	26305	3.63	0.0E+00	U1436969	EST_HUMAN	Homo sapiens vitamin D (1,25-dihydroxyvitamin D3) receptor (VDR), mRNA
6286	16150	26305	3.63	0.0E+00	U1436969	EST_HUMAN	Homo sapiens vitamin D (1,25-dihydroxyvitamin D3) receptor (VDR), mRNA
6302	16166	26323	25.51	0.0E+00	AI128344.1	EST_HUMAN	ip57407.x1 Soera, placenta, 2N8HP860W Homo sapiens cDNA clone IMAGE:171484 3'
6302	16166	26323	25.51	0.0E+00	AI128344.1	EST_HUMAN	ip57407.x1 Soera, placenta, 2N8HP860W Homo sapiens cDNA clone IMAGE:171484 3'
6304	16168	26326	18.70	0.0E+00	U1426302	EST_HUMAN	ip57407.x1 Soera, placenta, 2N8HP860W Homo sapiens cDNA clone IMAGE:171484 3'
6304	16168	26326	18.70	0.0E+00	U1426302	EST_HUMAN	ip57407.x1 Soera, placenta, 2N8HP860W Homo sapiens cDNA clone IMAGE:171484 3'
6306	16170	26327	14.06	0.0E+00	BF517375.1	EST_HUMAN	ip57407.x1 Soera, placenta, 2N8HP860W Homo sapiens cDNA clone IMAGE:171484 3'
6308	16172	26328	5.1	0.0E+00	AA128453.1	EST_HUMAN	ip57407.x1 Soera, placenta, 2N8HP860W Homo sapiens cDNA clone IMAGE:171484 3'
6328	16191	26355	6.72	0.0E+00	AF032113.1	NT	Homo sapiens myosin, heavy polypeptide 8, skeletal muscle, perinatal (MYH8), mRNA
6328	16191	26354	6.72	0.0E+00	AF032113.1	NT	Homo sapiens myosin, heavy polypeptide 8, skeletal muscle, perinatal (MYH8), mRNA
6337	16200	26360	7.85	0.0E+00	AF032113.1	NT	Homo sapiens myosin, heavy polypeptide 8, skeletal muscle, perinatal (MYH8), mRNA
6339	16202	26362	11.09	0.0E+00	U45448.1	NT	Homo sapiens myosin, heavy polypeptide 8, skeletal muscle, perinatal (MYH8), mRNA
6339	16202	26363	11.09	0.0E+00	U45448.1	NT	Homo sapiens myosin, heavy polypeptide 8, skeletal muscle, perinatal (MYH8), mRNA
6347	16210	26372	1.43	0.0E+00	AW56503.1	EST_HUMAN	Homo sapiens myosin, heavy polypeptide 8, skeletal muscle, perinatal (MYH8), mRNA
6349	16212	26374	2.54	0.0E+00	AW56503.1	EST_HUMAN	Homo sapiens myosin, heavy polypeptide 8, skeletal muscle, perinatal (MYH8), mRNA
6389	10231	26411	1.67	0.0E+00	AW236326.1	EST_HUMAN	Homo sapiens myosin, heavy polypeptide 8, skeletal muscle, perinatal (MYH8), mRNA
6400	16281	26422	1.8	0.0E+00	AU117593.1	EST_HUMAN	Homo sapiens myosin, heavy polypeptide 8, skeletal muscle, perinatal (MYH8), mRNA
6401	16282	26422	3.64	0.0E+00	U1427135	NT	Homo sapiens myosin, heavy polypeptide 8, skeletal muscle, perinatal (MYH8), mRNA
6411	16272	26434	54.66	0.0E+00	AA211893.1	EST_HUMAN	Homo sapiens myosin, heavy polypeptide 8, skeletal muscle, perinatal (MYH8), mRNA
6422	16321	26486	4.25	0.0E+00	AU752951.1	EST_HUMAN	Homo sapiens myosin, heavy polypeptide 8, skeletal muscle, perinatal (MYH8), mRNA

Table 4

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6462	16321	26497	4.26	0.0E+00	AJ525091.1	EST_HUMAN	en17.005.x1 Normal Homo sapiens cDNA clone NT1BC, en17.005 random
6469	16358	26530	1.59	0.0E+00	AF094205.1	NT	Homo sapiens dynactin 1 (DCTN1) gene, alternatively spliced products, exons 7 through 32 and complete
6469	16359	26531	1.59	0.0E+00	AF094205.1	NT	Homo sapiens dynactin 1 (DCTN1) gene, alternatively spliced products, exons 7 through 32 and complete
6515	16374	26551	1.3	0.0E+00	11417342	NT	Homo sapiens sense domain, seven thrombospondin repeats (type 1 and type 4-like), transmembrane domain
6530	16389	26569	1.98	0.0E+00	6012735	EST_HUMAN	(TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A), mRNA
6534	16392	26571	5.37	0.0E+00	BE217905.1	EST_HUMAN	Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA
6539	16397	26576	2.98	0.0E+00	AL112622.1	EST_HUMAN	en17.005.x1 Normal Homo sapiens cDNA clone NT28P-20345/13 5'
6550	16408	26586	6.46	0.0E+00	4501848	NT	Homo sapiens ATR-binding catalase, sus-family A (ABC1), member 3 (ABC1A), mRNA
6555	16413	26590	4.87	0.0E+00	BE739870.1	EST_HUMAN	en17.005.x1 Normal Homo sapiens cDNA clone NT28P-20345/13 5'
6555	16413	26591	4.87	0.0E+00	BE739870.1	EST_HUMAN	en17.005.x1 Normal Homo sapiens cDNA clone NT28P-20345/13 5'
6556	16414	26592	60.88	0.0E+00	AL112042.1	EST_HUMAN	en17.005.x1 Normal Homo sapiens cDNA clone NT28P-20345/13 5'
6559	16414	26593	60.88	0.0E+00	AL112042.1	EST_HUMAN	en17.005.x1 Normal Homo sapiens cDNA clone NT28P-20345/13 5'
6574	16422	26614	1.82	0.0E+00	BE737670.1	EST_HUMAN	en17.005.x1 Normal Homo sapiens cDNA clone NT28P-20345/13 5'
6574	16422	26615	1.82	0.0E+00	BE737670.1	EST_HUMAN	en17.005.x1 Normal Homo sapiens cDNA clone NT28P-20345/13 5'
6622	16502	26890	1.28	0.0E+00	AC146079.1	EST_HUMAN	en17.005.x1 Normal Homo sapiens cDNA clone NT28P-20345/13 5'
6645	16505	26719	3.72	0.0E+00	BE739546.1	EST_HUMAN	en17.005.x1 Normal Homo sapiens cDNA clone NT28P-20345/13 5'
6654	16534	26728	3.97	0.0E+00	MG4672.1	NT	Human amyloid-beta protein (APP) gene, exon 11
6654	16534	26730	3.97	0.0E+00	MG4672.1	NT	Human amyloid-beta protein (APP) gene, exon 11
6674	16554	26749	1.65	0.0E+00	AA397551.1	EST_HUMAN	en17.005.x1 Normal Homo sapiens cDNA clone NT28P-20345/13 5'
6677	16557	26750	7.54	0.0E+00	AF142402.1	EST_HUMAN	en17.005.x1 Normal Homo sapiens cDNA clone NT28P-20345/13 5'
6688	16568	26751	8.73	0.0E+00	BF73006.1	EST_HUMAN	en17.005.x1 Normal Homo sapiens cDNA clone NT28P-20345/13 5'
6714	16564	26783	1.99	0.0E+00	AF142024.1	EST_HUMAN	en17.005.x1 Normal Homo sapiens cDNA clone NT28P-20345/13 5'
6714	16564	26784	1.99	0.0E+00	AF142024.1	EST_HUMAN	en17.005.x1 Normal Homo sapiens cDNA clone NT28P-20345/13 5'
6720	16810	26810	1.31	0.0E+00	BE377693.1	EST_HUMAN	en17.005.x1 Normal Homo sapiens cDNA clone NT28P-20345/13 5'
6742	16821	26810	1.35	0.0E+00	AW500549.1	EST_HUMAN	en17.005.x1 Normal Homo sapiens cDNA clone NT28P-20345/13 5'
6747	16826	26813	14.35	0.0E+00	AW167233.1	EST_HUMAN	en17.005.x1 Normal Homo sapiens cDNA clone NT28P-20345/13 5'
6775	16854	26842	1.16	0.0E+00	BE746507.1	EST_HUMAN	en17.005.x1 Normal Homo sapiens cDNA clone NT28P-20345/13 5'
6775	16854	26843	1.16	0.0E+00	BE746507.1	EST_HUMAN	en17.005.x1 Normal Homo sapiens cDNA clone NT28P-20345/13 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID/NO.	Expression Signal	Most Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
0783	16662	26552	2.72	0.0E+00	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
0810	16689	26576	2.2	0.0E+00	BE574157.1	EST_HUMAN	7476504 x1 NCL CGAP, 1424 Homo sapiens cDNA clone IMAGE:3273962 3' similar to TR-065763 065763
0811	16690	26579	1.36	0.0E+00	AB86571.1	EST_HUMAN	W60b.10 x1 NCL CGAP, 3926 Homo sapiens cDNA clone IMAGE:2429276 3' similar to
0817	16696	26587	1.31	0.0E+00	BE563950.1	EST_HUMAN	SV-0027_HUMAN P0281 MATRIX METALLOPROTEINASE-14 PRECURSOR,
0817	16696	26588	1.31	0.0E+00	BE563950.1	EST_HUMAN	SV-0027_HUMAN P0281 MATRIX METALLOPROTEINASE-14 PRECURSOR,
0824	16703	26597	1.44	0.0E+00	11427235	NT	801334700F1 NIH, MGC, 39 Homo sapiens cDNA clone IMAGE:358965 5'
0824	16703	26598	1.44	0.0E+00	11427235	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
0851	16730		3.99	0.0E+00	AA339511.1	EST_HUMAN	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
0859	16735	26628	1.45	0.0E+00	AI336474.1	EST_HUMAN	PTF348 x1 Soares, Insulin, NMT Homo sapiens cDNA clone IMAGE:727936 3' similar to p6S36655
0859	16735	26629	1.45	0.0E+00	AI336474.1	EST_HUMAN	PROHEUTIN (HUMAN),
0859	16743	26626	1.45	0.0E+00	AI336474.1	EST_HUMAN	CV9.D70045.221593.016-37 DT0045 Homo sapiens cDNA
0859	16743	26642	1.21	0.0E+00	AI336474.1	EST_HUMAN	CV9.D70045.221593.016-37 DT0045 Homo sapiens cDNA
0859	16743	26643	1.21	0.0E+00	BE512586.1	EST_HUMAN	8014531251 NIH, MGC, 96 Homo sapiens cDNA clone IMAGE:3558179 5'
0879	16759	26645	1.25	0.0E+00	BE512586.1	EST_HUMAN	8014531251 NIH, MGC, 96 Homo sapiens cDNA clone IMAGE:3558179 5'
0879	16759	26646	1.25	0.0E+00	AL163209.2	NT	Homo sapiens chromosome 21 segment H521C09
0879	16759	26647	1.25	0.0E+00	AL163209.2	NT	Homo sapiens chromosome 21 segment H521C09
0893	16773	26691	2.01	0.0E+00	BE560797.1	EST_HUMAN	Homo sapiens chromosome 21 segment H521C09
0893	16773	26694	2.4	0.0E+00	4798959	NT	Homo sapiens mitogen-activated protein kinase kinase 18 (MAP3K13), mRNA
0813	16791	26695	2.4	0.0E+00	4798959	NT	Homo sapiens mitogen-activated protein kinase kinase 18 (MAP3K13), mRNA
0895	16833	27026	2.95	0.0E+00	X66022.1	NT	H sapiens mRNA for gamma-glutamyltransferase
0895	16833	27027	2.95	0.0E+00	X66022.1	NT	H sapiens mRNA for gamma-glutamyltransferase
0895	16833	27028	2.95	0.0E+00	X66022.1	NT	H sapiens mRNA for gamma-glutamyltransferase
0893	16870		1.30	0.0E+00	AW615813.1	EST_HUMAN	306601 x1 NCL CGAP, 191 Homo sapiens cDNA clone IMAGE:2707032 3' similar to gb.M14123_c44
0895	16872	27063	3.64	0.0E+00	D32650.1	EST_HUMAN	RETROVIRUS-RELATED POLYPROTEIN (HUMAN),
7011	16893	27091	4.46	0.0E+00	BC378495.1	EST_HUMAN	HUM84C03B2 Clontech human fetal brain polyA+ mRNA (#8535) Homo sapiens cDNA clone GEN-094C02
7016	16892	27093	1.31	0.0E+00	AA410545.1	EST_HUMAN	801239488F1 NIH, MGC, 41 Homo sapiens cDNA clone IMAGE:3609709 5'
7016	16893		4.32	0.0E+00	BF313946.1	EST_HUMAN	23264 x1 Soares, every tumor NHOT Homo sapiens cDNA clone IMAGE:724062 5'
7021	16899	27099	1.41	0.0E+00	AW139673.1	EST_HUMAN	80190057F1 NIH, MGC, 19 Homo sapiens cDNA clone IMAGE:4129744 5'
7021	16899	27099	1.41	0.0E+00	AW139673.1	EST_HUMAN	U1-H81-adr-e-12-01.1 x1 NCL CGAP, Sub33 Homo sapiens cDNA clone IMAGE:277687 3'
7021	16899	27099	1.41	0.0E+00	AW139673.1	EST_HUMAN	U1-H81-adr-e-12-01.1 x1 NCL CGAP, Sub33 Homo sapiens cDNA clone IMAGE:277687 3'
7038	16915	27104	2.39	0.0E+00	BE200272.1	EST_HUMAN	80150051F1 NIH, MGC, 59 Homo sapiens cDNA clone IMAGE:3502936 5'
7040	16917	27106	1.93	0.0E+00	BF700165.1	EST_HUMAN	80212766F1 NIH, MGC, 59 Homo sapiens cDNA clone IMAGE:4284642 5'

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon NO.	ORF SEQ ID NO.	Expression Signal	Mean (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7290	17166	27365	1.44	0.0E+00	AB011190.1	NT	Homo sapiens mRNA for KIAA0678 protein, partial cds
7291	17167	27366	2.36	0.0E+00	BE794823.1	EST_HUMAN	Homo sapiens cDNA clone IMAGE:3943483 5'
7292	17174	27374	1.24	0.0E+00	BE898343.1	EST_HUMAN	Homo sapiens cDNA clone IMAGE:3911986 5'
7293	17174	27375	1.24	0.0E+00	BE898343.1	EST_HUMAN	Homo sapiens cDNA clone IMAGE:3911986 5'
7294	17174	27383	1.24	0.0E+00	AA346011.1	EST_HUMAN	Homo sapiens cDNA 5' end
7295	17184	27384	1.6	0.0E+00	AA346011.1	EST_HUMAN	Homo sapiens cDNA 5' end
7300	17227	27420	1.38	0.0E+00	BE207063.1	EST_HUMAN	Homo sapiens cDNA clone IMAGE:2823872 5' similar to gbl.35049 Mus musculus
7301	17227	27427	1.38	0.0E+00	BE207063.1	EST_HUMAN	Homo sapiens cDNA clone IMAGE:2823872 5' similar to gbl.35049 Mus musculus
7302	17246	27551	2.71	0.0E+00	BE734013.1	EST_HUMAN	Homo sapiens cDNA clone IMAGE:4169307 5'
7303	17252	27457	3	0.0E+00	BF12515.1	EST_HUMAN	Homo sapiens cDNA clone IMAGE:3911986 5'
7405	17273	27475	11.81	0.0E+00	AL042278.1	EST_HUMAN	Homo sapiens cDNA clone IMAGE:1651249 3' similar to
7425	17292	27503	1.27	0.0E+00	AO89043.1	EST_HUMAN	Homo sapiens cDNA clone IMAGE:1651249 3' similar to
7426	18442	28528	2.95	0.0E+00	11560151	NT	Homo sapiens cDNA clone IMAGE:1651249 3' similar to
7429	18442	28529	2.95	0.0E+00	11560151	NT	Homo sapiens cDNA clone IMAGE:1651249 3' similar to
7431	18444	28532	8.86	0.0E+00	AF200093.1	EST_HUMAN	Homo sapiens cDNA clone IMAGE:1651249 3' similar to
7431	18444	28533	8.86	0.0E+00	AF200093.1	EST_HUMAN	Homo sapiens cDNA clone IMAGE:1651249 3' similar to
7432	18445	28534	1.89	0.0E+00	AF193035.1	EST_HUMAN	Homo sapiens cDNA clone IMAGE:1651249 3' similar to
7433	17250	27464	3.92	0.0E+00	AF103495.1	EST_HUMAN	Homo sapiens cDNA clone IMAGE:1651249 3' similar to
7434	17321	27529	4.9	0.0E+00	BE238625.1	EST_HUMAN	Homo sapiens cDNA clone IMAGE:1651249 3' similar to
7435	17323	27530	1.37	0.0E+00	BE781382.1	EST_HUMAN	Homo sapiens cDNA clone IMAGE:1651249 3' similar to
7436	17323	27530	1.37	0.0E+00	BE781382.1	EST_HUMAN	Homo sapiens cDNA clone IMAGE:1651249 3' similar to
7437	17324	27531	7.21	0.0E+00	AF165776.1	EST_HUMAN	Homo sapiens cDNA clone IMAGE:1651249 3' similar to
7438	17353	27541	2.85	0.0E+00	BE263191.1	EST_HUMAN	Homo sapiens cDNA clone IMAGE:1651249 3' similar to
7439	17353	27562	3.98	0.0E+00	CO8158.1	EST_HUMAN	Homo sapiens cDNA clone IMAGE:1651249 3' similar to
7440	17353	27563	3.98	0.0E+00	CO8158.1	EST_HUMAN	Homo sapiens cDNA clone IMAGE:1651249 3' similar to
7441	17353	27566	3.22	0.0E+00	BE746215.1	EST_HUMAN	Homo sapiens cDNA clone IMAGE:1651249 3' similar to
7442	17353	27566	3.22	0.0E+00	BE746215.1	EST_HUMAN	Homo sapiens cDNA clone IMAGE:1651249 3' similar to
7443	17353	27574	1.93	0.0E+00	11437282	NT	Homo sapiens cDNA clone IMAGE:1651249 3' similar to
7444	17353	27575	1.93	0.0E+00	11437282	NT	Homo sapiens cDNA clone IMAGE:1651249 3' similar to

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Max Similar (Top Hit) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7469	17369	27576	1.53	0.0E+00	11437282	NT	Homo sapiens solute carrier family 21 (organic anion transporter), member 9 (SLC21A9), mRNA
7514	17302	27568	1.47	0.0E+00	BE000549.1	EST_HUMAN	6016734/25/1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958233 5'
7530	17381	27591	2.59	0.0E+00	AF010094.1	NT	Homo sapiens keratin 2a (KRT2E) gene, complete cds
7530	17381	27592	2.56	0.0E+00	AF010094.1	NT	Homo sapiens keratin 2a (KRT2E) gene, complete cds
7548	17369	27612	1.47	0.0E+00	BE002377.1	EST_HUMAN	RC2-8710642-130003/1/1/01 BT0842 Homo sapiens cDNA
7559	17410	27626	1.78	0.0E+00	AW500283.1	EST_HUMAN	UHF-E80-493-b-120-U/1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078943 5'
7559	17410	27627	1.78	0.0E+00	AW500283.1	EST_HUMAN	UHF-E80-493-b-120-U/1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078943 5'
7563	17414	27620	1.25	0.0E+00	AF028008.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and tyrosinogen gene families
7563	17414	27630	1.25	0.0E+00	AF028008.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and tyrosinogen gene families
7580	17431	27548	2.45	0.0E+00	AF050826.1	EST_HUMAN	UHF-E80-493-c-07-U/1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077854 5'
7607	17458	27673	1.34	0.0E+00	AF069888.1	NT	Multiple sclerosis associated retinotic polyprotein (p5) mRNA, partial cds
7621	17472	27591	2.86	0.0E+00	ST76466.1	NT	ADP-adenosine-induced growth factor ALGF (human, placenta, GenomichRNA, 468 nt, segment 5 of 5)
7621	17472	27692	2.46	0.0E+00	ST76466.1	NT	ADP-adenosine-induced growth factor ALGF (human, placenta, GenomichRNA, 468 nt, segment 5 of 5)
7622	17473	27693	2.87	0.0E+00	BE053320.1	EST_HUMAN	6013348/69/1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3689850 5'
7630	17481	27701	1.82	0.0E+00	AW363158.1	EST_HUMAN	CH2-C10311-307169-043-M1 C10311 Homo sapiens cDNA
7630	17500	27722	2.17	0.0E+00	AU132349.1	EST_HUMAN	AU132348 NT2RP3 Homo sapiens cDNA clone NT2RP3004280 5'
7630	17500	27723	2.17	0.0E+00	AU132349.1	EST_HUMAN	AU132348 NT2RP3 Homo sapiens cDNA clone NT2RP3004280 5'
7638	17504	27734	7.73	0.0E+00	BE70460.1	EST_HUMAN	6015666/68/1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3949333 5'
7658	17509	27735	7.73	0.0E+00	BE70460.1	EST_HUMAN	6015666/68/1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3949333 5'
7668	17516	27743	1.76	0.0E+00	7662067	NT	Homo sapiens KIA00345 gene product (KIA00345), mRNA
7682	17532	27766	2.22	0.0E+00	AU132349.1	EST_HUMAN	AU132346 NT2RP3 Homo sapiens cDNA clone NT2RP3004280 5'
7683	17533	27757	1.89	0.0E+00	AF162308.1	NT	Homo sapiens protocadherin alpha 12 (PCDH-alpha12), mRNA, complete cds
7701	17551	27776	2.72	0.0E+00	AF066220.1	NT	Homo sapiens leukocyte immunoglobulin-like receptor-1 mRNA, complete cds
7701	17551	27777	2.72	0.0E+00	AF066220.1	NT	Homo sapiens leukocyte immunoglobulin-like receptor-1 mRNA, complete cds
7708	17558	27784	1.95	0.0E+00	BF62668.1	EST_HUMAN	MF4-TN0114-110900-101-s04 TN0114 Homo sapiens cDNA
7720	17570	27796	2.44	0.0E+00	BE280763.1	EST_HUMAN	6011552/27/1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138768 5'
7728	17578	27800	1.74	0.0E+00	AW286386.1	EST_HUMAN	wf2801.141 NG2 CGAP_CML1 Homo sapiens cDNA clone IMAGE:266997 3' similar to gb-X02162_cdf1.1
7735	17586	27810	1.91	0.0E+00	11427235	NT	LACTATE DEHYDROGENASE M CHAN (HUMAN)
7733	17603	27826	5.98	0.0E+00	AU134573.1	EST_HUMAN	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
7733	17603	27826	5.98	0.0E+00	AU134573.1	EST_HUMAN	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA

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Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8106	18054	28304	3.45	0.0E+00/AW59333.1	EST_HUMAN	h913402.x1 Source, NFI_T, GBC, S1 Homo sapiens cDNA clone IMAGE:2945475 3' similar to contains element MSRT1 repetitive element.	
8166	18054	28305	3.45	0.0E+00/AW59333.1	EST_HUMAN	h913402.x1 Source, NFI_T, GBC, S1 Homo sapiens cDNA clone IMAGE:2945475 3' similar to contains element MSRT1 repetitive element.	
8166	18054	28306	3.45	0.0E+00/AW59333.1	EST_HUMAN	h913402.x1 Source, NFI_T, GBC, S1 Homo sapiens cDNA clone IMAGE:2945475 3' similar to contains element MSRT1 repetitive element.	
8169	18057	28309	1.82	0.0E+00/Z34897.1	NT	H.sapiens mRNA for H1T1 Nidamrin receptor	
8176	18064	28313	2.8	0.0E+00/F13086.1	EST_HUMAN	H.sapiens mRNA for H1T1 Nidamrin receptor	
8176	18064	28313	2.12	0.0E+00/D10083.1	NT	Homo sapiens RGH1 gene, respiratory-like element	
8161	18077	28328	2.92	0.0E+00/AW33504.1	EST_HUMAN	h96901.x1 NCI CGAP, Pmt Homo sapiens cDNA clone IMAGE:2932983 3' similar to gb-X17115 G.MU	
8162	18078	28329	5.84	0.0E+00/AW45230.1	EST_HUMAN	U1H818.1b-01-01-01-01 NCI CGAP, S1b5 Homo sapiens cDNA clone IMAGE:2775549 3'	
8162	18078	28330	5.84	0.0E+00/AW45230.1	EST_HUMAN	U1H818.1b-01-01-01-01 NCI CGAP, S1b5 Homo sapiens cDNA clone IMAGE:2775549 3'	
8164	18079	28332	14.21	0.0E+00/460933.2	NT	Homo sapiens Ribosomal protein L31 (RPL31) mRNA	
8169	18081	28332	2.03	0.0E+00/AJ01497.1	NT	Homo sapiens mRNA for KIA0057 protein, paraf cells	
8208	18092	28346	2.36	0.0E+00/BE25849.1	EST_HUMAN	h9110248.F1 NHI, MGC, 17 Homo sapiens cDNA clone IMAGE:3029219 5'	
8224	18106	28365	1.86	0.0E+00/AJ011117.1	NT	Homo sapiens mRNA for KIA00545 protein, paraf cells	
8227	18108	28363	59.52	0.0E+00/Z20355.1	NT	Homo sapiens cDNA for cardiac alpha-myosin heavy chain gene	
8240	18120	28371	3.47	0.0E+00/BE702155.1	EST_HUMAN	h91182032.F1 NHI, MGC, 40 Homo sapiens cDNA clone IMAGE:3955539 5'	
8241	18121	28371	25.37	0.0E+00/BE704051.1	EST_HUMAN	h91182032.F1 NHI, MGC, 40 Homo sapiens cDNA clone IMAGE:3955539 5'	
8244	18124	28374	0.10	0.0E+00/AJ18383.1	EST_HUMAN	AJ118388 HEMBA1 Homo sapiens cDNA clone HEMBA1003480 5'	
8245	18125	28374	2.72	0.0E+00/AW23626.1	EST_HUMAN	h912801.x1 NCI CGAP, CMT1 Homo sapiens cDNA clone IMAGE:2969977 3' similar to gb-X02152_cds1 L	
8250	18130	28375	0.77	0.0E+00/AJ14680.1	EST_HUMAN	LACTATE DEHYDROGENASE M CHAIN (HUMAN);	
8250	18130	28379	0.77	0.0E+00/AJ14680.1	EST_HUMAN	h914303.x1 Source, testis, NHT Homo sapiens cDNA clone IMAGE:1752772 3'	
8251	18131	28380	3.05	0.0E+00/AJ391097.1	EST_HUMAN	h914303.x1 Source, testis, NHT Homo sapiens cDNA clone IMAGE:1752772 3'	
8252	18142	28380	4.62	0.0E+00/AJ14680.1	EST_HUMAN	h914303.x1 Source, testis, NHT Homo sapiens cDNA clone IMAGE:1752772 3'	
8253	18143	28386	-18.03	0.0E+00/1142879	NT	AJ118388 HEMBA1 Homo sapiens cDNA clone HEMBA1003480 5'	
8271	18151	28392	1.78	0.0E+00/AW804516.1	EST_HUMAN	Homo sapiens insulin receptor (INSR), mRNA	
8271	18151	28393	1.78	0.0E+00/AW804516.1	EST_HUMAN	CYU-UM00093-170400-191-408 UM0093 Homo sapiens cDNA	
8272	18152	28394	2.14	0.0E+00/BF340308.1	EST_HUMAN	CYU-UM00093-170400-191-408 UM0093 Homo sapiens cDNA	
8273	18153	28399	49.5	0.0E+00/BE281208.1	EST_HUMAN	h902307014.F1 NCI, CGAP, Bme4 Homo sapiens cDNA clone IMAGE:4184975 5'	
8282	18161	28403	2.83	0.0E+00/UM9326.1	NT	Homo protein kinase C substrate BOK-H (PRKCSH) gene, exon 15-17	
8283	18162	28404	68.7	0.0E+00/Z20355.1	NT	Homo sapiens of cardiac alpha-myosin heavy chain gene	

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Probe SEQ ID NO.	Even SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Htt BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Description
8287	18166	28400	3.32	0.0E+00	BE773036.1	EST_HUMAN	RC4-H1034-170700-012-60 FT1034 Homo sapiens cDNA
8287	18166	28410	3.32	0.0E+00	BE773036.1	EST_HUMAN	RC4-H1034-170700-012-60 FT1034 Homo sapiens cDNA
8304	18164	28431	24.35	0.0E+00	AA740782.1	EST_HUMAN	RC4-H1034-170700-012-60 FT1034 Homo sapiens cDNA
8313	18190	28439	3.12	0.0E+00	AF125203.1	NT	Human spleen signaling lymphocyte activation molecule (SLAM) gene, exon 2
8326	18240	28459	148.95	0.0E+00	Q59509.1	EST_HUMAN	Q59509 Human heart cDNA (Yukamamura) Homo sapiens cDNA clone 3NH4-0417
8333	18210	28460	2.17	0.0E+00	AA740375.1	EST_HUMAN	cd36901.1 NC1 CGAP CGBT Homo sapiens cDNA clone IMAGE:1306009 5'
8333	18210	28461	2.17	0.0E+00	AA740375.1	EST_HUMAN	cd36901.1 NC1 CGAP CGBT Homo sapiens cDNA clone IMAGE:1306009 5'
8341	18218	28470	2.41	0.0E+00	MF78448.1	EST_HUMAN	EST00569 Fetal brain, Striatum (cat#63826) Homo sapiens cDNA clone HBC038
8341	18218	28471	2.41	0.0E+00	MF78448.1	EST_HUMAN	EST00569 Fetal brain, Striatum (cat#63826) Homo sapiens cDNA clone HBC038
8344	18221	28472	1.82	0.0E+00	BF133625.1	EST_HUMAN	QV24-H1026-020800-005-407 HT0698 Homo sapiens cDNA
8344	18222	28473	8.08	0.0E+00	AF137698.1	EST_HUMAN	QV24-H1026-020800-005-407 HT0698 Homo sapiens cDNA
8357	18243	28482	10.33	0.0E+00	AF101698.1	EST_HUMAN	DKFZP761216.1 T81 (synonym: hamp2) Homo sapiens cDNA clone DKFZP761216.1 5'
8375	18262	28493	1.80	0.0E+00	BF130953.1	EST_HUMAN	U3-NT10104-200500-010-407 NT10104 Homo sapiens cDNA
8395	18271	28523	3.78	0.0E+00	BE123390.1	EST_HUMAN	U3-NT10104-200500-010-407 NT10104 Homo sapiens cDNA
8395	18271	28524	3.78	0.0E+00	BE123390.1	EST_HUMAN	U3-NT10104-200500-010-407 NT10104 Homo sapiens cDNA
8405	18285	28539	3.40	0.0E+00	BE068423.1	EST_HUMAN	FM10-HT0645-000500-002-E05 HT0645 Homo sapiens cDNA
8410	18293	28540	1.74	0.0E+00	AA153007.1	EST_HUMAN	801439052F.1 NIH MGCC 72 Homo sapiens cDNA
8410	18293	28540	1.74	0.0E+00	AA153007.1	EST_HUMAN	801439052F.1 NIH MGCC 72 Homo sapiens cDNA clone IMAGE:3924142 5'
8442	18316	28574	4	0.0E+00	BE087933.1	EST_HUMAN	U1HF-BNO-409-4-02-DU-1T NIH MGCC 50 Homo sapiens cDNA clone IMAGE:3077616 5'
8442	18316	28574	4	0.0E+00	BE087933.1	EST_HUMAN	U1HF-BNO-409-4-02-DU-1T NIH MGCC 50 Homo sapiens cDNA clone IMAGE:3077616 5'
8443	18317	28575	1.98	0.0E+00	AA459545.1	EST_HUMAN	cd69011.1 Schiller meningioma Homo sapiens cDNA clone IMAGE:3628404 3'
8443	18317	28576	1.98	0.0E+00	AA459545.1	EST_HUMAN	cd69011.1 Schiller meningioma Homo sapiens cDNA clone IMAGE:3628404 3'
8455	18326	28587	88.73	0.0E+00	F00884.1	EST_HUMAN	HSB7YE122 STRATAGENE Human skeletal muscle cDNA library, cat. #638215, Homo sapiens cDNA clone
8455	18326	28588	88.73	0.0E+00	F00884.1	EST_HUMAN	HSB7YE122 STRATAGENE Human skeletal muscle cDNA library, cat. #638215, Homo sapiens cDNA clone
8460	18334	28613	3.98	0.0E+00	4T59827.1	NT	Homo sapiens neuraxial III (NRX3) mRNA
8461	18354	28615	4.54	0.0E+00	BF240491.1	EST_HUMAN	601076049F.1 NIH MGCC 19 Homo sapiens cDNA clone IMAGE:4101433 5'
8463	18356	28620	16	0.0E+00	AA120774.1	EST_HUMAN	U1H-B2-209-1-01-DU-1T NIH MGCC 50 Homo sapiens cDNA clone IMAGE:274312 3'
8464	18357	28621	3.77	0.0E+00	AF1064975.1	EST_HUMAN	RCO-GT0380-210100-038-010 GT0380 Homo sapiens cDNA
8464	18357	28622	3.77	0.0E+00	AF1064975.1	EST_HUMAN	RCO-GT0380-210100-038-010 GT0380 Homo sapiens cDNA
8465	18351	28626	6.91	0.0E+00	AB012860.1	NT	Homo sapiens mRNA for KIA00717 protein, partial cds
8465	18351	28626	6.91	0.0E+00	AB012860.1	NT	Homo sapiens mRNA for KIA00717 protein, partial cds

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar Top Hit E-Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8490	18393	28628	2.59	0.0E+00	BE208946.1	EST_HUMAN	b604d07.yt NIH_MGC. 7 Homo sapiens cDNA clone IMAGE:2823373 5' similar to TR:078022 078022 E1B-59K0A-ASSOCIATED PROTEIN ;
8490	18393	28629	2.59	0.0E+00	BE208946.1	EST_HUMAN	b604d07.yt NIH_MGC. 7 Homo sapiens cDNA clone IMAGE:2823373 5' similar to TR:078022 078022 E1B-59K0A-ASSOCIATED PROTEIN ;
8511	18399	28649	2.85	0.0E+00	11024711	NT	59K0A-ASSOCIATED PROTEIN ;
8514	18399	28651	2.01	0.0E+00	BF059357.1	EST_HUMAN	Homo sapiens myelin, heavy polysialide 4, skeletal muscle (MYH4), mRNA
8518	18399	28653	2.9	0.0E+00	BE148076.1	EST_HUMAN	QV01M0091.120900-385-b12 UM0091 Homo sapiens cDNA
8518	18399	28654	2.9	0.0E+00	BE148076.1	EST_HUMAN	RC3-H10230-040500-110-N04 HT0230 Homo sapiens cDNA
8529	18398	28665	6.47	0.0E+00	AA105906.1	EST_HUMAN	RC3-H10230-040500-110-N04 HT0230 Homo sapiens cDNA
8546	18418	28687	4.47	0.0E+00	BF007975.1	EST_HUMAN	295911.11 Skeletal muscle 937209 Homo sapiens cDNA clone IMAGE:427833 5' similar to gb:203740
8546	18418	28688	4.47	0.0E+00	BF007975.1	EST_HUMAN	MYO5IN HEAVY CHAIN, SKELETAL MUSCLE (HUMAN);
8553	18423	28692	2.16	0.0E+00	KU133170.1	EST_HUMAN	U1H-B14-9kb-b2-10-UL1 NCL CGAP. S108 Homo sapiens cDNA clone IMAGE:3085028 3'
8557	18427	28696	5.62	0.0E+00	BE172401.1	EST_HUMAN	U1H-B14-9kb-b2-10-UL1 NCL CGAP. S108 Homo sapiens cDNA clone IMAGE:3085028 3'
8557	18427	28697	5.62	0.0E+00	BE172401.1	EST_HUMAN	U1H-B14-9kb-b2-10-UL1 NCL CGAP. S108 Homo sapiens cDNA clone IMAGE:3085028 3'
8566	18435	28713	10.32	0.0E+00	BE240361.1	EST_HUMAN	U1H-B14-9kb-b2-10-UL1 NCL CGAP. S108 Homo sapiens cDNA clone IMAGE:3085028 3'
8577	18445	28714	3.05	0.0E+00	BE037737.1	NT	U1H-B14-9kb-b2-10-UL1 NCL CGAP. S108 Homo sapiens cDNA clone IMAGE:3085028 3'
8581	18449	28716	3.49	0.0E+00	11430898	NT	U1H-B14-9kb-b2-10-UL1 NCL CGAP. S108 Homo sapiens cDNA clone IMAGE:3085028 3'
8595	18463	28734	6.1	0.0E+00	4503544	NT	U1H-B14-9kb-b2-10-UL1 NCL CGAP. S108 Homo sapiens cDNA clone IMAGE:3085028 3'
8603	18470	28741	2.49	0.0E+00	BF076257.1	EST_HUMAN	U1H-B14-9kb-b2-10-UL1 NCL CGAP. S108 Homo sapiens cDNA clone IMAGE:3085028 3'
8605	18472	28744	5.44	0.0E+00	AA132873.1	EST_HUMAN	U1H-B14-9kb-b2-10-UL1 NCL CGAP. S108 Homo sapiens cDNA clone IMAGE:3085028 3'
8608	18475		120.95	0.0E+00	AA50983.1	NT	U1H-B14-9kb-b2-10-UL1 NCL CGAP. S108 Homo sapiens cDNA clone IMAGE:3085028 3'
8612	18479	28750	3.16	0.0E+00	AA600068.1	EST_HUMAN	U1H-B14-9kb-b2-10-UL1 NCL CGAP. S108 Homo sapiens cDNA clone IMAGE:3085028 3'
8614	18481	28752	3.94	0.0E+00	BF009956.1	EST_HUMAN	U1H-B14-9kb-b2-10-UL1 NCL CGAP. S108 Homo sapiens cDNA clone IMAGE:3085028 3'
8614	18481	28753	3.94	0.0E+00	BF009956.1	EST_HUMAN	U1H-B14-9kb-b2-10-UL1 NCL CGAP. S108 Homo sapiens cDNA clone IMAGE:3085028 3'
8620	18488	28758	20.88	0.0E+00	BF034022.1	EST_HUMAN	U1H-B14-9kb-b2-10-UL1 NCL CGAP. S108 Homo sapiens cDNA clone IMAGE:3085028 3'
8639	18504		4.07	0.0E+00	BE087051.1	EST_HUMAN	U1H-B14-9kb-b2-10-UL1 NCL CGAP. S108 Homo sapiens cDNA clone IMAGE:3085028 3'
8648	18512	28793	2.85	0.0E+00	86228698	NT	U1H-B14-9kb-b2-10-UL1 NCL CGAP. S108 Homo sapiens cDNA clone IMAGE:3085028 3'
8650	18514		2.24	0.0E+00	BF127062.1	EST_HUMAN	U1H-B14-9kb-b2-10-UL1 NCL CGAP. S108 Homo sapiens cDNA clone IMAGE:3085028 3'
8661	18550	28833	4.01	0.0E+00	BE208946.1	EST_HUMAN	U1H-B14-9kb-b2-10-UL1 NCL CGAP. S108 Homo sapiens cDNA clone IMAGE:3085028 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top Hit BLAST E Value)	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8661	18550	28834	4.51	0.0E+00	BE006948.1	EST_HUMAN	hs04007.v1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2803373 5' similar to TR-076022 076022 E1B
8663	18552	28836	3	0.0E+00	AW750028.1	EST_HUMAN	58KDA-ASSOCIATED PROTEIN;1
8668	18557		2.36	0.0E+00	AA588707.1	EST_HUMAN	h42c08.x1 NCI CGAP P41 Homo sapiens cDNA clone IMAGE:1046342 similar to gh-MG5178 ALPHA-
8669	15148	24615	5	0.0E+00	AA349554.1	EST_HUMAN	ACTININ.1, CYTOSKELETAL ISOFORM (HUMAN)
8670	18559	28942	7.41	0.0E+00	AW327865.1	EST_HUMAN	h42c08.x1 NCI CGAP P41 Homo sapiens cDNA clone IMAGE:246084 3'
8700	18519	28900	4.73	0.0E+00	BE06955.1	EST_HUMAN	w05908.x1 NIH_MGC_3 Homo sapiens cDNA clone IMAGE:246084 3'
8712	18520	28812	4.74	0.0E+00	AL046540.1	EST_HUMAN	ILK-HTO731-020600-077-466 HTO731 Homo sapiens cDNA
8712	18520	28813	4.74	0.0E+00	AL046540.1	EST_HUMAN	DKFZ4843178.t1.84 (apocynin, hsa3) Homo sapiens cDNA clone IMAGE:246084 3'
8722	18539	28823	12.53	0.0E+00	AA023116.1	EST_HUMAN	w05908.x1 NCI CGAP P41 Homo sapiens cDNA clone IMAGE:246084 3' similar to gh-S37451 LAMININ
8724	18550	28893	4.18	0.0E+00	AA750033.1	EST_HUMAN	h42c08.x1 NCI CGAP P41 Homo sapiens cDNA clone IMAGE:1287468 3' similar to TRQ13986
8724	18550	28894	4.18	0.0E+00	AA750033.1	EST_HUMAN	Q13986 ALB8 HOMOLOG PROTEIN;1
8726	18564	28980	2.33	0.0E+00	BE070546.1	EST_HUMAN	Q13986 ALB8 HOMOLOG PROTEIN;1
8737	17898	28130	5.67	0.0E+00	BE076347.1	EST_HUMAN	h42c08.x1 NCI CGAP P41 Homo sapiens cDNA clone IMAGE:3595919 3' similar to TR-000409 000409
8772	18559	28976	2.78	0.0E+00	U36991.1	NT	CHECKPOINT SUPPRESSOR 1;1
8772	18559	28976	2.78	0.0E+00	U36991.1	NT	Homo sapiens polyoma kidney disease-associated protein (PKD1) gene, complete cds
8774	18560	28978	4.02	0.0E+00	AA136211.1	EST_HUMAN	Homo sapiens polyoma kidney disease-associated protein (PKD1) gene, complete cds
8797	18911	28902	1.91	0.0E+00	AA136211.1	EST_HUMAN	h42c08.x1 NCI CGAP P41 Homo sapiens cDNA clone IMAGE:3595919 3' similar to TR-000409 000409
8827	18940	28924	10.47	0.0E+00	BE022317.1	EST_HUMAN	h42c08.x1 NCI CGAP P41 Homo sapiens cDNA clone IMAGE:3595919 3' similar to TR-000409 000409
8837	18950	28925	10.47	0.0E+00	BE022317.1	EST_HUMAN	h42c08.x1 NCI CGAP P41 Homo sapiens cDNA clone IMAGE:3595919 3' similar to TR-000409 000409
8837	18950	28937	2.37	0.0E+00	AA141882.1	EST_HUMAN	h42c08.x1 NCI CGAP P41 Homo sapiens cDNA clone IMAGE:3595919 3' similar to TR-000409 000409
8837	18950	28939	2.37	0.0E+00	AA141882.1	EST_HUMAN	h42c08.x1 NCI CGAP P41 Homo sapiens cDNA clone IMAGE:3595919 3' similar to TR-000409 000409
8840	18953	28941	2.35	0.0E+00	AA141882.1	EST_HUMAN	h42c08.x1 NCI CGAP P41 Homo sapiens cDNA clone IMAGE:3595919 3' similar to TR-000409 000409
8843	19474	28943	3.84	0.0E+00	BF002853.1	EST_HUMAN	h42c08.x1 NCI CGAP P41 Homo sapiens cDNA clone IMAGE:3595919 3' similar to TR-000409 000409
8861	18973	28957	3.19	0.0E+00	AA13778.1	EST_HUMAN	h42c08.x1 NCI CGAP P41 Homo sapiens cDNA clone IMAGE:3595919 3' similar to TR-000409 000409
8861	18973	28963	3.19	0.0E+00	AA13778.1	EST_HUMAN	h42c08.x1 NCI CGAP P41 Homo sapiens cDNA clone IMAGE:3595919 3' similar to TR-000409 000409
8878	18990	28982	2.57	0.0E+00	11435241	NT	Homo sapiens KIA0247 gene product (KIA0247), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8878	18900	28883	2.57	0.0E+00	11435244	NT	Homo sapiens KIA0247 gene product (KIA0247), mRNA
8883	18904	28887	5.52	0.0E+00	U36253.1	NT	Human beta-prime-adipin (BAM22) gene, exon 5
8885	18906	28890	2.04	0.0E+00	BE379254.1	EST_HUMAN	Human beta-prime-adipin (BAM22) gene, exon 5
8895	18906	28890	2.04	0.0E+00	BE379254.1	EST_HUMAN	Human beta-prime-adipin (BAM22) gene, exon 5
8896	16272	26434	63.21	0.0E+00	AA211663.1	EST_HUMAN	265022_r1 Striatum muscle 937209 Homo sapiens cDNA clone IMAGE:862203 5' similar to gb-X03740
8900	15993	26009	4.08	0.0E+00	AV150430.1	EST_HUMAN	MYOSIN HEAVY-CHAIN, SKELETAL MUSCLE (HUMAN);
8902	18710	25005	3.25	0.0E+00	BE794738.1	EST_HUMAN	UHP-ENO-ams-c1-0111 NH1.MGC 50 Homo sapiens cDNA clone IMAGE:3091217 5'
8903	18711	25006	37.53	0.0E+00	BE794738.1	EST_HUMAN	UHP-ENO-ams-c1-0111 NH1.MGC 50 Homo sapiens cDNA clone IMAGE:3091217 5'
8904	18712	25007	2.63	0.0E+00	M65676.1	NT	Human von Willebrand factor pseudogene corresponding to bases 23 through 34
8915	18723	25014	6.35	0.0E+00	BE400963.1	EST_HUMAN	901269403F1 NH1.MGC 21 Homo sapiens cDNA clone IMAGE:352864 5'
8916	18724	25015	1.93	0.0E+00	11427346	NT	Homo sapiens protein kinase, AUP-activated, alpha 2 catalytic subunit (PRKAA2), mRNA
8916	18724	25015	1.93	0.0E+00	11427346	NT	Homo sapiens protein kinase, AUP-activated, alpha 2 catalytic subunit (PRKAA2), mRNA
8916	18724	25017	1.93	0.0E+00	11427346	NT	Homo sapiens protein kinase, AUP-activated, alpha 2 catalytic subunit (PRKAA2), mRNA
8917	18725	25018	2.32	0.0E+00	AF23391.1	NT	Homo sapiens calcium channel, epsilon1E subunit (CACNA1E) gene, exons 74b, and partial cdb, alternatively spliced
8917	18725	25019	2.32	0.0E+00	AF23391.1	NT	Homo sapiens calcium channel, epsilon1E subunit (CACNA1E) gene, exons 74b, and partial cdb, alternatively spliced
8918	18727	25020	5.66	0.0E+00	BF568141.1	EST_HUMAN	902157122F1 NH1.MGC 83 Homo sapiens cDNA clone IMAGE:3266726 5'
8919	18727	25021	5.90	0.0E+00	BF568141.1	EST_HUMAN	902157122F1 NH1.MGC 83 Homo sapiens cDNA clone IMAGE:3266726 5'
8924	18732	25026	3.22	0.0E+00	BF563372.1	EST_HUMAN	901676305F1 NH1.MGC 21 Homo sapiens cDNA clone IMAGE:358809 5'
8933	18741	25034	8.18	0.0E+00	BF312562.1	EST_HUMAN	901697504F1 NH1.MGC 10 Homo sapiens cDNA clone IMAGE:4127069 5'
8933	18741	25035	8.18	0.0E+00	BF312562.1	EST_HUMAN	901697504F1 NH1.MGC 10 Homo sapiens cDNA clone IMAGE:4127069 5'
8944	18742	25036	3.02	0.0E+00	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
8944	18742	25037	3.02	0.0E+00	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
8944	18742	25037	3.02	0.0E+00	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
8945	18745	25062	20.36	0.0E+00	BF309120.1	EST_HUMAN	901805054F1 NH1.MGC 17 Homo sapiens cDNA clone IMAGE:4131416 5'
8955	18771	28062	1.95	0.0E+00	BE698891.1	EST_HUMAN	RC4-NN0025-129000-016-307 NN0025 Homo sapiens cDNA
8955	18771	28062	1.95	0.0E+00	BE698891.1	EST_HUMAN	RC4-NN0025-129000-016-307 NN0025 Homo sapiens cDNA
8959	18776	25068	31.95	0.0E+00	BC591775.1	EST_HUMAN	901174707F1 NH1.MGC 17 Homo sapiens cDNA clone IMAGE:3532568 5'
8961	18786	25076	35.47	0.0E+00	7695065	NT	Homo sapiens myosin, heavy polypeptide 1, skeletal muscle, adult (MYH1), mRNA
8961	18786	25077	35.47	0.0E+00	7695065	NT	Homo sapiens myosin, heavy polypeptide 1, skeletal muscle, adult (MYH1), mRNA
8962	18787	25078	34.26	0.0E+00	11024711	NT	Homo sapiens myosin, heavy polypeptide 4, skeletal muscle (MYH4), mRNA
8987	18792	25081	31.32	0.0E+00	F03884.1	EST_HUMAN	HSB7/E122 STRATAGENE Human skeletal muscle cDNA library, cat. 8636215, Homo sapiens cDNA clone 77E12

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6887	18792	25082	31.52	0.0E+00	P00834.1	EST_HUMAN	H887E12 STRATAGENE Human skeletal muscle cDNA library, cat. #88215. Homo sapiens cDNA clone 77E12
9000	18903	25093	7.35	0.0E+00	U84744.1	NT	Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete cds
9002	18905	20068	92.6	0.0E+00	Z20856.1	NT	Homo sapiens of cardiac embryonic heavy chain gene
9017	19177	24863	2.54	0.0E+00	E312542.1	EST_HUMAN	60119023F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3503020 5'
9031	18594		2.87	0.0E+00	AL193266.2	NT	Homo sapiens chromosome 21 segment H521C048
9033	18605		3.43	0.0E+00	A109293.1	EST_HUMAN	gel7012.1 Soares. fetal lung, NH4-139 Homo sapiens cDNA clone IMAGE:179231 3'
9043	18629		2.24	0.0E+00	A8011599.1	NT	Homo sapiens gene for F-45 complex cys
9062	18943		2.2	0.0E+00	AL163346.2	NT	Homo sapiens chromosome 21 segment H521C048
9071	18948		2.73	0.0E+00	A1117663	NT	Homo sapiens calcitonin binding protein 1 (CBP1), nuclear gene encoding mitochondrial protein, mRNA
9090	18964		5.48	0.0E+00	5802373	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2), nuclear gene encoding mitochondrial protein, mRNA
9123	18963	25068	1.63	0.0E+00	AF240786.1	NT	Genes, complete cds
9133	18971		2.82	0.0E+00	AL01931.1	EST_HUMAN	DN72434-0319 J1 434 (synonym: hscs) Homo sapiens cDNA clone DKFZ:254940818 5'
9159	18971		3.07	0.0E+00	11416319	NT	Homo sapiens G-2 and S-phase expressed 1 (G1SET), mRNA
9187	18910		4.38	0.0E+00	AL046844.1	EST_HUMAN	DN72434-0210 J1 634 (synonym: hscs) Homo sapiens cDNA clone DKFZ:254940818 5'
9190	18910		2.36	0.0E+00	A803487.1	EST_HUMAN	LS1100-271068-001 B1030 Homo sapiens cDNA
9218	19732		1.3	0.0E+00	N64484.1	EST_HUMAN	Y40608.61 Soares fetal liver spleen TNP15 Homo sapiens cDNA clone IMAGE:245222 3' similar to SW-FOL_BAEVM P10272 POL POLYPROTEIN
9233	18922		3.38	0.0E+00	AF106931.1	NT	Homo sapiens adenovocutaneous lymphoma gene, complete cds
9238	10752	20091	3.21	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TAM1) mRNA
9238	10752	20092	3.21	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TAM1) mRNA
9248	19612		2.75	0.0E+00	10092587	NT	Homo sapiens nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2 (NFATC2), mRNA
9276	10477		2.7	0.0E+00	AF003328.1	NT	Homo sapiens Minked antihidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
9309	19412	25183	2.48	0.0E+00	11430480	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
9370	19544	25064	3.23	0.0E+00	AW50082.1	EST_HUMAN	hg3106.x1 NCI_GCAP_G08 Homo sapiens cDNA clone IMAGE:2847234 3' similar to contains Alu repetitive element/contains element MER22 repetitive element;
9382	18956		1.61	0.0E+00	BE590210.1	EST_HUMAN	RC00407711-290300-071 L05 B7011 Homo sapiens cDNA
9426	19007		2.33	0.0E+00	AF088767.1	NT	Homo sapiens somatostatin receptor subunit 3 (SSTR3) gene, 5' flanking region and partial cds
9461	19092		1.56	0.0E+00	9635487	NT	Human endogenous retrovirus, complete genome
9486	19090		1.59	0.0E+00	A1204914.1	EST_HUMAN	ar0504.x1 StrataGene schizo brain S11 Homo sapiens cDNA clone IMAGE:1884769 3'
9529	19135		1.38	0.0E+00	A804646.1	EST_HUMAN	QV-BT065-020359-103 BT065 Homo sapiens cDNA

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CLAIMS

1. A spatially-addressable set of single exon nucleic-acid probes for measuring gene expression in a sample derived
5 from human heart comprising a plurality single exon nucleic probes, said probes comprising any one of the nucleotide sequences set out in SEQ ID NOS: 1 - 9,980 or a complementary sequence, or a portion of such a sequence.
- 10 2. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 1 wherein each of said plurality of probes is separately and addressably amplifiable.
- 15 3. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 1 wherein each of said plurality of probes is separately and addressably isolatable from said plurality.
- 20 4. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 3 wherein said probes comprise any one of the nucleotide sequences set out in SEQ ID NOS.: 9,981 - 19,771.
- 25 5. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 4, wherein each of said plurality of probes is amplifiable using at least one common primer.
- 30 6. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 5 wherein the set comprises between 50 - 20,000 single exon nucleic acid probes.
- 35 7. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 6, wherein the

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average length of the single exon nucleic acid probes is between 200 and 500 bp.

8. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 7, wherein at least 50% of said single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence.
9. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 8, wherein at least 50% of said single exon nucleic acid probes lack homopolymeric stretches of A or T.
10. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 - 9 characterised in that said set of probes is addressably disposed upon a substrate.
11. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 10 wherein said substrate is selected from glass, amorphous silicon, crystalline silicon and plastic.
12. A microarray comprising a spatially addressable set of single exon nucleic acid probes as claimed in any of claims 1 - 11.
13. A single exon nucleic acid probe for measuring human gene expression in a sample derived from human heart comprising a nucleotide sequence as set out in any of SEQ ID NOs.: 1 - 9,980 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid molecule expressed in the human heart.

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14. A single exon nucleic acid probe as claimed in claim 13 comprising a nucleotide sequence as set out in any of SEQ ID NOs.: 9,981 - 19,771 or a complementary sequence or a fragment thereof.
- 5
15. A single exon nucleic acid probe for measuring human gene expression in a sample derived from human heart which is a nucleic acid molecule having a sequence encoding a peptide comprising a peptide sequence as set out in any of
- 10 SEQ ID NOs.: 19,772 - 29,119, or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human heart.
16. A single exon nucleic acid probe as claimed in any one
- 15 of claims 13 to 15 wherein said single exon nucleic acid probe comprises between 15 and 25 contiguous nucleotides of said SEQ ID NO.
17. A single exon nucleic acid probe as claimed in any one
- 20 of claims 13 to 15, wherein said probe is between 3 - 25 kb in length.
18. A single exon nucleic acid probe as claimed in any one of claims 13 - 17, wherein said probe is DNA, RNA or PNA.
- 25
19. A single exon nucleic acid probe as claimed in any one of claims 13 - 18, wherein said probe is detectably labeled.
- 30
20. A single exon nucleic acid probe as claimed in any one of claims 13 - 19, wherein said probe lacks prokaryotic and bacteriophage vector sequence.
21. A single exon nucleic acid probe as claimed in any one
- 35 of claims 13 - 20, wherein said probe lacks homopolymeric

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stretches of A or T.

22. A method of measuring gene expression in a sample derived from human heart, comprising:

- 5 contacting the microarray of claim 12, with a first collection of detectably labeled nucleic acids, said first collection of nucleic acids derived from mRNA of human heart; and then measuring the label detectably bound to each probe of
10 said microarray.

23. A method of identifying exons in a eukaryotic genome, comprising:

- 15 algorithmically predicting at least one exon from genomic sequence of said eukaryote; and then detecting specific hybridization of detectably labeled nucleic acids to a single exon probe, wherein said detectably labeled nucleic acids are derived from mRNA from the heart of said eukaryote, said probe is a
20 single exon probe having a fragment identical in sequence to, or complementary in sequence to, said predicted exon, said probe is included within a microarray according to claim 12, and said fragment is selectively hybridizable at high stringency.

25

24. A method of assigning exons to a single gene, comprising:

- identifying a plurality of exons from genomic sequence according to the method of claim 23; and
30 then measuring the expression of each of said exons in a plurality of tissues and/or cell types using hybridization to single exon microarrays having a probe with said exon,
35 wherein a common pattern of expression of said exons in

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said plurality of tissues and/or cell types indicates that the exons should be assigned to a single gene.

25. A nucleic acid sequence as set out in any of SEQ ID
5 NOS: 1 - 19,771 which encodes a peptide.

26. A peptide encoded by a sequence as set out in any of
SEQ ID Nos: 1 - 19,771.

10 27. A peptide comprising a sequence as set out in any of
SEQ ID Nos: 19,772 - 29,119.

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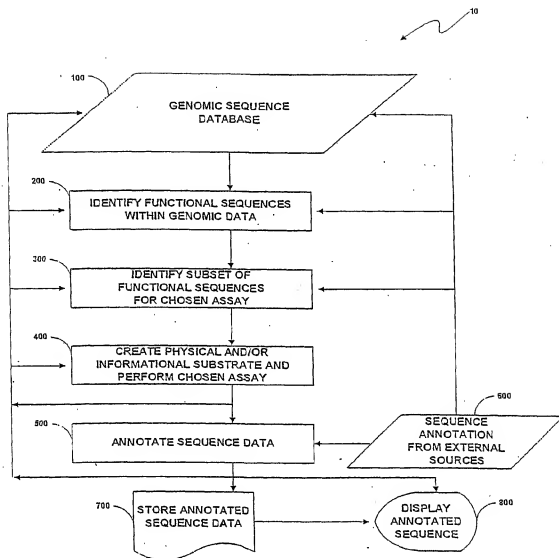


Fig. 1

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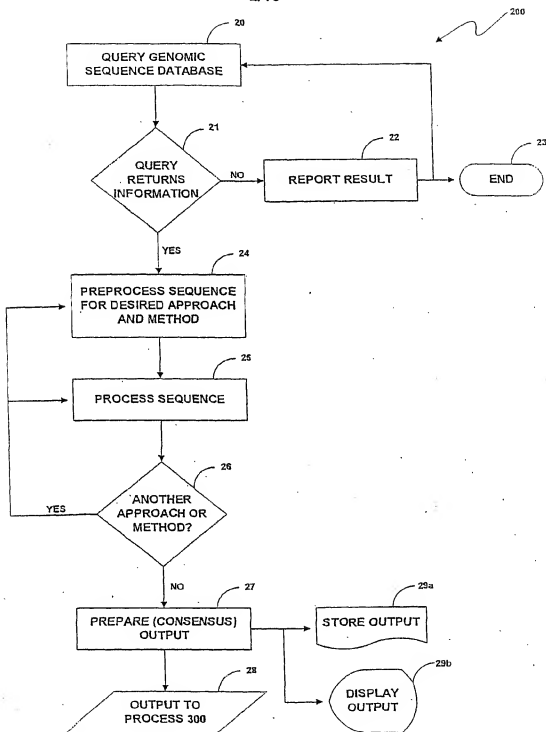


Fig. 2

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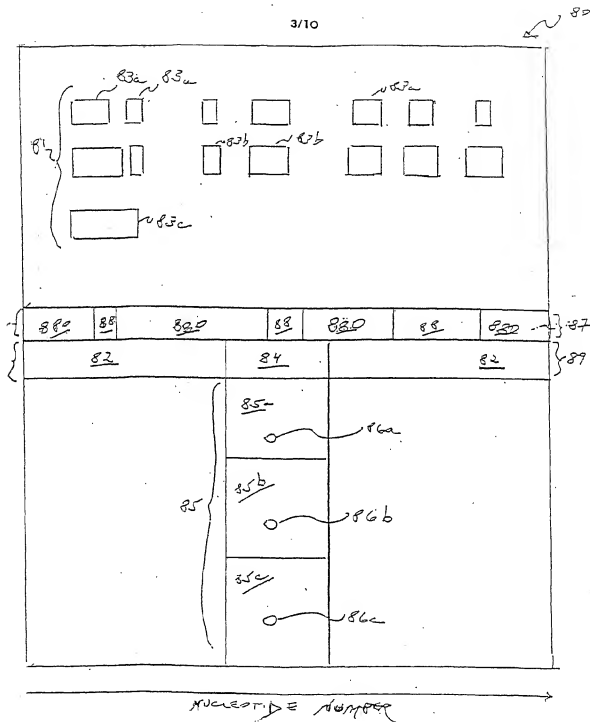


Fig. 3

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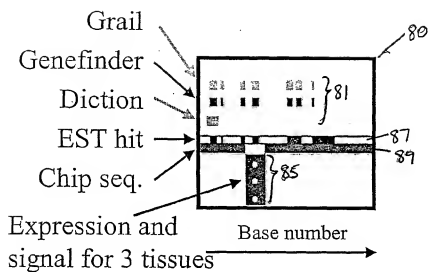


Fig. 4

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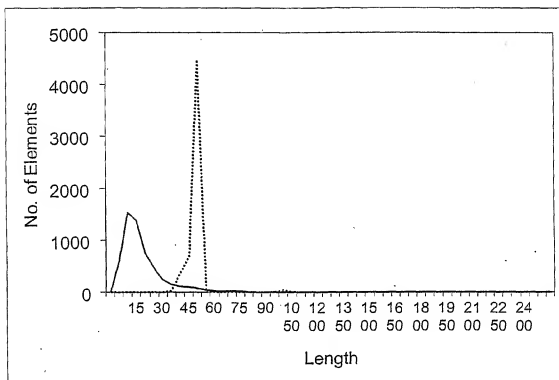


Fig. 5

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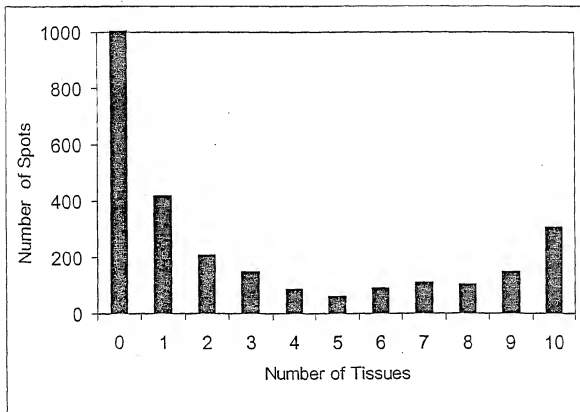


Fig. 6

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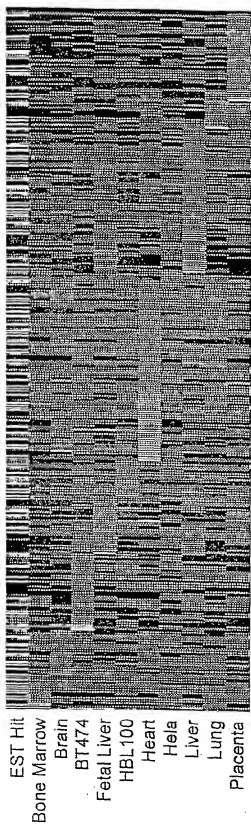


Fig. 7a

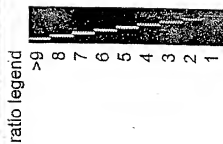


Fig. 7b

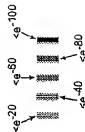


Fig. 7c

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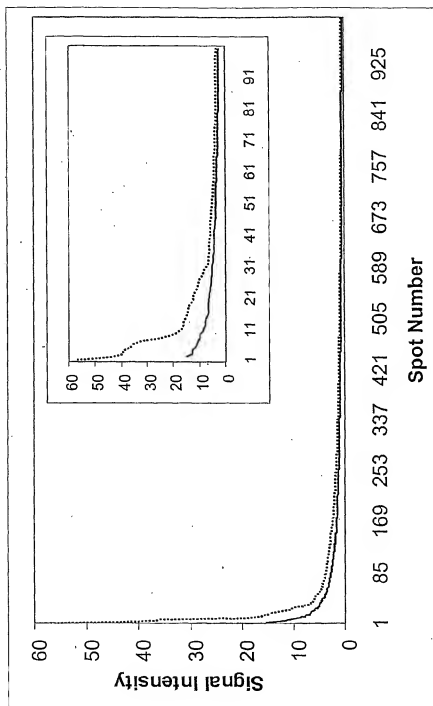


Fig. 8

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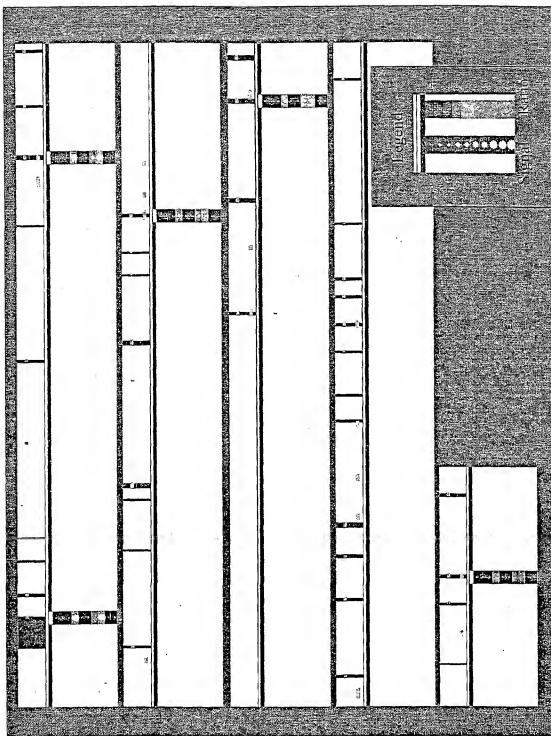


Fig. 9

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Fig. 10

